

This Page Is Inserted by IFW Operations
and is not a part of the Official Record

BEST AVAILABLE IMAGES

Defective images within this document are accurate representations of the original documents submitted by the applicant.

Defects in the images may include (but are not limited to):

- BLACK BORDERS
- TEXT CUT OFF AT TOP, BOTTOM OR SIDES
- FADED TEXT
- ILLEGIBLE TEXT
- SKEWED/SLANTED IMAGES
- COLORED PHOTOS
- BLACK OR VERY BLACK AND WHITE DARK PHOTOS
- GRAY SCALE DOCUMENTS

IMAGES ARE BEST AVAILABLE COPY.

**As rescanning documents *will not* correct images,
please do not report the images to the
Image Problem Mailbox.**

THIS PAGE BLANK (USPTO)

O'Bryen, Barbara

From: Yu, Misook
Sent: Monday, September 29, 2003 2:35 PM
To: O'Bryen, Barbara
Subject: RE: 09402713

Barb, would you please add oligo-search for DNA encoding SEQ ID NO:7 in US issued nucleic acid data base also as we discussed over the phone. Thank you.

Examiner Misook Yu, Ph.D.
703-308-2454 (Phone)
Art Unit 1642
CM1-8E18 (Room)
CM1-8E12 (Mail Box)

-----Original Message-----

Fr m: O'Bryen, Barbara
Sent: Monday, September 29, 2003 2:30 PM
T : Yu, Misook
Subject: RE: 09402713

Misook,
Results 16-45 are not saved anywhere (this is true of *all* searches). In order to get those extra results, the search has to be rerun. That will take at least 24 hours. I will contact you when the new results are ready.
Barb

-----Original Message-----

From: Yu, Misook
Sent: Monday, September 29, 2003 2:23 PM
To: O'Bryen, Barbara
Subject: RE: 09402713

Barb, would you please print out the Result NO. 16-45 of SEQ ID NOs 1, 3, 4, 6 and DNA encoding SEQ ID NO:2 from Issued Patent NA only. Review of the search result indicates 1-15 is from two patents that are not prior art. Thank you.

Examiner Misook Yu, Ph.D.
703-308-2454 (Phone)
Art Unit 1642
CM1-8E18 (Room)
CM1-8E12 (Mail Box)

-----Original Message-----

From: O'Bryen, Barbara
Sent: Monday, September 29, 2003 1:57 PM
To: Yu, Misook
Cc: Hale, Mary
Subject: RE: 09402713

Misook,
This search is finished. You can pick it up from the table outside the door to the 6th floor STIC cluster.
Barb

-----Original Message-----

From: Yu, Misook
Sent: Monday, September 29, 2003 1:45 PM
To: O'Bryen, Barbara
Subject: FW: 09402713
Importance: High

Barb, is the search result ready to be pick up?

Examiner Misook Yu, Ph.D.
703-308-2454 (Phone)
Art Unit 1642
CM1-8E18 (Room)
CM1-8E12 (Mail Box)

THIS PAGE BLANK (USPTO)

-----Original Message-----

From: Hale, Mary
Sent: Monday, September 29, 2003 1:38 PM
To: Yu, Misook
Subject: FW: 09402713
Importance: High

You search has been completed by Barb. You can call her at 308-4291

-----Original Message-----

From: STIC-Biotech/ChemLib
Sent: Monday, September 29, 2003 1:24 PM
To: Hale, Mary
Subject: FW: 09402713
Importance: High

I thought I should send this to you..Linda

-----Original Message-----

From: Yu, Misook
Sent: Monday, September 29, 2003 1:23 PM
To: STIC-Biotech/ChemLib
Subject: FW: 09402713
Importance: High

Is there any hope that I could get the search result of this case by tomorrow morning (9/30)?

Examiner Misook Yu, Ph.D.
703-308-2454 (Phone)
Art Unit 1642
CM1-8E18 (Room)
CM1-8E12 (Mail Box)

-----Original Message-----

From: Page, Thurman
Sent: Friday, September 26, 2003 9:42 AM
To: STIC-Biotech/ChemLib
Cc: Yu, Misook
Subject: FW: 09402713
Importance: High

RUSH SEARCH APPROVED

Thurman K. Page
SPE Art Units 1615 & 1616
Technology Center 1600

-----Original Message-----

From: Yu, Misook
Sent: Friday, September 26, 2003 9:40 AM
To: Page, Thurman
Subject: 09402713

Please approve rush Oligo-search for SEQ ID NOs 1, 3, 4, 6 and DNA encoding SEQ ID NO:2. It is due this biweek.

Examiner Misook Yu, Ph.D.
703-308-2454 (Phone)
Art Unit 1642
CM1-8E18 (Room)
CM1-8E12 (Mail Box)

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 26, 2003, 21:01:08 ; Search time 13035.4 Seconds
(without alignments)
11241.524 Million cell updates/sec

Title: US-09-402-713a-6

Perfect score: 3582
Sequence: 1 acagagaagaatagcaagtcg.....tgattcttggtacacttt 3582

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 2888711 seqs, 20454813386 residues

Word size : 0

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : GenEmbl:*

1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vl:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
21: em_or:*
22: em_ov:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sts:*
28: em_un:*
29: em_vl:*
30: em_htg_hum:*
31: em_htg_inv:*
32: em_htg_other:*
33: em_htg_mus:*
34: em_htg_pin:*
35: em_htg_rtd:*
36: em_htg_mam:*
37: em_htg_vrt:*
38: em_sy:*
39: em_htgo_hum:*
40: em_htgo_mus:*
41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	3582	100.0	3582	6	BD082485	BD082485 PCA3, PCA
2	3036	84.8	3923	6	AR261156	AR261156 Sequence
3	3036	84.8	3923	6	AR278697	AR278697 Sequence
4	3036	84.8	3923	6	AX200988	AX200988 Sequence
5	3036	84.8	3923	6	AX267716	AX267716 Sequence
6	3036	84.8	3923	9	AF103907	AF103907 Homo sapi
7	2570	71.7	5435	9	AF103908	AF103908 Homo sapi
8	1629	45.5	2037	6	BD082482	BD082482 PCA3, PCA
9	1367	38.2	1872	6	BD082483	BD082483 PCA3, PCA
10	1364	38.1	3112	6	AR261036	AR261036 Sequence
11	1364	38.1	3112	6	AR278557	AR278557 Sequence
12	1364	38.1	3112	6	AX106204	AX106204 Sequence
13	1364	38.1	3112	6	AX106687	AX106687 Sequence
14	1364	38.1	3112	6	AX140978	AX140978 Sequence
15	1364	38.1	3112	6	AX200838	AX200838 Sequence
16	1364	38.1	3112	6	AX267494	AX267494 Sequence
17	1357	37.9	2426	6	AR261038	AR261038 Sequence
18	1357	37.9	2426	6	AR278559	AR278559 Sequence
19	1357	37.9	2426	6	AX106206	AX106206 Sequence
20	1357	37.9	2426	6	AX106689	AX106689 Sequence
21	1357	37.9	2426	6	AX140980	AX140980 Sequence
22	1357	37.9	2426	6	AX200840	AX200840 Sequence
23	1357	37.9	2426	6	AX267496	AX267496 Sequence
24	1123	31.4	2229	6	AR261037	AR261037 Sequence
25	1123	31.4	2229	6	AR278558	AR278558 Sequence
26	1123	31.4	2229	6	AX106205	AX106205 Sequence
27	1123	31.4	2229	6	AX106688	AX106688 Sequence
28	1123	31.4	2229	6	AX140979	AX140979 Sequence
29	1123	31.4	2229	6	AX200839	AX200839 Sequence
30	1123	31.4	2229	6	AX267495	AX267495 Sequence
31	991	27.7	128480	9	AL359314	AL359314 Human DNA
32	874	24.4	129109	9	AL359239	AL359239 Human DNA
33	723	20.2	820	6	BD082484	BD082484 PCA3, PCA
34	720	20.1	812	6	AR261039	AR261039 Sequence
35	720	20.1	812	6	AR278570	AR278570 Sequence
36	720	20.1	812	6	AX106207	AX106207 Sequence
37	720	20.1	812	6	AX106690	AX106690 Sequence
38	720	20.1	812	6	AX140981	AX140981 Sequence
39	720	20.1	812	6	AX200841	AX200841 Sequence
40	720	20.1	812	6	AX267497	AX267497 Sequence
41	533	14.9	542	11	G56926	G56926 SHGC-102486
42	473	13.2	597	6	BD078456	BD078456 101 human
43	452	12.6	546	11	G56925	G56925 SHGC-102485
44	241	6.7	481	6	BD119166	BD119166 EST and e
45	233	6.5	359	6	AX018075	AX018075 Sequence

ALIGNMENTS

RESULT 1
BD082485
LOCUS
DEFINITION
PCA3, PCA3 genes, and methods of use.
ACCESSION
BD082485
VERSION
BD082485.1 GI:22628095
KEYWORDS
JP 2001522240-A/4.
SOURCE
Mastadenovirus
ORGANISM
Mastadenovirus
viruses; dsDNA viruses, no RNA stage; Adenoviridae.
REFERENCE
1 (bases 1 to 3582)
AUTHORS
Bussemakers,M.J.G.
TITLE
PCA3, PCA3 genes, and methods of use
PATENT: JP 2001522240-A 4 13-NOV-2001;
JOURNAL
DIAGNOCURE INC

COMMENT

PN JP 2001522240-A/4
PD 13-NOV-2001
PF 09-APR-1998 JP 1998542194
PR 10-APR-1997 US 60/041836
PI MARION J G. BUSEMAKERS
PC C12N15/00,C12N15/12,C12N5/12,C12N1/21,C07K14/47,C07K16/18, PC
C1201/68,
PC G01N33/577,A61K39/395,A01K67/027
CC Strandedness: Double;
CC Topology: Linear;
FH Key Location/Qualifiers
FT CDS 401..553. Location/Qualifiers

FEATURES
source 1..3582
/organism="Mastadenovirus"
/mol_type="genomic DNA"
/db_xref="taxon:10509"

BASE COUNT 1052 a 787 c 680 g 1063 t
ORIGIN

Query Match 100.0%; Score 3582; DB 6; Length 3582;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3582; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACAGAGAAATAGCAAGTGGCGAGAGCTGCATCAGAAAAACAGAGGGAGATTGTGT 60
Db 1 ACAGAGAAATAGCAAGTGGCGAGAGCTGCATCAGAAAAACAGAGGGAGATTGTGT 60

QY 61 GGCTGACGCCGAGGAGACAGAAAGATCTGCATGTTGGAGAGACCTGATACAGAG 120
Db 61 GGCTGACGCCGAGGAGACAGAAAGATCTGCATGTTGGAGAGACCTGATACAGAG 120

QY 121 GAATTACACACATATATCTTAGTGTTCATGAACACACAGATAAATAGTAAGAGCTA 180
Db 121 GAATTACACACATATATCTTAGTGTTCATGAACACACAGATAAATAGTAAGAGCTA 180

QY 181 GTCCGCTGTAGTCTCTCTCAGTACAGAGGCTGCATCAGAGGCACTTTCTAG 240
Db 181 GTCCGCTGTAGTCTCTCTCAGTACAGAGGCTGCATCAGAGGCACTTTCTAG 240

QY 181 GTCCGCTGTAGTCTCTCTCAGTACAGAGGCTGCATCAGAGGCACTTTCTAG 240
Db 181 GTCCGCTGTAGTCTCTCTCAGTACAGAGGCTGCATCAGAGGCACTTTCTAG 240

QY 241 TACTCAGTGCAGCAAGAAAGACTACAGACATCTCAATGCGAGGGGTGAGAAATAGAAA 300
Db 241 TACTCAGTGCAGCAAGAAAGACTACAGACATCTCAATGCGAGGGGTGAGAAATAGAAA 300

QY 301 GGCTGCTGACTTACCATCTGAGGCCACACATCTGTGAATGAGATATTAACATCAC 360
Db 301 GGCTGCTGACTTACCATCTGAGGCCACACATCTGTGAATGAGATATTAACATCAC 360

QY 361 TAGAAACAGCAAGATGCAATATATATGCTTAAGTAGACATGTTTTTGGACATTTCCAG 420
Db 361 TAGAAACAGCAAGATGCAATATATATGCTTAAGTAGACATGTTTTTGGACATTTCCAG 420

QY 421 CCCCTTTAAATATCCACACACAGAAAGCACAAAAGGAACACAGAGATCCCTGGAGA 480
Db 421 CCCCTTTAAATATCCACACACAGAAAGCACAAAAGGAACACAGAGATCCCTGGAGA 480

QY 481 AATGCCCGGCCCATCTTGGGTGTCATGATGAGCCTGCCCTGTGCCGTCCTGTGT 540
Db 481 AATGCCCGGCCCATCTTGGGTGTCATGATGAGCCTGCCCTGTGCCGTCCTGTGT 540

QY 541 GAGGGAAGGACATTAGAAATGATGATGCTGCTTAAAGATGGGCAAGAAAACAGA 600
Db 541 GAGGGAAGGACATTAGAAATGATGATGCTTAAAGATGGGCAAGAAAACAGA 600

QY 601 TCCGTGTGTGATATTTATTTGAACGGGATTACAGATTTGAATGAAGTCCAAAGTAG 660
Db 601 TCCGTGTGTGATATTTATTTGAACGGGATTACAGATTTGAATGAAGTCCAAAGTAG 660

QY 661 CATTTACCAATGAGGAGAAACAGACGAGAAAATCTTGAATGCTTACAAAGCATGCA 720
Db 661 CATTTACCAATGAGGAGAAACAGACGAGAAAATCTTGAATGCTTACAAAGCATGCA 720

QY 721 AACAAATGAATCTGTGATGACATGAGGCAAGCACTGGGAGAGATTAACACAGGG 780

Db 721 AACAAATGAATCTGTGATGACATGAGGCAAGCACTGGGAGAGATTAACACAGGG 780

QY 781 GCACAGGCTCAGAGATTTGCGCCCTGCTGCCCTTAACATGCGCTTATTAACCAATCATTT 840
Db 781 GCACAGGCTCAGAGATTTGCGCCCTGCTGCCCTTAACATGCGCTTATTAACCAATCATTT 840

QY 841 ATATTTTCAACCCCAAAACAAAGCTGTTGTAATATGATCTACAGGTCCTTGGG 900
Db 841 ATATTTTCAACCCCAAAACAAAGCTGTTGTAATATGATCTACAGGTCCTTGGG 900

QY 901 CCCAATCTTCATATATATTCAGCCACACATGATTTTAATATTAAGTCCAGATCTGTA 960
Db 901 CCCAATCTTCATATATATTCAGCCACACATGATTTTAATATTAAGTCCAGATCTGTA 960

QY 961 CTGAGACCTTCTACACGTGATGATTAATACATATCTTTGTTCAAGACCTTCGTGT 1020
Db 961 CTGAGACCTTCTACACGTGATGATTAATACATATCTTTGTTCAAGACCTTCGTGT 1020

QY 1021 GCTGCTTAATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1080
Db 1021 GCTGCTTAATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1080

QY 1081 AACAGGCTGGAGACATCTCAAGATCTTCCAGGGTTATCTACTAGCACACAGCATGA 1140
Db 1081 AACAGGCTGGAGACATCTCAAGATCTTCCAGGGTTATCTACTAGCACACAGCATGA 1140

QY 1141 TCATTAGGAGTGAATATATCAATCAATCATCTGATGATGATGATGATGATGATGAT 1200
Db 1141 TCATTAGGAGTGAATATATCAATCAATCATCTGATGATGATGATGATGATGATGAT 1200

QY 1201 TCATTTCCACTTTTGTGCCCCATTCCTCAAGACCTCAAAATGTCCATTAATATGACA 1260
Db 1201 TCATTTCCACTTTTGTGCCCCATTCCTCAAGACCTCAAAATGTCCATTAATATGACA 1260

QY 1261 GGATTAACCTTTTAAAACTGGAAGATTTCAATGATGATGATGATGATGATGATGAT 1320
Db 1261 GGATTAACCTTTTAAAACTGGAAGATTTCAATGATGATGATGATGATGATGATGAT 1320

QY 1321 ATATCAATATTTGTTTCCAGTCAAGATGATGATGATGATGATGATGATGATGATGAT 1380
Db 1321 ATATCAATATTTGTTTCCAGTCAAGATGATGATGATGATGATGATGATGATGATGAT 1380

QY 1381 GATTTTTCCTCAATTAATTAATGCTTACCTGTTAGTCAAGGCTGTATACAGCAC 1440
Db 1381 GATTTTTCCTCAATTAATTAATGCTTACCTGTTAGTCAAGGCTGTATACAGCAC 1440

QY 1441 AGCCTTCCCATGCTCCACAGCTTATCTGATGATGATGATGATGATGATGATGATGAT 1500
Db 1441 AGCCTTCCCATGCTCCACAGCTTATCTGATGATGATGATGATGATGATGATGATGAT 1500

QY 1501 AACCAAAATCAATCTTAATCTTGAACATGTCAGAGCATATATTCCTTCTGCT 1560
Db 1501 AACCAAAATCAATCTTGAATCTTGAACATGTCAGAGCATATATTCCTTCTGCT 1560

QY 1561 GAGAAAGCTCTTCTGCTCTTAATCTAGATGATGATGATGATGATGATGATGATGAT 1620
Db 1561 GAGAAAGCTCTTCTGCTCTTAATCTAGATGATGATGATGATGATGATGATGATGAT 1620

QY 1621 TCTTACTTCATGCAAAAGGAGGACATATGATGATGATGATGATGATGATGATGATGAT 1680
Db 1621 TCTTACTTCATGCAAAAGGAGGACATATGATGATGATGATGATGATGATGATGATGAT 1680

QY 1681 CTTAAAGTGTATTTGATTAATAGATTTAGATTAATATATATATATATATATATATAT 1740
Db 1681 CTTAAAGTGTATTTGATTAATAGATTTAGATTAATATATATATATATATATATATAT 1740

QY 1741 GGAATGTTTATGAGGACAGTTTGTAAAGCTGAGATGTAAGCAAGAGGACAGACTCA 1800
Db 1741 GGAATGTTTATGAGGACAGTTTGTAAAGCTGAGATGTAAGCAAGAGGACAGACTCA 1800

QY 1801 TAGATCTTAATATATATATCTTCTATCTATCTATCTATCTATCTATCTATCTATCT 1860
Db 1801 TAGATCTTAATATATATATCTTCTATCTATCTATCTATCTATCTATCTATCTATCTATCT 1860

D	b	1801	TAGATCTTAATATAATACTTCAATTTCTCATCTATCTATACAAATATACCAAGCTTTT	1860
Q	y	1861	CACGAATTCCTGCGAGTGCAAATCCCAAGAGTAACCTTTATCCATTTCAATGAGTAGC	1920
D	b	1861	CACGAATTCATCGCAGTGCAAATCCCAAGAGTAACCTTTATCCATTTCAATGAGTAGC	1920
Q	y	1921	GCTTTAGCAATTTTGGCAATCATCTGCTCATTTATCTCAACTTTGAGATGTGTTGTCC	1980
D	b	1921	GCTTTAGCAATTTTGGCAATCATCTGCTCATTTATCTCAACTTTGAGATGTGTTGTCC	1980
Q	y	1981	TTTGAGTAAATTTGAAAGAAATAGGGCACTCTGTGAGCCACTTTAGAGTTCACTCCGCG	2040
D	b	1981	TTTGAGTAAATTTGAAAGAAATAGGGCACTCTGTGAGCCACTTTAGAGTTCACTCCGCG	2040
Q	y	2041	AATTAAGAAATTTACAAAGAGCTACTCGAGCACTGTTTAAAGACTCTGTGTGTGTGT	2100
D	b	2041	AATTAAGAAATTTACAAAGAGCTACTCGAGCACTGTTTAAAGACTCTGTGTGTGTGT	2100
Q	y	2101	GTTGTGTGTGAGTGTACATGCCAAAGTGTGCTCTCTCTTGACCACTTATTTTCAGAC	2160
D	b	2101	GTTGTGTGTGAGTGTACATGCCAAAGTGTGCTCTCTCTTGACCACTTATTTTCAGAC	2160
Q	y	2161	TTTAAACAAGATGTTTTCAAAATGGCACTATGAGCTGCCAATGATATCACCACTAT	2220
D	b	2161	TTTAAACAAGATGTTTTCAAAATGGCACTATGAGCTGCCAATGATATCACCACTAT	2220
Q	y	2221	CTCATTTATTCGCCAGTAAATGATGATTAATATGTCATGTTAAATATAAAAGATTGAC	2280
D	b	2221	CTCATTTATTCGCCAGTAAATGATGATTAATATGTCATGTTAAATATAAAAGATTGAC	2280
Q	y	2281	TTTCACAAAGACAGCTGGAATTGACAACACCAATATGCAATTAATCTTACTCCATCA	2340
D	b	2281	TTTCACAAAGACAGCTGGAATTGACAACACCAATATGCAATTAATCTTACTCCATCA	2340
Q	y	2341	GCTACACACTGCTTACCATATATTTGTTAGAACACCTCGCATTTGTGTGGTCTCTTAAGC	2400
D	b	2341	GCTACACACTGCTTACCATATATTTGTTAGAACACCTCGCATTTGTGTGGTCTCTTAAGC	2400
Q	y	2401	AAATTACTGTGATTAGGCTCAGCTGGGGCTGCTCATCAGCGGGTTTGAGAAATATCA	2460
D	b	2401	AAATTACTGTGATTAGGCTCAGCTGGGGCTGCTCATCAGCGGGTTTGAGAAATATCA	2460
Q	y	2461	TTTCTCAGCAGAACCCAGAAATTTGAATTCCTTCATCTTTAGGAATCAATTTACAGGTTTG	2520
D	b	2461	TTTCTCAGCAGAACCCAGAAATTTGAATTCCTTCATCTTTAGGAATCAATTTACAGGTTTG	2520
Q	y	2521	GAGAGGATTCAGACAGCTCAGGTGCTTCTACTAATGTCTCTGAATCTTGCTGCTCTTGG	2580
D	b	2521	GAGAGGATTCAGACAGCTCAGGTGCTTCTACTAATGTCTCTGAATCTTGCTGCTCTTGG	2580
Q	y	2581	TGTTCAATGAGATGTCGAATTAATATGTTTATCTTGAACGATGCTCATAGGAGAGATA	2640
D	b	2581	TGTTCAATGAGATGTCGAATTAATATGTTTATCTTGAACGATGCTCATAGGAGAGATA	2640
Q	y	2641	TAAAGACTCTGAGTGATATCAACAATTTAGAGATTTCAAGAAATATTTAGATTTAACTACA	2700
D	b	2641	TAAAGACTCTGAGTGATATCAACAATTTAGAGATTTCAAGAAATATTTAGATTTAACTACA	2700
Q	y	2701	CTGTCTAAAGGAACCAAGATACAAAGACTCTGAGTGTATGTCCTCCACTCTCTGTGA	2760
D	b	2701	CTGTCTAAAGGAACCAAGATACAAAGACTCTGAGTGTATGTCCTCCACTCTCTGTGA	2760
Q	y	2761	GCCCAACCAACAGCAGAGCCCAAGCGATGCTGAGATCTTTAATATCAGGAAACCAAGTG	2820
D	b	2761	GCCCAACCAACAGCAGAGCCCAAGCGATGCTGAGATCTTTAATATCAGGAAACCAAGTG	2820
Q	y	2821	TCATGAGTTGAATTTCTCTTAATATGAGATGTAGTCTTGCGCACTCTGGCTCTCTCTT	2880
D	b	2821	TCATGAGTTGAATTTCTCTTAATATGAGATGTAGTCTTGCGCACTCTGGCTCTCTCTT	2880
Q	y	2881	GACACATATTAAGCTTAGCGCTTGGCTTCCACGACTTTATCTTTCTCCACACATGCG	2940
D	b	2881	GACACATATTAAGCTTAGCGCTTGGCTTCCACGACTTTATCTTTCTCCACACATGCG	2940

QY	2941	TTACCAATCCTCTCTGCTCTGTGTGCTTTGGACTTCCCCACAAGAAATTTCAACGACTCT	3000		
DB	2941	TTACCAATCCTCTCTGCTCTGTGTGCTTTGGACTTCCCCACAAGAAATTTCAACGACTCT	3000		
QY	3001	CAAGTCTTTTCTTCATCCCCACCACTGTAATGCTGCTAAGCCCTTATTTTATTTAA	3060		
DB	3001	CAAGTCTTTTCTTCATCCCCACCACTGTAATGCTGCTAAGCCCTTATTTTATTTAA	3060		
QY	3061	TTTCCAAATAGATGCTGCTATGAGGCTATATGCTTTATAGATGAACATTAGATTTTAAAG	3120		
DB	3061	TTTCCAAATAGATGCTGCTATGAGGCTATATGCTTTATAGATGAACATTAGATTTTAAAG	3120		
QY	3121	TCTAAGAGGTTCAAAATTCACAACCTATTATCTTCTCTTCTTCACTCCCTGCTCTCT	3180		
DB	3121	TCTAAGAGGTTCAAAATTCACAACCTATTATCTTCTCTTCTTCACTCCCTGCTCTCT	3180		
QY	3181	CCCTATATATTACTGATTCAGTACGATGAGATGCTCCCAAGATGCGATCAATGGAAC	3240		
DB	3181	CCCTATATATTACTGATTCAGTACGATGAGATGCTCCCAAGATGCGATCAATGGAAC	3240		
QY	3241	CAGTGGCCCTTGATGATCATGATGCAAGACGCTGGAAGCCAGAGGTGATGATTAACG	3300		
DB	3241	CAGTGGCCCTTGATGATCATGATGCAAGACGCTGGAAGCCAGAGGTGATGATTAACG	3300		
QY	3301	CCTATGAGGTGAGAGGACCACTCCTGCGCTTGCTGATTTGTCAGAGACAAGACCTGAGA	3360		
DB	3301	CCTATGAGGTGAGAGGACCACTCCTGCGCTTGCTGATTTGTCAGAGACAAGACCTGAGA	3360		
QY	3361	TGCTGCCCTGCTGAGTGTGCTCTGTCATCTCCCTTTCTAATGAAGATCCATAGAAATTTG	3420		
DB	3361	TGCTGCCCTGCTGAGTGTGCTCTGTCATCTCCCTTTCTAATGAAGATCCATAGAAATTTG	3420		
QY	3421	CTAATTTTGAGAAATTTCCAAATTAGAACTGACATGTTTATCTGCTTATCAATTTTTAA	3480		
DB	3421	CTAATTTTGAGAAATTTCCAAATTAGAACTGACATGTTTATCTGCTTATCAATTTTTAA	3480		
QY	3481	ACTTGCGAAATTAAGTTTTTTCAAAATCGTCTGTAATTAATTACTTTTCTTACAGTG	3540		
DB	3481	ACTTGCGAAATTAAGTTTTTTCAAAATCGTCTGTAATTAATTACTTTTCTTACAGTG	3540		
QY	3541	TCTTGCCATCTATATCAACTTTGATCTTTGTTTACAACCTTT	3582		
DB	3541	TCTTGCCATCTATATCAACTTTGATCTTTGTTTACAACCTTT	3582		
RESULT 2	AR261166	3923 bp	DNA	linear	PAT 29-JAN-2003
LOCUS	AR261166				
DEFINITION	Sequence 690 from patent US 6321716.				
ACCESSION	AR261166				
VERSION	AR261166.1	GI:28071929			
KEYWORDS	Unknown.				
SOURCE	Unknown.				
ORGANISM	Unknown.				
REFERENCE	Unclassified.				
AUTHORS	1 (bases 1 to 3923)				
TITLE	Mashiki,Z. and Harada,J.				
JOURNAL	Negative pressure control apparatus for engine mounted in vehicle				
FEATURES	Patent: US 6321716-A 690 27-NOV-2001;				
	Location/Qualifiers				
	1..3923				
BASE COUNT	1157 a	840 c	740 g	1186 t	
ORIGIN					
Query Match	84.8%;	Score 3036;	DB 6;	Length 3923;	
Best Local Similarity	100.0%;	Pred. No. 0;			
Matches 3036;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;	
QY	1	ACAGAGAATAATGACAGTGTCCGAGAGAGCTGGCATCAGAAAAACAGAGGGAGATTTGTGT	60		
DB	1	ACAGAGAATAATGACAGTGTCCGAGAGAGCTGGCATCAGAAAAACAGAGGGAGATTTGTGT	60		

QY	61	GGCTGACAGCCGAGGGAGACACAGGAAGATCTGCATGCTGGGAAGACCTGATGATACAGAG	120
Db	61	GGCTCCACCGCGGGGAGACACAGGAAGATCTGCATGCTGGGAAGACCTGATGATACAGAG	120
QY	121	GAATTACAAACATATTACTGTGTGTTCAATCAACCAAGAATAATTAATGACAGCTA	180
Db	121	GAATTACAAACATATTACTGTGTGTTCAATCAACCAAGAATAATTAATGACAGCTA	180
QY	181	GTCCGCTGTGAGTCTCTCACTGATGACACAGGGGTGTGATACCATGACGGCACTTCTGAG	240
Db	181	GTCCGCTGTGAGTCTCTCACTGATGACACAGGGGTGTGATACCATGACGGCACTTCTGAG	240
QY	241	TACTAGTGCAGCAAAAGAAAGACTTCAACATCTTCAATGCGAGGGGTGAGAAATAGAAA	300
Db	241	TACTAGTGCAGCAAAAGAAAGACTTCAACATCTTCAATGCGAGGGGTGAGAAATAGAAA	300
QY	301	GGCTGCTACATTTTACCATCTGAGGGGCACACATCTGCTGAATGTGAGATTAATTAACATAC	360
Db	301	GGCTGCTACATTTTACCATCTGAGGGGCACACATCTGCTGAATGTGAGATTAATTAACATAC	360
QY	361	TAGAAACAGCAGATGACATTTAAATGTCTAATGATGACATGTTTTTGCACATTTCCAG	420
Db	361	TAGAAACAGCAGATGACATTTAAATGTCTAATGATGACATGTTTTTGCACATTTCCAG	420
QY	421	CCCCCTTAAATATCCACACACACAGGAGCAACAAAGGAAACACAGATCCCTGGGAGA	480
Db	421	CCCCCTTAAATATCCACACACACAGGAGCAACAAAGGAAACACAGATCCCTGGGAGA	480
QY	481	AATGCCCGCGCCCATCTTTGGGTCATCCANTAGCCTCCGCCCTGTGCTCCGCTTGT	540
Db	481	AATGCCCGCGCCCATCTTTGGGTCATCCANTAGCCTCCGCCCTGTGCTCCGCTTGT	540
QY	541	GAGGGAAGACATTAGAAAATGATGATGTGTTCTTTAAAGATGGCGAGAAAAACAGA	600
Db	541	GAGGGAAGACATTAGAAAATGATGATGTGTTCTTTAAAGATGGCGAGAAAAACAGA	600
QY	601	TCCTTTTGTGGATTTTATTTTGAACGGGATTAACGATTTGAAATGAATCCAAATGATAG	660
Db	601	TCCTTTTGTGGATTTTATTTTGAACGGGATTAACGATTTGAAATGAATCCAAATGATAG	660
QY	661	CATTACCAATGAGAGGAAAAACAGACAGAAATCTTGATGGCTTCACAGACATGCAACA	720
Db	661	CATTACCAATGAGAGGAAAAACAGACAGAAATCTTGATGGCTTCACAGACATGCAACA	720
QY	721	AACAAAATGGAATCTGTGATGACATGAGCCAGCCAGCTGGGGAGAGATPAACAGGG	780
Db	721	AACAAAATGGAATCTGTGATGACATGAGCCAGCCAGCTGGGGAGAGATPAACAGGG	780
QY	781	GCAAGGGGTGAGGATTTCTGGCCCTGCTGCTTAAACTGTGCTTCAATCCAAATCATTTTC	840
Db	781	GCAAGGGGTGAGGATTTCTGGCCCTGCTGCTTAAACTGTGCTTCAATCCAAATCATTTTC	840
QY	841	ATATTTCTAACCCCTCAAAACAAAGCTGTTGTAAATATCTGATCTAGCGTTCCTTGGG	900
Db	841	ATATTTCTAACCCCTCAAAACAAAGCTGTTGTAAATATCTGATCTAGCGTTCCTTGGG	900
QY	901	CCCAACATTTCCATATATCCAGCCACACATCTTTTAAATTTAGTTCCAGATCTGTA	960
Db	901	CCCAACATTTCCATATATCCAGCCACACATCTTTTAAATTTAGTTCCAGATCTGTA	960
QY	961	CTTGACCTTTCTACACTGTAGATTAACATTAATTTGTGTCAAGAACCCCTTCGTGT	1020
Db	961	CTTGACCTTTCTACACTGTAGATTAACATTAATTTGTGTGTCAAGAACCCCTTCGTGT	1020
QY	1021	GCTGCTTAATATATAGCTGACTGTTTTTCTTAAAGAGATGTTCTGGCCAGGGGATCTGTG	1080
Db	1021	GCTGCTTAATATATAGCTGACTGTTTTTCTTAAAGAGATGTTCTGGCCAGGGGATCTGTG	1080
QY	1081	AACAGGCTGGAGACATCTCAAGATCTTTTCCAGGGTTAATCTACTAGACACAGCATGA	1140
Db	1081	AACAGGCTGGAGACATCTCAAGATCTTTTCCAGGGTTAATCTACTAGACACAGCATGA	1140

QY	1141	TCATTACGAGAGGAAATTATCTAATACAAATCATCTCAAGTGTCTTTGGCCACTAGAAAT	1200
Db	1141	TCATTACGAGAGGAAATTATCTAATACAAATCATCTCAAGTGTCTTTGGCCACTAGAAAT	1200
QY	1201	TCATTGCCACCTTTGTGCGCAATCTCAAGACCTCAAAATGTCATTCATTAAATATCA	1260
Db	1201	TCATTGCCACCTTTGTGCGCAATCTCAAGACCTCAAAATGTCATTCATTAAATATCA	1260
QY	1261	GGATTAACTTTTTTTTTTAACTGAGAAATTCATGTATACATGACGCTATGGAAATTTA	1320
Db	1261	GGATTAACTTTTTTTTTTAACTGAGAAATTCATGTATACATGACGCTATGGAAATTTA	1320
QY	1321	ATTACATATTTTGTGTTTCCAGTCGCAAAATGACATACGCTTTATCCCTCCCTTTGTT	1380
Db	1321	ATTACATATTTTGTGTTTCCAGTCGCAAAATGACATACGCTTTATCCCTCCCTTTGTT	1380
QY	1381	GATTTTTTTTCCAGATATAAGTTAAATGCTAGACCTGTACTGAGGCTGTATACAGAC	1440
Db	1381	GATTTTTTTTCCAGATATAAGTTAAATGCTAGACCTGTACTGAGGCTGTATACAGAC	1440
QY	1441	AGCCTCTGCCATCCCTCCAGCCTTATCTGTATCACCATCAACCCCTCCCATACACCT	1500
Db	1441	AGCCTCTGCCATCCCTCCAGCCTTATCTGTATCACCATCAACCCCTCCCATACACCT	1500
QY	1501	AAACAAATCTAATCTGTATATTCCTGTGAACATGTACAGACATACATATATTCCTCTGCT	1560
Db	1501	AAACAAATCTAATCTGTATATTCCTGTGAACATGTACAGACATACATATATTCCTCTGCT	1560
QY	1561	GAGAAAGCTCTTCCTGTCTCTTAAATCTAGAAATGATGTAAGTTTGAATTAAGTTGACTA	1620
Db	1561	GAGAAAGCTCTTCCTGTCTCTTAAATCTAGAAATGATGTAAGTTTGAATTAAGTTGACTA	1620
QY	1621	TCTTACTTCATGCAAAAGAGGACACATATGAGATTCTCATCATGACATGAGACAGCAATA	1680
Db	1621	TCTTACTTCATGCAAAAGAGGACACATATGAGATTCTCATCATGACATGAGACAGCAATA	1680
QY	1681	CTAAAGAGCTAATTTGATTATTAAGAGTTTAATATAATATATGAATATGCAAGCCACAGA	1740
Db	1681	CTAAAGAGCTAATTTGATTATTAAGAGTTTAATATAATATATGAATATGCAAGCCACAGA	1740
QY	1741	GGGAATGTTTATNGGGGACGTTTGTGAACCTGTGGGATGTGAAGCAAAAGCAGGAACTCA	1800
Db	1741	GGGAATGTTTATNGGGGACGTTTGTGAACCTGTGGGATGTGAAGCAAAAGCAGGAACTCA	1800
QY	1801	TAGTATCTTATATATATATCTTCAATTTCTATCTATCTATCAACAATATCAACAAGCTTTT	1860
Db	1801	TAGTATCTTATATATATATCTTCAATTTCTATCTATCTATCTATCAACAATATCAACAAGCTTTT	1860
QY	1861	CACAGAATCTATGCAATGCAATATCCCAAGAGTAACCTTTATTCATATTTCAATGTTAGTC	1920
Db	1861	CACAGAATCTATGCAATGCAATATCCCAAGAGTAACCTTTATTCATATTTCAATGTTAGTC	1920
QY	1921	GCTTAGAATTTTGGCAAAATCATCTGCTCATCTATCTCAACCTTGAGAGTGTGTTTCC	1980
Db	1921	GCTTAGAATTTTGGCAAAATCATCTGCTCATCTATCTCAACCTTGAGAGTGTGTTTCC	1980
QY	1981	TTGTAGTAAATTTGAAAGAAATAGGGCACTCTTGTAGACCACTTTAGAGTTCACTCTGGC	2040
Db	1981	TTGTAGTAAATTTGAAAGAAATAGGGCACTCTTGTAGACCACTTTAGAGTTCACTCTGGC	2040
QY	2041	AATTAAGAAATTTACAAAGAGCTACTCAAGGACAGTGTTAAGAGCTCTGTGTGTGTGT	2100
Db	2041	AATTAAGAAATTTACAAAGAGCTACTCAAGGACAGTGTTAAGAGCTCTGTGTGTGTGTGT	2100
QY	2101	GTTGTGTGTGTAGTGTATATGCAATGCAAAAGTGTGCTCTCTCTTGTGACCATTTATTTGAC	2160
Db	2101	GTTGTGTGTGTAGTGTATATGCAATGCAAAAGTGTGCTCTCTCTTGTGACCATTTATTTGAC	2160
QY	2161	TTTAAACACAGATGTTTTTCAAAATGGCACTATGACCTGCAATGATGTATACCAACCATAT	2220
Db	2161	TTTAAACACAGATGTTTTTCAAAATGGCACTATGACCTGCAATGATGTATACCAACCATAT	2220
QY	2221	CTCATATATCTCCAGTAATGTATTAATATGTATCATCTGTTAACATTAATAAAGTTTGAC	2280

|||||
Db 2221 CTCATTATTCCTCAATTAATGTGATATATATCTCATCTTTAAACAATAAAAAAGTTGAC 2280
|||||
Qy 2281 TTCACAAAAGCAGCTGGAATATGACACACAATATGACATAATCTTAACCTCCATCATCA 2340
|||||
Db 2281 TTCACAAAAGCAGCTGGAATATGACACACAATATGACATAATCTTAACCTCCATCATCA 2340
|||||
Qy 2341 GCTACACACTGCTTGACATATTTGTTAGAACACCTCGCATTTGGGTTCTCTTAAC 2400
|||||
Db 2341 GCTACACACTGCTTGACATATTTGTTAGAACACCTCGCATTTGGGTTCTCTTAAC 2400
|||||
Qy 2401 AAAAATCTTGATTAAGTCTGAGCTGGGCTTGACATGAGGCTTGAATAATTTCA 2460
|||||
Db 2401 AAAAATCTTGATTAAGTCTGAGCTGGGCTTGACATGAGGCTTGAATAATTTCA 2460
|||||
Qy 2461 TTCTCAGCAGAGACCCAGAAATTTGAATTCCTCATCTTTTGAATCATTTTACAGGTTTG 2520
|||||
Db 2461 TTCTCAGCAGAGACCCAGAAATTTGAATTCCTCATCTTTTGAATCATTTTACAGGTTTG 2520
|||||
Qy 2521 GAGAGATTCAGACAGCTCAGGCTTTCACATAATGTCTCTGAACCTTCTGCTCCCTTTG 2580
|||||
Db 2521 GAGAGATTCAGACAGCTCAGGCTTTCACATAATGTCTCTGAACCTTCTGCTCCCTTTG 2580
|||||
Qy 2581 TGTTCATGGATAGTCCAAATTAATTAATGTATCTTTGAACCTGATGCTATAGAGAGAAATA 2640
|||||
Db 2581 TGTTCATGGATAGTCCAAATTAATTAATGTATCTTTGAACCTGATGCTATAGAGAGAAATA 2640
|||||
Qy 2641 TAAGAACTCTGAGTATATCAACATTTAGGATTTCAAGAAATATTAGATTTAAGCTCACA 2700
|||||
Db 2641 TAAGAACTCTGAGTATATCAACATTTAGGATTTCAAGAAATATTAGATTTAAGCTCACA 2700
|||||
Qy 2701 CTGGCTCAAAAGGAACCAAGATATCAAAAGAACTGTAGCTGTATCGTCCCATCTCTGTGA 2760
|||||
Db 2701 CTGGCTCAAAAGGAACCAAGATATCAAAAGAACTGTAGCTGTATCGTCCCATCTCTGTGA 2760
|||||
Qy 2761 GCCAACAACAGCAGCAGAGCCACAGCATGTCTGAGATCCTTAATTAAGAGAAACAGTG 2820
|||||
Db 2761 GCCAACAACAGCAGCAGAGCCACAGCATGTCTGAGATCCTTAATTAAGAGAAACAGTG 2820
|||||
Qy 2821 TCATAGATTTGAATTTCTCATATTAATGATGCTAGCTTGGCCATCTGCGCTCTCTCTT 2880
|||||
Db 2821 TCATAGATTTGAATTTCTCATATTAATGATGCTAGCTTGGCCATCTGCGCTCTCTCTT 2880
|||||
Qy 2881 GACACATATTAACCTTCTAGCTTGTGCTTCCAGACCTTTATCTTTTCCACACATGCG 2940
|||||
Db 2881 GACACATATTAACCTTCTAGCTTGTGCTTCCAGACCTTTATCTTTTCCACACATGCG 2940
|||||
Qy 2941 TTACCAATCTCTCTCTGCTCTGTTGCTTTGGACTTCCACAGAAATTTCAACGACTCT 3000
|||||
Db 2941 TTACCAATCTCTCTCTGCTCTGTTGCTTTGGACTTCCACAGAAATTTCAACGACTCT 3000
|||||
Qy 3001 CAAGTCTTTTCTTCATCCCGCAGCTAAGCTGAAT 3036
|||||
Db 3001 CAAGTCTTTTCTTCATCCCGCAGCTAAGCTGAAT 3036
|||||

RESULT 3
AR278697 3923 bp DNA linear PAT 10-APR-2003
LOCUS AR278697
DEFINITION Sequence 690 from patent US 6512094.
ACCESSION AR278697
VERSION AR278697.1 GI:29712943
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 3923)
AUTHORS Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y.,
Kalos,M.D., Fanger,G.R., Retter,M.W., Stolk,J.A., Day,C.H.,
Vedler,T.S., Garter,D., Li,S.X., Wang,A., Skelley,Y.A.W.,
Hepler,W.T., and Henderson,R.A.
TITLE Compositions and methods for the therapy and diagnosis of prostate cancer

JOURNAL Patent: US 6512094-A 690 28-JAN-2003;
FEATURES Location/Qualifiers
source 1..3923 /organism="unknown"
BASE COUNT 1157 a 840 c 740 g 1186 t
ORIGIN
Query Match 84.8%; Score 3036; DB 6; Length 3923;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3036; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1 ACAGAAAGAAATATGCAAGTCCGAGAAAGCTGGCATCGAAGAAACAGAGGAGATTTGTGT 60
1 ACAGAAAGAAATATGCAAGTCCGAGAAAGCTGGCATCGAAGAAACAGAGGAGATTTGTGT 60
61 GGCTGAGCGGAGGAGGAGACAGAGAAATGTCATGCTGGGAAAGACCTGATATACAGAG 120
61 GGCTGAGCGGAGGAGGAGACAGAGAAATGTCATGCTGGGAAAGACCTGATATACAGAG 120
121 GAATTACAAACATATACTTACTTGTTCATTAATGACACCAAGATTAATAGTGAAGACTA 180
121 GAATTACAAACATATACTTACTTGTTCATTAATGACACCAAGATTAATAGTGAAGACTA 180
181 GTCCGCTGAGCTCTCCAGTGAACAGAGGCTGGATCACAATCGACGCGACTTCTGTAG 240
181 GTCCGCTGAGCTCTCCAGTGAACAGAGGCTGGATCACAATCGACGCGACTTCTGTAG 240
241 TACTCAGTCCAGCAAGAAAGAAAGACTACAGACATCTCAATGGCAGGAGGTTGAATAAGAAA 300
241 TACTCAGTCCAGCAAGAAAGAAAGACTACAGACATCTCAATGGCAGGAGGTTGAATAAGAAA 300
301 GGCTGTGACTTTTACCATCTGAGGCGACACATCTGCTGAATAGGAGATTAATTAATCAG 360
301 GGCTGTGACTTTTACCATCTGAGGCGACACATCTGCTGAATAGGAGATTAATTAATCAG 360
361 TAGAAACACAGATATGACATTAATATGTTAGTATGATGATGATGTTTTCACATTTCCAG 420
361 TAGAAACACAGATATGACATTAATATGTTAGTATGATGATGATGTTTTCACATTTCCAG 420
421 CCCCTTTAATATTCACACACACAGAGACACAAAAGGAAGACAGAGATCCCTGGGAGA 480
421 CCCCTTTAATATTCACACACACAGAGACACAAAAGGAAGACAGAGATCCCTGGGAGA 480
481 AATGCCCGGCGGCAATCTGGGTCATGATGAGCCGCGCTGCTGCTGCTGCTGCTGCTGCT 540
481 AATGCCCGGCGGCAATCTGGGTCATGATGAGCCGCGCTGCTGCTGCTGCTGCTGCTGCT 540
541 GAGGAGAGACATTAAGAAATGAATGATGTCTCTTAAGAGATGGGAGGAGAAACAGA 600
541 GAGGAGAGACATTAAGAAATGAATGATGTCTCTTAAGAGATGGGAGGAGAAACAGA 600
601 TCCTGTGTGATATTTATTTGACGGGATTCACAGATTTGAATGACAGTCAACAACTGAG 660
601 TCCTGTGTGATATTTATTTGACGGGATTCACAGATTTGAATGACAGTCAACAACTGAG 660
661 CATTAACATGAGAGGAGAAACAGAGAGAAATCTTGATGGCTTCAACAGATGGAACA 720
661 CATTAACATGAGAGGAGAAACAGAGAGAAATCTTGATGGCTTCAACAGATGGAACA 720
721 AACCAAAATGATATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 780
721 AACCAAAATGATATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 780
781 GCAGAGGCTCAGGATTTGCGCCCTGCTGCTTAACCTGCTTCAATTAACCAATATTTTC 840
781 GCAGAGGCTCAGGATTTGCGCCCTGCTGCTTAACCTGCTTCAATTAACCAATATTTTC 840
841 ATATTCTTAACCTCAAAACAAAGCTGTGTAATATCTGATCTGACGTTCTCTCTGAG 900
841 ATATTCTTAACCTCAAAACAAAGCTGTGTAATATCTGATCTGACGTTCTCTCTGAG 900
901 CCCAATCTTCCATATATCCAGCACACTCATTTTAAATTAATTTAGTTCCAGATCTGTA 960
901 CCCAATCTTCCATATATCCAGCACACTCATTTTAAATTAATTTAGTTCCAGATCTGTA 960

Dh 901 CCAACATTCATATATATCCAGCCACACTGATTTTATATATTTAGTTCCAGATCTGTGA 960
Qy 961 CTGTGACCTTTCTACACTGTAGAAATACATTAATCTGATTTGTTCAAAGACCCCTTGCTGT 1020
Dh 961 CTGTGACCTTTCTACACTGTAGAAATACATTAATCTGATTTGTTCAAAGACCCCTTGCTGT 1020
Qy 1021 GCTGCTTAATATAGTGTGACGTGTTTTCCTTAAGAGTGTCTGGCCCAAGGGGATCTGTG 1080
Dh 1021 GCTGCTTAATATAGTGTGACGTGTTTTCCTTAAGAGTGTCTGGCCCAAGGGGATCTGTG 1080
Qy 1081 AACAGGCTGGGAAGCATCTCAAGATCTTCCAGGGGTATTAATCTTACTATAGACACAGCATGA 1140
Dh 1081 AACAGGCTGGGAAGCATCTCAAGATCTTCCAGGGGTATTAATCTTACTATAGACACAGCATGA 1140
Qy 1141 TCATTTACGAGTGAATTAATCTAATCAATCATATCTCAGTGTCTTGGCCATAGTGAAT 1200
Dh 1141 TCATTTACGAGTGAATTAATCTAATCAATCATATCTCAGTGTCTTGGCCATAGTGAAT 1200
Qy 1201 TCATTTCCACATTTTGTGCCATTTCTCAAGACCTCAAAATGTGATTCATTAATATCTACA 1260
Dh 1201 TCATTTCCACATTTTGTGCCATTTCTCAAGACCTCAAAATGTGATTCATTAATATCTACA 1260
Qy 1261 GGATTTAACTTTTTTTTTTAACTGGGAAGAAATTCATGTACATGAGCTATGGGAATTTA 1320
Dh 1261 GGATTTAACTTTTTTTTTTAACTGGGAAGAAATTCATGTACATGAGCTATGGGAATTTA 1320
Qy 1321 ATTACATATTTTGTTCCTCACTGCAAGATGACATAGTCTTTATCCCTCTGCTTGTGT 1380
Dh 1321 ATTACATATTTTGTTCCTCACTGCAAGATGACATAGTCTTTATCCCTCTGCTTGTGT 1380
Qy 1381 GATTTTTCAGATTAATTAAGTTAAATGCTTAGCGTTGTAAGGCTGTATACAGAC 1440
Dh 1381 GATTTTTCAGATTAATTAAGTTAAATGCTTAGCGTTGTAAGGCTGTATACAGAC 1440
Qy 1441 AGCCTTCGCCACCTCCCTCCAGCCTTATCTGTATCACCATCAACCCCTCCCATACACCT 1500
Dh 1441 AGCCTTCGCCACCTCCCTCCAGCCTTATCTGTATCACCATCAACCCCTCCCATACACCT 1500
Qy 1501 AAACAAATCTAACTGTGAATCTCTGAAACATGTGACGACATTAATTCCTCTGCTGCT 1560
Dh 1501 AAACAAATCTAACTGTGAATCTCTGAAACATGTGACGACATTAATTCCTCTGCTGCT 1560
Qy 1561 GAGAAGCTCTCCCTGCTCTTAATCTAGAAATGATGAAGTTTGAATGAATGACTGA 1620
Dh 1561 GAGAAGCTCTCCCTGCTCTTAATCTAGAAATGATGAAGTTTGAATGAATGACTGA 1620
Qy 1621 TCTTACTTCATGCAAGAGGACACATATGAGATTCATCATACATGAGACAGCAATA 1680
Dh 1621 TCTTACTTCATGCAAGAGGACACATATGAGATTCATCATACATGAGACAGCAATA 1680
Qy 1681 CTAAAGTGTATATTTGATTAATAGATTAATATATATATGAATGCAAGGCCACAGA 1740
Dh 1681 CTAAAGTGTATATTTGATTAATAGATTAATATATATATGAATGCAAGGCCACAGA 1740
Qy 1741 GGAAGTGTATATGGGACGTTTGTAAAGCCTGGATGGAAGCAAGGCAAGGCAACCTCA 1800
Dh 1741 GGAAGTGTATATGGGACGTTTGTAAAGCCTGGATGGAAGCAAGGCAAGGCAACCTCA 1800
Qy 1801 TAGTATCTATATATATATATCTATCTATCTATCAATCAATATCAACAAGCTTTT 1860
Dh 1801 TAGTATCTATATATATATATCTATCTATCTATCAATCAATATCAACAAGCTTTT 1860
Qy 1861 CACAGAAATTCATGAGAGCAAAATCCCAAGGTAACTTTATTCATTTCAAGGTGAGTGC 1920
Dh 1861 CACAGAAATTCATGAGAGCAAAATCCCAAGGTAACTTTATTCATTTCAAGGTGAGTGC 1920
Qy 1921 GCTTTAGAAATTTGGCAAAATCAATCTGTGACCTTATCTCAACTTTGAGATGTGTTGTCC 1980
Dh 1921 GCTTTAGAAATTTGGCAAAATCAATCTGTGACCTTATCTCAACTTTGAGATGTGTTGTCC 1980
Qy 1981 TTGTAGTTAATGAAAGAAATAGGGCACTCTGTGAGCCACTTTAGGGTTCACTCTGCGC 2040
Dh 1981 TTGTAGTTAATGAAAGAAATAGGGCACTCTGTGAGCCACTTTAGGGTTCACTCTGCGC 2040

Qy 2041 AATAAAGATTTTACAAAGACTACTCAGGACAGTTGTTAAGAGCTGTGTGTGTGT 2100
Dh 2041 AATAAAGATTTTACAAAGACTACTCAGGACAGTTGTTAAGAGCTGTGTGTGTGTGT 2100
Qy 2101 GT 2160
Dh 2101 GT 2160
Qy 2161 TTAACAACAAGCATGTTTCAAAATGSCACATATGAGCTGGCAATGATGTATCCACACATAT 2220
Dh 2161 TTAACAACAAGCATGTTTCAAAATGSCACATATGAGCTGGCAATGATGTATCCACACATAT 2220
Qy 2221 CTCATTAATCTCCCAATAATGTGATTAATATGTCATCTGTAAACATTAATAAAGTTTAC 2280
Dh 2221 CTCATTAATCTCCCAATAATGTGATTAATATGTCATCTGTAAACATTAATAAAGTTTAC 2280
Qy 2281 TTCACAAAAGCAGCTGGAAATGTGACACACACATATGATTAATCTAATCTCTACATCA 2340
Dh 2281 TTCACAAAAGCAGCTGGAAATGTGACACACACATATGATTAATCTAATCTCTACATCA 2340
Qy 2341 GCTACACACTGCTTGACATATATGTTTGAAGACACTGSCATTTGTGTGTGTGTGTGTGT 2400
Dh 2341 GCTACACACTGCTTGACATATATGTTTGAAGACACTGSCATTTGTGTGTGTGTGTGTGT 2400
Qy 2401 AAAATACTTGATTAAGTCTCAGCTGGGGCTGTGCATCAGGCGGTTTGAGAAATATTCAA 2460
Dh 2401 AAAATACTTGATTAAGTCTCAGCTGGGGCTGTGCATCAGGCGGTTTGAGAAATATTCAA 2460
Qy 2461 TTCACAGCAAGCAGAAATTTGAATTCCTCATCTTTAGGAATCATTTACCGAGTTTG 2520
Dh 2461 TTCACAGCAAGCAGAAATTTGAATTCCTCATCTTTAGGAATCATTTACCGAGTTTG 2520
Qy 2521 GAGAAGATTCAGACAGCTCAGGTGCTTCAATATGTCATGCAATCTCTGCTCTTTG 2580
Dh 2521 GAGAAGATTCAGACAGCTCAGGTGCTTCAATATGTCATGCAATCTCTGCTCTTTG 2580
Qy 2581 TGTTCATGATATGTCATTAATAATGTTATCTTTGAACATGATCTCATAGAGAGATA 2640
Dh 2581 TGTTCATGATATGTCATTAATAATGTTATCTTTGAACATGATCTCATAGAGAGATA 2640
Qy 2641 TTAAGACCTGTAGATATCAACATTAAGGATTTCAAGAAATATTAATTAATTAACCTACA 2700
Dh 2641 TTAAGACCTGTAGATATCAACATTAAGGATTTCAAGAAATATTAATTAATTAACCTACA 2700
Qy 2701 CTGCTCAAAAGAACCAAGATATCAAGAACTGTAGCTGTATCTGCTCTGTGA 2760
Dh 2701 CTGCTCAAAAGAACCAAGATATCAAGAACTGTAGCTGTATCTGCTCTGTGA 2760
Qy 2761 GCCAACACCAACAGCAGACCAAGCATGTCTGAGATCTTAAATCAAGGAAACCAAGT 2820
Dh 2761 GCCAACACCAACAGCAGACCAAGCATGTCTGAGATCTTAAATCAAGGAAACCAAGT 2820
Qy 2821 TCATGAGTGTGAATCTCTCTATTAATGATGATGATGCTGCGCATCTGCGCTCTCTCT 2880
Dh 2821 TCATGAGTGTGAATCTCTCTATTAATGATGATGATGCTGCGCATCTGCGCTCTCTCT 2880
Qy 2881 GACACATATATGCTTTAGAGCTTGTGCTTCCAGCACTTTATCTTTCCAAACATATGCG 2940
Dh 2881 GACACATATATGCTTTAGAGCTTGTGCTTCCAGCACTTTATCTTTCCAAACATATGCG 2940
Qy 2941 TTACCAATCTCTCTGT 3000
Dh 2941 TTACCAATCTCTCTGT 3000
Qy 3001 CAAGCTTTTCTTCCATCCCAACACATTAACCTGAT 3036
Dh 3001 CAAGCTTTTCTTCCATCCCAACACATTAACCTGAT 3036
RESULT 4
AX200988
LOCUS AX200988 3923 bp DNA linear PAT 29-AUG-2001

DEFINITION Sequence 618 from Patent WO0151633.
ACCESSION AX200988
VERSION AX200988.1 GI:15390814
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1
AUTHORS Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y.,
Reed,S.G., Kalos,M.D., Fanger,G.R., Day,C.H., Reller,M.W.,
Stolk,D.A., Skeiky,Y.A., Wang,A. and Meagher,M.J.
TITLE Compositions and methods for the therapy and diagnosis of prostate
cancer
JOURNAL Patent: WO 0151633-A 618 19-JUL-2001;
CORLIX CORPORATION (US)
FEATURES
source 1..3923
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
BASE COUNT 1157 a 840 c 740 g 1186 t
ORIGIN
Query Match 84.8%; Score 3036; DB 6; Length 3923;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3036; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ACAGAGAATATAGCAAGTCCGAGAGCTGCGATCAGAAAAACAGAGGAGATTGTGT 60
DB 1 ACAGAGAATATAGCAAGTCCGAGAGCTGCGATCAGAAAAACAGAGGAGATTGTGT 60
QY 61 GGCTGAGCGGAGGAGGAGACAGAGATGTCATGGTGGGAAGACCTGATATAGAG 120
DB 61 GGCTGAGCGGAGGAGGAGACAGAGATGTCATGGTGGGAAGACCTGATATAGAG 120
QY 121 GAATTACACACATATACTAGTGTTCATGAACACCAAGATTAATAGTGAAGACTA 180
DB 121 GAATTACACACATATACTAGTGTTCATGAACACCAAGATTAATAGTGAAGACTA 180
QY 181 GTCGCTGTGAGTCTCTTAGTGACACAGAGGCTGGATCCATCCAGCGCATTTTGAG 240
DB 181 GTCGCTGTGAGTCTCTTAGTGACACAGAGGCTGGATCCATCCAGCGCATTTTGAG 240
QY 241 TACTCAGTCAGCAAGAAAGACTACAGACATCTCATGCGAGGGGTGAATAAGAAA 300
DB 241 TACTCAGTCAGCAAGAAAGACTACAGACATCTCATGCGAGGGGTGAATAAGAAA 300
QY 301 GGCTGCTGACTTTACCATCTGAGGCCACATCTGCTGAATGAGATTAATTACATCAC 360
DB 301 GGCTGCTGACTTTACCATCTGAGGCCACATCTGCTGAATGAGATTAATTACATCAC 360
QY 361 TAGAAACAGCAAGATACAAATATATGTCTAAGTAGACATGTTTTGCACATTTCCAG 420
DB 361 TAGAAACAGCAAGATACAAATATATGTCTAAGTAGACATGTTTTGCACATTTCCAG 420
QY 421 CCCCTTTAATATCCACACACAGAGCAACAAAAGAGACACACAGATCCCTGGGAGA 480
DB 421 CCCCTTTAATATCCACACACAGAGCAACAAAAGAGACACACAGATCCCTGGGAGA 480
QY 481 AATGCCGCCGCCCATCTTGGGTGATCGATGAGCCCTGCGCTGTGCTCCCGTTGT 540
DB 481 AATGCCGCCGCCCATCTTGGGTGATCGATGAGCCCTGCGCTGTGCTCCCGTTGT 540
QY 541 GAGGGAAGGACATTGAAAAATGATGATGTTCTCTTAAGGATGGCAGAAAAACAGA 600
DB 541 GAGGGAAGGACATTGAAAAATGATGATGTTCTCTTAAGGATGGCAGAAAAACAGA 600
QY 601 TCCGTGTGATATTTATTTTGAACGGATTAAGATTGAATGAAGTACACAAATGTAG 660
DB 601 TCCGTGTGATATTTATTTTGAACGGATTAAGATTGAATGAAGTACACAAATGTAG 660
QY 661 CATTAACATGAGAGGAAAAACAGAGAAAAATCTTGATGGCTTCACAGACATGCAACA 720

DB 661 CATTAACATGAGAGGAAAAACAGAGAAAAATCTTGATGGCTTCACAGACATGCAACA 720
QY 721 AACAAATGGAATATCTGTATGACATAGAGGACCAAGCTGGGAGAGATTAACACGGG 780
DB 721 AACAAATGGAATATCTGTATGACATAGAGGACCAAGCTGGGAGAGATTAACACGGG 780
QY 781 GCAGAGGTCAGGATCTGGCCCTGCTGCTAAACGTGCGTTCATACCAATCATTTTC 840
DB 781 GCAGAGGTCAGGATCTGGCCCTGCTGCTAAACGTGCGTTCATACCAATCATTTTC 840
QY 841 ATATTCTTAACCTCAAAAACAAAGCTGTGTATATCTGATCTCAAGCTTCCCTGGG 900
DB 841 ATATTCTTAACCTCAAAAACAAAGCTGTGTATATCTGATCTCAAGCTTCCCTGGG 900
QY 901 CCCACATCTCCATATATATCCAGCCACACTCATTTTAAATTAATTAATCCAGATCTGA 960
DB 901 CCCACATCTCCATATATATCCAGCCACACTCATTTTAAATTAATTAATCCAGATCTGA 960
QY 961 CTGTGACCTTTCTACACTGTAGATTAACATTAATCTCATTTTGTCAAGACCTTCGTGT 1020
DB 961 CTGTGACCTTTCTACACTGTAGATTAACATTAATCTCATTTTGTCAAGACCTTCGTGT 1020
QY 1021 GCTGCTAATATGATGACTGACTGTTTTCCTAAGAGATGTCGGCCAGGGATCTGTG 1080
DB 1021 GCTGCTAATATGATGACTGACTGTTTTCCTAAGAGATGTCGGCCAGGGATCTGTG 1080
QY 1081 AACAGGCTGGGAACATCTCAAGATCTTTCAGGCTTAATCTTACTAGACACAGATGA 1140
DB 1081 AACAGGCTGGGAACATCTCAAGATCTTTCAGGCTTAATCTTACTAGACACAGATGA 1140
QY 1141 TCATTACGAGTGAATATATCTAATCAACATCCACATGCTTCCCATCTCAAT 1200
DB 1141 TCATTACGAGTGAATATATCTAATCAACATCCACATGCTTCCCATCTCAAT 1200
QY 1201 TCATTCCCACTTTTGTGCCATCTCAAGACCTCAAAATGTCATTCATTAATACAGA 1260
DB 1201 TCATTCCCACTTTTGTGCCATCTCAAGACCTCAAAATGTCATTCATTAATACAGA 1260
QY 1261 GGAATTAACCTTTTAAACCTGGAAGATTAATCAATGAGAGCTATGGGAATTA 1320
DB 1261 GGAATTAACCTTTTAAACCTGGAAGATTAATCAATGAGAGCTATGGGAATTA 1320
QY 1321 ATTACATATTTTCTTCCAGTCAAGATGACTAGTCTTATCCCTCCCTTGTGT 1380
DB 1321 ATTACATATTTTCTTCCAGTCAAGATGACTAGTCTTATCCCTCCCTTGTGT 1380
QY 1381 GATTTTTTCCAGTAAAGTTAAATGCTTAGCCTTGACTGAGGCTGTATACAGAC 1440
DB 1381 GATTTTTTCCAGTAAAGTTAAATGCTTAGCCTTGACTGAGGCTGTATACAGAC 1440
QY 1441 AGCCTTCCCATCCTCCAGCCTTATCTGTATCAACATCAACCCCTCCATACACCT 1500
DB 1441 AGCCTTCCCATCCTCCAGCCTTATCTGTATCAACATCAACCCCTCCATACACCT 1500
QY 1501 AAACAAATCTAATCTGTAATCTTGAACATCTGAGCATCATTAATCTTCCGCT 1560
DB 1501 AAACAAATCTAATCTGTAATCTTGAACATCTGAGCATCATTAATCTTCCGCT 1560
QY 1561 GAGAACTCTTCTCTCTTAATCTGAATGATGAAGTTTGAATTAAGTTGACTA 1620
DB 1561 GAGAACTCTTCTCTCTTAATCTGAATGATGAAGTTTGAATTAAGTTGACTA 1620
QY 1621 TCTTACTATGCAAGAAAGGACACATATGATTCATCATGAGACGCAAAATA 1680
DB 1621 TCTTACTATGCAAGAAAGGACACATATGATTCATCATGAGACGCAAAATA 1680
QY 1681 CTAAAGTGAATTTATATTAAGATTAAGATTAATATATGAAGTGAAGGCGCAGCA 1740
DB 1681 CTAAAGTGAATTTATATTAAGATTAAGATTAATATATGAAGTGAAGGCGCAGCA 1740
QY 1741 GGGAAATGTTATGGGCGAGCTTGTAAAGCTGGAGTGAAGCAAGGCGAGGAACTCA 1800
DB 1741 GGGAAATGTTATGGGCGAGCTTGTAAAGCTGGAGTGAAGCAAGGCGAGGAACTCA 1800

Db 1741 GGGATGTTTGGGGCAGCTTTGTAAGCTGGGATGTGAAGCAAGGACAGGAACTCTCA 1800
Qy 1801 TAGATCTTATATATATATCTTCAATTTCTATCTATCTATCAATATCAACAAGCTTTT 1860
Db 1801 TAGATCTTATATATATATCTTCAATTTCTATCTATCTATCAATATCAACAAGCTTTT 1860
Qy 1861 CACGAAATTCATGCAAGTGAATCCCAAGGTAACCTTTATCCATTTTCATGGTGAATGC 1920
Db 1861 CACGAAATTCATGCAAGTGAATCCCAAGGTAACCTTTATCCATTTTCATGGTGAATGC 1920
Qy 1921 GCTTGAATTTTGGCAATCATCTGCTGCTATATCAACTTTGAGATGTTGCTGCC 1980
Db 1921 GCTTGAATTTTGGCAATCATCTGCTGCTATATCAACTTTGAGATGTTGTTGCC 1980
Qy 1981 TTGTAGTTAATTTGAAGAAATAGGGCACTTTGTGAGCCACTTAAAGGCTCATCTGCC 2040
Db 1981 TTGTAGTTAATTTGAAGAAATAGGGCACTTTGTGAGCCACTTAAAGGCTCATCTGCC 2040
Qy 2041 AATTAAGATTTTACAAAGAGCTACTCAGAGCCAGTTGTTAAGAGCTGTGTGTGTGT 2100
Db 2041 AATTAAGATTTTACAAAGAGCTACTCAGAGCCAGTTGTTAAGAGCTGTGTGTGTGT 2100
Qy 2101 GTGTGTGTGTGAGTGTACATGCCAAAGTGTGCTGTCTGTGAGCCCATTTATTTCAAGC 2160
Db 2101 GTGTGTGTGTGAGTGTACATGCCAAAGTGTGCTGTCTGTGAGCCCATTTATTTCAAGC 2160
Qy 2161 TTTAAACAGAGCATTTTCAAAATGGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 2220
Db 2161 TTTAAACAGAGCATTTTCAAAATGGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 2220
Qy 2221 CTCTATTTTCTCCAGTAAATGTGATTAATATGCTATCTGTTAAACATTAAGTTTGCAC 2280
Db 2221 CTCTATTTTCTCCAGTAAATGTGATTAATATGCTATCTGTTAAACATTAAGTTTGCAC 2280
Qy 2281 TTCAAAAGAGAGCTGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 2340
Db 2281 TTCAAAAGAGAGCTGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 2340
Qy 2341 GCTACACAGCTGTGACATATATTTGTTAGAAAGCAGCTGTGAGGTTCTCTTAAAGC 2400
Db 2341 GCTACACAGCTGTGACATATATTTGTTAGAAAGCAGCTGTGAGGTTCTCTTAAAGC 2400
Qy 2401 AAAATCTGATATAGTCTCAGTGGGCTGTGCTATCAGGCGGTTTGAGAAATATTTCAA 2460
Db 2401 AAAATCTGATATAGTCTCAGTGGGCTGTGCTATCAGGCGGTTTGAGAAATATTTCAA 2460
Qy 2461 TTTTCACAGAGAGAGCAATTTGAATTCCTCATCTTTAGGAATCAATTTTCCAGGTTTG 2520
Db 2461 TTTTCACAGAGAGAGCAATTTGAATTCCTCATCTTTAGGAATCAATTTTCCAGGTTTG 2520
Qy 2521 GAGAGATTCAGACAGCTCAGGTCCTTTCAGTAATGTCTGTAACCTTCTGCTCTTTG 2580
Db 2521 GAGAGATTCAGACAGCTCAGGTCCTTTCAGTAATGTCTGTAACCTTCTGCTCTTTG 2580
Qy 2581 TGTTCATGATATAGTCCAAATTAATGTATCTTGAACGATGCTCATAGAGAGATA 2640
Db 2581 TGTTCATGATATAGTCCAAATTAATGTATCTTGAACGATGCTCATAGAGAGATA 2640
Qy 2641 TAAAGATTCAGATATCAACATTTAGGATTTCAAGAAATATTTAGATTTAAGCTTACA 2700
Db 2641 TAAAGATTCAGATATCAACATTTAGGATTTCAAGAAATATTTAGATTTAAGCTTACA 2700
Qy 2701 CTGTGCTAAAAGAAACAAGATACAAAGACTGTGAGCTGTGATGCTCCCATCTCTGTA 2760
Db 2701 CTGTGCTAAAAGAAACAAGATACAAAGACTGTGAGCTGTGATGCTCCCATCTCTGTA 2760
Qy 2761 GGCACAAACCAAG 2820
Db 2761 GGCACAAACCAAG 2820
Qy 2821 TCATGATGATATCTCTATTTATGATGCTAGCTTTGGGCAATCTGTGCTCTCTCTT 2880
Db 2821 TCATGATGATATCTCTATTTATGATGCTAGCTTTGGGCAATCTGTGCTCTCTCTT 2880

Qy 2881 GACACATATTAAGCTTTCAGCTTTGCTTCCAGAGCTTTTATCTTTTCCAAACATGCG 2940
Db 2881 GACACATATTAAGCTTTCAGCTTTGCTTCCAGAGCTTTTATCTTTTCCAAACATGCG 2940
Qy 2941 TTACCAATCT 3000
Db 2941 TTACCAATCT 3000
Qy 3001 CAAGCTTTCT 3036
Db 3001 CAAGCTTTCT 3036

RESULT 5
AX267716
LOCUS AX267716 690 bp DNA linear PAT 26-OCT-2001
DEFINITION Sequence 690 from Patent WO0173032.
ACCESSION AX267716
VERSION AX267716.1 GI:16516388
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1
Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y.,
Kalos,M.D., Fanger,G.R., Retter,M.W., Stolk,J.A., Day,C.H.,
Vedvick,T.S., Carter,D., Li,S.X., Wang,A., Skeiky,Y.A., Hepler,W.T.,
and Henderson,R.A.
Compositions and methods for the therapy and diagnosis of prostate
cancer
Patent: WO 0173032-A 690 04-OCT-2001;
JOURNAL CORIXA CORPORATION (US)
FEATURES
SOURCE 1. 3923
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
BASE COUNT 1157 a 840 c 740 g 1186 t
ORIGIN

Query Match 84.8%; Score 3036; DB 6; Length 3923;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3036; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ACAGAAATAATAGCAAGTGGCGAGAGAGCTGGCAGCAAGAAACAGAGGAGATTTGCT 60
Db 1 ACAGAAATAATAGCAAGTGGCGAGAGAGCTGGCAGCAAGAAACAGAGGAGATTTGCT 60
Qy 61 GCGTGCAGCGAGGAGAGACAGAGAAATCTGCATGTGTGGAGAGACCTGATGATACAGAG 120
Db 61 GCGTGCAGCGAGGAGAGACAGAGAAATCTGCATGTGTGGAGAGACCTGATGATACAGAG 120
Qy 121 GAATTACACACATATATCTTATGTTTCAATGAACACCAAGATTAATAGTGAAGACTTA 180
Db 121 GAATTACACACATATATCTTATGTTTCAATGAACACCAAGATTAATAGTGAAGACTTA 180
Qy 181 GTCCGCTGTGATCTCTCTGATGACAGAGGCTGATCAGATGAGGAGGCTTTGAG 240
Db 181 GTCCGCTGTGATCTCTCTGATGACAGAGGCTGATCAGATGAGGAGGCTTTGAG 240
Qy 241 TACTCAGTGCAGCAAGAAAGACTTACAGATCTCAATGTCAGAGGGTGAGAAATTAAGAAA 300
Db 241 TACTCAGTGCAGCAAGAAAGACTTACAGATCTCAATGTCAGAGGGTGAGAAATTAAGAAA 300
Qy 301 GCGTGTGATCTTACATCTGAGGCGACACATCTGCTGAATAGAGATTAATTAACATCAC 360
Db 301 GCGTGTGATCTTACATCTGAGGCGACACATCTGCTGAATAGAGATTAATTAACATCAC 360
Qy 361 TAGAAACAGCAAGATGACATATTAATGTTAAGTGAAGATGTTTGGACATTTCCAG 420
Db 361 TAGAAACAGCAAGATGACATATTAATGTTAAGTGAAGATGTTTGGACATTTCCAG 420

QY	421	CCCTTTAAATATTCACACACACAGAACACAAAGGAGACAGATCCCTGGAGA	480
Db	421	CCCTTTAAATATTCACACACACAGGAAAGACAAAGAGACATCCCTGGGAGA	480
QY	481	AATGCCGGCGGCATCTTGGGTCATGAGCTGCGCCTGGCGCGCGCTGT	540
Db	481	AATGCCGGCGGCATCTTGGGTCATGATGAGCCTGCGCCTGGCGCGCGCTGT	540
QY	541	GAGGGAAGGACATTAGAAAAATGAAATGATGTGTTCTTAAAGATGGGCAAGAAACAGA	600
Db	541	GAGGGAAGGACATTAGAAAAATGAAATGATGTGTTCTTAAAGATGGGCAAGAAACAGA	600
QY	601	TCTGTGTGTGATATTTATTTGAAACGGGATTACAGATTTGAATGAAGTACAAAGTGAG	660
Db	601	TCTGTGTGTGATATTTATTTGAAACGGGATTACAGATTTGAATGAAGTACAAAGTGAG	660
QY	661	CATTACCAATGAGAGAAAAACAGACGAGAAATTTGATGGCTTCACACAGCATGCACA	720
Db	661	CATTACCAATGAGAGAAAAACAGACGAGAAATTTGATGGCTTCACACAGCATGCACA	720
QY	721	AACAAAATGGAATCTGTGATGACATGAGCAGCCAGCTGGGGAGAGATAACACGGG	780
Db	721	AACAAAATGGAATCTGTGATGACATGAGGAGCCAGCTGGGGAGAGATAACACGGG	780
QY	781	GCAGAGGCTGAGATTTGCGCCCTGCGCTAAACTGTCGCTTATFACCAAAATCATTTT	840
Db	781	GCAGAGGCTGAGATTTGCGCCCTGCGCTAAACTGTCGCTTATFACCAAAATCATTTT	840
QY	841	ATATTTCTTAAACCTCAAAACAAAGCTGTGTAATATGTGATCTGTACGGTTCCTTGGG	900
Db	841	ATATTTCTTAAACCTCAAAACAAAGCTGTGTAATATGTGATCTGTACGGTTCCTTGGG	900
QY	901	CCCAACATTCCTCATATATCAGCAGACATCTTAAATTTAGTTCCAGATCTGTA	960
Db	901	CCCAACATTCCTCATATATCAGCAGACATCTTAAATTTAGTTCCAGATCTGTA	960
QY	961	CTGTGACCTTCTCACTGTAGAAATTAACATTTACTCATTTGTTCAAGACCTTCGTTT	1020
Db	961	CTGTGACCTTCTCACTGTAGAAATTAACATTTACTCATTTGTTCAAGACCTTCGTTT	1020
QY	1021	GTGTCTTAATATGATGACTGTTTTTCTTAAGAGTGTTCGGCCAGGGATCTGTG	1080
Db	1021	GTGTCTTAATATGATGACTGTTTTTCTTAAGAGTGTTCGGCCAGGGATCTGTG	1080
QY	1081	AACAGGCTGGGAACCATCTCAAGATCTTTCACAGGTTATCTTCTGTGACACACAGCATGA	1140
Db	1081	AACAGGCTGGGAACCATCTCAAGATCTTTCACAGGTTATCTTCTGTGACACACAGCATGA	1140
QY	1141	TCATTTACGGAGTAATATCTAATCAACATCATCTCAGTGTCTTGGCCATCTGAAT	1200
Db	1141	TCATTTACGGAGTAATATCTAATCAACATCATCTCAGTGTCTTGGCCATCTGAAT	1200
QY	1201	TCATTTCCCACTTTTGTGCCATCTCTCAAGACCTCAAAATGTCAATTCATTAATATACA	1260
Db	1201	TCATTTCCCACTTTTGTGCCATCTCTCAAGACCTCAAAATGTCAATTCATTAATATACA	1260
QY	1261	GGATTAACTTTTTTTTAAACCTGGAAGAAATTCATGTACATCAGCATAGGGAATTTA	1320
Db	1261	GGATTAACTTTTTTTTAAACCTGGAAGAAATTCATGTACATCAGCATAGGGAATTTA	1320
QY	1321	ATTACATATTTTGTTTTCCAGTGCAGAAATGACTAAGTCCTTTATCCCTCCCTTGT	1380
Db	1321	ATTACATATTTTGTTTTCCAGTGCAGAAATGACTAAGTCCTTTATCCCTCCCTTGT	1380
QY	1381	GATTTTTTTTCCAGTATAAAGTTAAATGCTTACCTGTACATGAGGCTGTATACAGAC	1440
Db	1381	GATTTTTTTTCCAGTATAAAGTTAAATGCTTACCTGTACATGAGGCTGTATACAGAC	1440
QY	1441	AGCCTCTCCCATCCCTCAGCCCTTATCTGTCAATCAGCATCAACCCCTCCCATCACT	1500
Db	1441	AGCCTCTCCCATCCCTCAGCCCTTATCTGTCAATCAGCATCAACCCCTCCCATCACT	1500

OY	1501	AAACAAATCTAACTTGTGAATTCCTTGAACATGTCAGACATACATTATTCCTTGCCCT	1560
Db	1501	AAACAAATCTAACTTGTGAATTCCTTGAACATGTCAGACATACATTATTCCTTGCCCT	1560
OY	1561	GAGAAAGCTCCCTGCTGCTCTTAATGTAGAAATGATGTAAAGTTTGAAATGAGTGA	1620
Db	1561	GAGAAAGCTCCCTGCTGCTCTTAATGTAGAAATGATGTAAAGTTTGAAATGAGTGA	1620
OY	1621	TCTTACTTTCATGCAAGAGGAGACACATATAGATTCATCTCATGAGACAGACAATA	1680
Db	1621	TCTTACTTTCATGCAAGAGGAGACACATATAGATTCATCTCATGAGACAGACAATA	1680
OY	1681	CTAAAGGTATATTTGATTATAGAGTTTACATTAATATATATAGAAATGCAAGAGCCACAGA	1740
Db	1681	CTAAAGGTATATTTGATTATAGAGTTTACATTAATATATATAGAAATGCAAGAGCCACAGA	1740
OY	1741	GGGAATGTTTATGGGGGCACTTTGTAAAGCTGGGATGTGAAGCAAGAGGAGAACTCA	1800
Db	1741	GGGAATGTTTATGGGGGCACTTTGTAAAGCTGGGATGTGAAGCAAGAGGAGAACTCA	1800
OY	1801	TAGATATCTTATATATATATCTTCAATTCCTATGCTATCATCAATATTCACAAGCTTTT	1860
Db	1801	TAGATATCTTATATATATATCTTCAATTCCTATGCTATCATCAATATTCACAAGCTTTT	1860
OY	1861	CACAGAAATTCAGCAGTCGCAAAATCCCAAGAGTAACCTTATATCCATTTTCATGTGATGC	1920
Db	1861	CACAGAAATTCAGCAGTCGCAAAATCCCAAGAGTAACCTTATATCCATTTTCATGTGATGC	1920
OY	1921	GCTTACGAATTTGGCAAAATCATCTGGTCACTTATCCAACTTGTGAGATGTGTTGCC	1980
Db	1921	GCTTACGAATTTGGCAAAATCATCTGGTCACTTATCCAACTTGTGAGATGTGTTGCC	1980
OY	1981	TTGTAGTTAAATTTGAAGAAATAGGGGCACTCTTGAGCCACACTTAAAGGTTTCACCTGCGC	2040
Db	1981	TTGTAGTTAAATTTGAAGAAATAGGGGCACTCTTGAGCCACACTTAAAGGTTTCACCTGCGC	2040
OY	2041	AATAAAGATTTACAAAGAGCTACTCAGAGCAGTTGTTAAGAGCTCTGTGTGTGTGT	2100
Db	2041	AATAAAGATTTACAAAGAGCTACTCAGAGCAGTTGTTAAGAGCTCTGTGTGTGTGT	2100
OY	2101	GTCGTGTGTAGGTACATGCCAAAGTGTGCCCTCTCTCTTGAACCATTAATTTTCAGAC	2160
Db	2101	GTCGTGTGTAGGTACATGCCAAAGTGTGCCCTCTCTCTTGAACCATTAATTTTCAGAC	2160
OY	2161	TTAAACACAGATGTTTTCAATAGGACATAGACTGTGCAAATGTAGTATCCACCACTAT	2220
Db	2161	TTAAACACAGATGTTTTCAATAGGACATAGACTGTGCAAATGTAGTATCCACCACTAT	2220
OY	2221	CTCATTTATTCGCCAGTAATGTGATTAATATGTATGTATGTCATGCTTAACATAAAAAATTTGAC	2280
Db	2221	CTCATTTATTCGCCAGTAATGTGATTAATATGTATGTATGTCATGCTTAACATAAAAAATTTGAC	2280
OY	2281	TTCACAAAAGCAGCTGGAATATGACAAACACAAATATGATTAATCTAACTCCACATCA	2340
Db	2281	TTCACAAAAGCAGCTGGAATATGACAAACACAAATATGATTAATCTAACTCCACATCA	2340
OY	2341	GCTACACACGCTGTACATATATGTGTAAAGCAACCTGCACTTGTGGTGTCTCTTAAGC	2400
Db	2341	GCTACACACGCTGTACATATATGTGTAAAGCAACCTGCACTTGTGGTGTCTCTTAAGC	2400
OY	2401	AAATATCTTGCATTAGGTCACGTGGGGCTGTGCATCAGCGGTTTTGAGAAATATTCAA	2460
Db	2401	AAATATCTTGCATTAGGTCACGTGGGGCTGTGCATCAGCGGTTTTGAGAAATATTCAA	2460
OY	2461	TTCTCAGCAGAGCCAGATTTGAATTCCTCATCTTTTAGGAATCATTTTACAGGTTTTG	2520
Db	2461	TTCTCAGCAGAGCCAGATTTGAATTCCTCATCTTTTAGGAATCATTTTACAGGTTTTG	2520
OY	2521	GAGAGAAATTCAGACAGCTCAGCTGCTTCACTATATGTCTCTGAACTCTGTGCCCTCTTG	2580
Db	2521	GAGAGAAATTCAGACAGCTCAGCTGCTTCACTATATGTCTCTGAACTCTGTGCCCTCTTG	2580
OY	2581	TGTTTCATGGAATGTCATAAATATATGTATATCTTTGAACATGATCTCATAGGAGAGATA	2640

|||||
Db 2561 TGTTCATGAGATAGTCCAAATAATATTTATCTTGAAGTGTGATGCTCATAGAGAGATA 2640
OY 2641 TAAGAACTCTGAGTATATCAACATTTAGGATTCAAAGAAATATAGATTTAGCTACA 2700
Db 2641 TAAGAACTCTGAGTATATCAACATTTAGGATTCAAAGAAATATAGATTTAGCTACA 2700
OY 2701 CTGCTCAAAAGAACCAAGATACAAAGACTGTGATCTGATCTGCTCCCATCTCTGTA 2760
Db 2701 CTGCTCAAAAGAACCAAGATACAAAGACTGTGATCTGATCTGCTCCCATCTCTGTA 2760
OY 2761 GCCAACCAACAGAGAGAGACCAAGCATGTCTGATCTCTTAATTCAGAGAACCATG 2820
Db 2761 GCCAACCAACAGAGAGAGACCAAGCATGTCTGATCTCTTAATTCAGAGAACCATG 2820
OY 2821 TCATGAGTTGAATCTCTTATATGATGATGATCTGATCTGATCTGATCTGATCTG 2880
Db 2821 TCATGAGTTGAATCTCTTATATGATGATGATCTGATCTGATCTGATCTGATCTG 2880
OY 2881 GACACATATATGCTTCTAGCTTGTGCTTCCACGACTTTATCTTCTCCAAACATCGC 2940
Db 2881 GACACATATATGCTTCTAGCTTGTGCTTCCACGACTTTATCTTCTCCAAACATCGC 2940
OY 2941 TTACCAATCTCTCTGCTGCTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGT 3000
Db 2941 TTACCAATCTCTCTGCTGCTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGT 3000
OY 3001 CAAGCTTTTCTTCCATCCCAACCACTAATCTGAAT 3036
Db 3001 CAAGCTTTTCTTCCATCCCAACCACTAATCTGAAT 3036
RESULT 6
AF103907 3923 bp mRNA linear PRI 14-AUG-2000
LOCUS Homo sapiens non-coding RNA DD3 sequence.
DEFINITION AF103907
ACCESSION AF103907
VERSION AF103907.1 GI:6165973
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE Bussemaekers,M.J., Van Bokhoven,A., Verhaegh,G.W., Smit,F.P.,
AUTHORS Kattelus,H.F., Schalken,J.A., Debruyne,F.M., Ru,N. and Isaacs,W.B.
DD3: a new prostate-specific gene, highly overexpressed in prostate
TITLE Cancer
JOURNAL Cancer Res. 59 (23), 5975-5979 (1999)
MEDLINE 20072260
PUBMED 10606244
REFERENCE 2 (bases 1 to 3923)
AUTHORS Bussemaekers,M.J.G., Van Bokhoven,A., Verhaegh,G.W., Smit,F.P.,
Kattelus,H.F.M., Schalken,J.A., Debruyne,F.M.J., Ru,N. and
Isaacs,W.B.
TITLE Direct Submission
JOURNAL Submitted (28-OCT-1998) Urology Research Laboratory, University
Hospitaal Nijmegen, P.O. Box 9101, Nijmegen 6500 HB, Netherlands
FEATURES
source
1. .3923
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/chromosome="9"
/map="9q21-q22"
/tissue_type="prostate"
/note="non-coding RNA DD3"
repeat_region
3756..3911
/note="LINE"
/rpt_family="L1"
/rpt_type="dispersed"
polya_site
BASE COUNT 1157 a 840 c 740 g 1186 t

ORIGIN
Query Match 84.8%; Score 3036; DB 9; Length 3923;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3036; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 ACAGAGAAATAGCAAGTCCGAGAGAGTGGCATCAGAAAAACAGAGGGAGATTTGTGT 60
Db 1 ACAGAGAAATAGCAAGTCCGAGAGAGTGGCATCAGAAAAACAGAGGGAGATTTGTGT 60
OY 61 GGCTGACCCGAGAGACACAGAGATCTGATGTTGGAAGACCTGATGATACAGAG 120
Db 61 GGCTGACCCGAGAGACACAGAGATCTGATGTTGGAAGACCTGATGATACAGAG 120
OY 121 GAATTACAAACATTTACTTGTAGTCTTCAATGAACACCAAGTAAATAGTAAGAGCTA 180
Db 121 GAATTACAAACATTTACTTGTAGTCTTCAATGAACACCAAGTAAATAGTAAGAGCTA 180
OY 181 GTCCGCTGTGAGTCTCTCACTGACACAGGGCTGGATCACCATCGACGCACTTCTGAG 240
Db 181 GTCCGCTGTGAGTCTCTCACTGACACAGGGCTGGATCACCATCGACGCACTTCTGAG 240
OY 241 TACTCAGTGCAGCAAGAAAGAACTACACATCTCTCAATGCGAGGGGTAGAAATAGAAA 300
Db 241 TACTCAGTGCAGCAAGAAAGAACTACACATCTCTCAATGCGAGGGGTAGAAATAGAAA 300
OY 301 GGCTGCTGACTTTTACCATCTGAGGCGACACATCTGCTGAATGAGATATTAACATCAC 360
Db 301 GGCTGCTGACTTTTACCATCTGAGGCGACACATCTGCTGAATGAGATATTAACATCAC 360
OY 361 TAGAAACGCAAGATGACAAATATATGTCTAAGTAGACATGTTTTCACATTTCCAG 420
Db 361 TAGAAACGCAAGATGACAAATATATGTCTAAGTAGACATGTTTTCACATTTCCAG 420
OY 421 CCCCTTTAATATTCACACACACAGAGAGCAACAAAAGAGACACAGAGATCCCTGGGAGA 480
Db 421 CCCCTTTAATATTCACACACACAGAGAGCAACAAAAGAGAGACACAGAGATCCCTGGGAGA 480
OY 481 AATGCCGCGCCGATCTTGGGTATGATGATGATGATGATGATGATGATGATGATGATGAT 540
Db 481 AATGCCGCGCCGATCTTGGGTATGATGATGATGATGATGATGATGATGATGATGATGAT 540
OY 541 GAGGAGAGACATTAGAAATGAATGATGATGATGATGATGATGATGATGATGATGATGAT 600
Db 541 GAGGAGAGACATTAGAAATGAATGATGATGATGATGATGATGATGATGATGATGATGAT 600
OY 601 TCCTGTTGTGATATTTATTTTGAACGGGATTAAGATTTGAATGAAGTCAACAAAGTAG 660
Db 601 TCCTGTTGTGATATTTATTTTGAACGGGATTAAGATTTGAATGAAGTCAACAAAGTAG 660
OY 661 CATTACCAATGAGAGGAAACAGACGAGAAATCTTGAATGCTTCACAGACATGACACA 720
Db 661 CATTACCAATGAGAGGAAACAGACGAGAAATCTTGAATGCTTCACAGACATGACACA 720
OY 721 AACCAAAATGCAATCTGTGATGACATGAGGACCAAGCTGGGAGAGATTAACACGGG 780
Db 721 AACCAAAATGCAATCTGTGATGACATGAGGACCAAGCTGGGAGAGATTAACACGGG 780
OY 781 GCAGAGGGTACAGATTTGCGCCCTGCTGCTTAACTGCTTAACTGCTTAACTGCTTAACT 840
Db 781 GCAGAGGGTACAGATTTGCGCCCTGCTGCTTAACTGCTTAACTGCTTAACTGCTTAACT 840
OY 841 ATATTTCTAACCCCTCAAAACAAACGCTGTTGAATATGATCTCTAGCGTTCTTGGG 900
Db 841 ATATTTCTAACCCCTCAAAACAAACGCTGTTGAATATGATCTCTAGCGTTCTTGGG 900
OY 901 CCCAACAATCTCCATATATTCACGACACACTATTTTAAATATTTAGTTCCAGATCTGTA 960
Db 901 CCCAACAATCTCCATATATTCACGACACACTATTTTAAATATTTAGTTCCAGATCTGTA 960
OY 961 CTGTGACCTTTCTACACTGTAGAAATACATTTAGCATTTTGTGTAAGAGCCCTTGCTT 1020
Db 961 CTGTGACCTTTCTACACTGTAGAAATACATTTAGCATTTTGTGTAAGAGCCCTTGCTT 1020

ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
AUTHORS	1 (bases 1 to 5435) Bussemakers,M.J., Van Bokhoven,A., Verhaegh,G.W., Smit,F.P., Karthaus,H.F.M., Schalken,J.A., Debruyne,F.M., Ru,N. and Isaacs,W.B.
TITLE	DD3: a new prostate-specific gene, highly overexpressed in prostate cancer
JOURNAL	Cancer Res. 59 (23), 5975-5979 (1999)
MEDLINE	20072260
PUBMED	10606244
REFERENCE	2 (bases 1 to 5435) Bussemakers,M.J.G., Van Bokhoven,A., Verhaegh,G.W., Smit,F.P., Karthaus,H.F.M., Schalken,J.A., Debruyne,F.M., Ru,N. and Isaacs,W.B.
JOURNAL	Direct Submission
FEATURES	Submitted (28-OCT-1998) Urology Research Laboratory, University Hospital Nijmegen, P.O. Box 9101, Nijmegen 6500 HB, Netherlands
Source	Location/Qualifiers 1..5435 /organism="Homo sapiens" /mol_type="genomic DNA" /db_xref="taxon:9606" /chromosome="9" /map="9q21-q22" 1..78 /rpt_family="Alu" /rpt_type-dispersed 533..697 /note="alternative exon present in 5% of cDNA clones" /number=2 1035..1294 /rpt_family="Alu" /rpt_type-dispersed join(1571..1753,1981..5435) /product="non-coding RNA DD3" /note="transcript II1" join(1571..1753,1981..3579) /product="non-coding RNA DD3" /note="transcript (major) II" join(1571..1753,1981..2517) /product="non-coding RNA DD3" /note="transcript I" 1571..1753 /number=3 1981..5435 /number=4 2495..2499 /note="transcript I" 2517 /note="transcript I" 3553..3558 /note="transcript (major) II" 3579 /note="transcript (major) II" 5268..5423 /note="LINE" /rpt_family="L1" /rpt_type-dispersed 5435 /note="transcript III" BASE COUNT 1546 a 1188 c 1036 g 1654 t 11 others ORIGIN
Query Match	71.7%: Score 2570; DB 9; Length 5435;
Best Local Similarity	100.0%: Freq. No. 0;
Matches 2570; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
467	AGATCCCTGGGAGAAATGTCGGCGGCATCTTGGTGCATGAGAGACCTGCGCCCTGTC
1979	AGATCCCTGGGAGAAATGTCGGCGGCATCTTGGTGCATGAGAGACCTGCGCCCTGTC
527	CTGGTCCCGCTTGTAGGAGGAGACATTAGAAAATGATGATGATGTTCTTAAAGGATG

D	b			2039	CTGGTCCGGCTTGTGAGGGAAGACATTAGAAATGAATTGATGTGTTCTTTAAAGATG	2098
Q	y			587	GGCAGGAAAAAGATCCTGTGTGTGGATATTTATTTGAACGGGATTTACAGATTTGAAATGA	646
D	b			2099	GGCAGGAAAAAGATCCTGTGTGTGGATATTTATTTGAACGGGATTTACAGATTTGAAATGA	2158
Q	y			647	AGTCAAAAGTGGAGATTACCAATGAGAGAAAAAGACGCGAAATCTTGATGGCTTCA	706
D	b			2139	AGTCAAAAGTGGAGATTACCAATGAGAGAAAAAGACGCGAAATCTTGATGGCTTCA	2218
Q	y			707	CAAGACATGCAACAAACAAATGGAATCTGTGATGACATGAGGACGCCAAGCTGGGAG	766
D	b			2219	CAAGACATGCAACAAACAAATGGAATCTGTGATGACATGAGGACGCCAAGCTGGGAG	2278
Q	y			767	GAGATAACCAAGGGGCACAGGGTCAAGATCTGTGGCCCGTGGCCCTAAACGTGGCTCAT	826
D	b			2279	GAGATAACCAAGGGGCACAGGGTCAAGATCTGTGGCCCGTGGCCCTAAACGTGGCTCAT	2338
Q	y			837	AACCAATCATTTTCATTTCTTAACCCCTCAACAAACAAAGCTGTGTAATATGATCTCTA	886
D	b			2339	AACCAATCATTTTCATTTCTTAACCCCTCAACAAACAAAGCTGTGTAATATGATCTCTA	2398
Q	y			887	CGGTTCTCTTGGGGCCCAACATTTCCATATATCCAGCCACATCTATTTTAAATATTAAG	946
D	b			2399	CGGTTCTCTTGGGGCCCAACATTTCCATATATCCAGCCACATCTATTTTAAATATTAAG	2458
Q	y			947	TTCCAGATCTGTACTGTGACCTTTCACATCTGATAGAAATACATTAACATATTTGTGCA	1006
D	b			2459	TTCCAGATCTGTACTGTGACCTTTCACATCTGATAGAAATACATTAACATATTTGTGCA	2518
Q	y			1007	AGACCTTCTGTGTGTGCTCTAATATGTAGCTGACTGTTTTTCTTAAGAGATGTTCTGGC	1066
D	b			2519	AGACCTTCTGTGTGTGCTCTAATATGTAGCTGACTGTTTTTCTTAAGAGATGTTCTGGC	2578
Q	y			1067	CCAGGGGATCTGTGAACAGGCTGGGAACATCTCAAGCTCTTCCAGGGTAAATCTACT	1126
D	b			2579	CCAGGGGATCTGTGAACAGGCTGGGAACATCTCAAGCTCTTCCAGGGTAAATCTACT	2638
Q	y			1127	AGCACACAGCATGATCATTACGGAGTGAATATCTTAATCAACATCATCTCAGTGTCTT	1186
D	b			2639	AGCACACAGCATGATCATTACGGAGTGAATATCTTAATCAACATCATCTCAGTGTCTT	2698
Q	y			1187	GCCCATACTGAAATTTCAATTTCCCACTTTTGCGCCATTTCTCAGACTCAAAATGTCAAT	1246
D	b			2699	GCCCATACTGAAATTTCAATTTCCCACTTTTGCGCCATTTCTCAGACTCAAAATGTCAAT	2758
Q	y			1247	CCATTAAATATACAGATTAACCTTTTTTTTAACTCGGAAGATTTCAATGTTACATGCA	1306
D	b			2759	CCATTAAATATACAGATTAACCTTTTTTTTAACTCGGAAGATTTCAATGTTACATGCA	2818
Q	y			1307	GCTATAGGGAATTAATTACATATTTTGTTCACAGTSCAAAGATGACTAAGTCTTATTC	1366
D	b			2819	GCTATAGGGAATTAATTACATATTTTGTTCACAGTSCAAAGATGACTAAGTCTTATTC	2878
Q	y			1367	CCGCCCTTGTGTGATTTTTTTTCCAGTATAAAGTTAAATGCTTAGCCTGTACTGAG	1426
D	b			2879	CCGCCCTTGTGTGATTTTTTTTCCAGTATAAAGTTAAATGCTTAGCCTGTACTGAG	2938
Q	y			1427	GCTGTATACAGACAGGCTCTCCCAATCCCTCCAGGCTATATCTCTCATACACATCAACC	1486
D	b			2939	GCTGTATACAGACAGGCTCTCCCAATCCCTCCAGGCTATATCTCTCATACACATCAACC	2998
Q	y			1487	CTCCCATACACACTAAACAAATATCTTAATCTGTAAATCTTGAACATGTACAGACATACAT	1546
D	b			2999	CTCCCATACACACTAAACAAATATCTTAATCTGTAAATCTTGAACATGTACAGACATACAT	3058
Q	y			1547	TATTCCTTTCGCCGAGAAGCTCTCTGTCTCTTAAATCTTGAAATGATGTAAGTTTTT	1606
D	b			3059	TATTCCTTTCGCCGAGAAGCTCTCTGTCTCTTAAATCTTGAAATGATGTAAGTTTTT	3118
Q	y			1607	GAATTAAGTGAATCTTCTTACTTCATCTGCAAGAAGGAGACATATGAAATTCATCATACCA	1666

[illegible]

OY	2747	CCCCATCTCTGTGAGCCACAAACACAGCAGAGACCACGATCTCTGAGATCTCTTAAT	2806
Db	4259	CCCCATCTCTGTGAGCCACAAACACAGCAGGACCACGACGATCTCTGAGATCTCTTAAT	4318
OY	2807	CAAGGAACACGATCTCAATGAGTTGAATTCTCTTATATGAGATGCTACTCTCTGGCCATCT	2865
Db	4319	CAAGGAACACGATCTCAATGAGTTGAATTCTCTTATATGAGATGCTACTCTCTGGCCATCT	4378
OY	2867	CTGGCTCTCTCTTGCACACATATTAGCTTTAGCCTTTGCTTCCAGACATTTTATCTTTT	2926
Db	4379	CTGGCTCTCTCTTGCACACATATTAGCTTTAGCCTTTGCTTCCAGACATTTTATCTTTT	4438
OY	2927	CTCCAAACATACGTTACCAATCTCTCTGCTCTGTGCTCTTGCATTTGGACTTCCCCACAGA	2986
Db	4439	CTCCAAACATACGTTACCAATCTCTCTGCTCTGTGCTCTTGGACTTCCCCACAGA	4498
OY	2987	ATTTCGAACGACTCGAAGTCTTTTCTTCACATCCCCACCACTAAGCTTAAT	3036
Db	4499	ATTTCGAACGACTCGAAGTCTTTTCTTCACATCCCCACCACTAAGCTTAAT	4548

[illegible]

203 GACACAGGCTGGATCACCATCGACGGCATCTTCTGACTACTGACGACCAAGAAAGA 262
181 GACACAGGCTGGATCACCATCGACGGCATCTTCTGACTACTGACGACCAAGAAAGA 240
263 CTACAGACATCTCATAGGAGGAGGAGAAATAGAAAGGCTGGAGACTTTACCTCTGA 322
241 CTACAGACATCTCATAGGAGGAGGAGAAATAGAAAGGCTGGAGACTTTACCTCTGA 300
323 GGCACACATCTGCTGAAGTGGAGATTAATTAACATCACTAGAAACAGCAAGATGACATA 382
301 GGCACACATCTGCTGAAGTGGAGATTAATTAACATCACTAGAAACAGCAAGATGACATA 360
383 TAAATCTAAGTAACTGACATGTTTGTGACATTTTCAGACCCCTTTAAATATCCACACA 442
361 TAAATCTAAGTAACTGACATGTTTGTGACATTTTCAGACCCCTTTAAATATCCACACA 420
443 CAGAGACCAAAAGGAAGACAGAGATCCCTGGAGAAATGCCCGGCGGCATCTTGG 502
421 CAGAGACCAAAAGGAAGACAGAGATCCCTGGAGAAATGCCCGGCGGCATCTTGG 480
503 TCATCGATGAGCTCGCCCTGCTGCTGCCCTTGTGAGGAAAGACATTAAGAAATG 562
481 TCATCGATGAGCTCGCCCTGCTGCTGCCCTTGTGAGGAAAGACATTAAGAAATG 540
563 AATGATGTGTCTCTTAAGGATGGGAGAAACAGATCTGTTGTGATTTATTTG 622
541 AATGATGTGTCTCTTAAGGATGGGAGAAACAGATCTGTTGTGATTTATTTG 600
623 AACGGATTACAGATTTGAATGAAGTCACAAAGTGACATTTACCAATGAGAGAAACA 682
601 AACGGATTACAGATTTGAATGAAGTCACAAAGTGACATTTACCAATGAGAGAAACA 660
683 GACGAGAAATCTTGATGGCTTCAAGACATGCAACAAACAAATGGAAATCTGTATG 742
661 GACGAGAAATCTTGATGGCTTCAAGACATGCAACAAACAAATGGAAATCTGTATG 720
743 ACATGAGGACCCAGAGCTGGGAGAGATTAACCAAGGGGCGAGAGGTGAGATTTGGCC 802
721 ACATGAGGACCCAGAGCTGGGAGAGATTAACCAAGGGGCGAGAGGTGAGATTTGGCC 780
803 CTGCTGCTTAACAGTGGCTTCATTAACCAATTCATTTCTTAACCTTCAAAACAA 862
781 CTGCTGCTTAACAGTGGCTTCATTAACCAATTCATTTCTTAACCTTCAAAACAA 840
863 AGCTGTGTAATATCTGATCTCTACGGTTCCTTGGGCCCAACATTCCTCATATATCA 922
841 AGCTGTGTAATATCTGATCTCTACGGTTCCTTGGGCCCAACATTCCTCATATATCA 900
923 GCCACATCATTTTATATTTAGTCCAGATCTGTAATGTGACCTTTTACACTGTAG 982
901 GCCACATCATTTTATATTTAGTCCAGATCTGTAATGTGACCTTTTACACTGTAG 960
983 AATACATTTACTCTTTTGTCAAGACCCCTTCTGTTGCTGCTTAATATGACTGACT 1042
961 AATACATTTACTCTTTTGTCAAGACCCCTTCTGTTGCTGCTTAATATGACTGACT 1020
1043 GTTTTCTTAAGAGTGTCTGGCCAGGGATCTGTGAACAGGCTGGGAACATCTCAA 1102
1021 GTTTTCTTAAGAGTGTCTGGCCAGGGATCTGTGAACAGGCTGGGAACATCTCAA 1080
1103 GATCTTCCAGGGTTATCTACTAGACACAGATGATCATTTACGAGATTAATATCTA 1162
1081 GATCTTCCAGGGTTATCTACTAGACACAGATGATCATTTACGAGATTAATATCTA 1140
1163 ATCAACATCATCTCAGTGTCTTGGCCATCTGAATTCCTTTCCACTTTTGGCCA 1222
1141 ATCAACATCATCTCAGTGTCTTGGCCATCTGAATTCCTTTCCACTTTTGGCCA 1200
1223 TTCTCAGACCTCAAAATGTCATTCATTAATATCAGAGATTAATTTTAACT 1282
1201 TTCTCAGACCTCAAAATGTCATTCATTAATATCAGAGATTAATTTTAACT 1260
1283 TGGAGAAATTCATGTTTCAATGCAAGCTATGGGAATTAATTTTGTTTCCAGT 1342

1261 TGGAGAAATTCATGTTTCAATGCAAGCTATGGGAATTAATTTTGTTTCCAGT 1320
1343 GCAAGATGACATTAATCTTATATCCCTCCCTTGTGATTTTTCAGATTAAGT 1402
1321 GCAAGATGACATTAATCTTATATCCCTCCCTTGTGATTTTTCAGATTAAGT 1380
1403 TAAATGCTTAGCCCTTGTACTGAGGCTGATACAGACAGGCTCCCATCCCTCAGC 1462
1381 TAAATGCTTAGCCCTTGTACTGAGGCTGATACAGACAGGCTCCCATCCCTCAGC 1440
1463 CTATCTGTCATACATCAACCCCTCCCATACACCTTAACCAAAATCTAATTTAAT 1522
1441 CTATCTGTCATACATCAACCCCTCCCATACACCTTAACCAAAATCTAATTTAAT 1500
1523 CTTGAACATGTCAGGACATCATTAATTCCTTGTGCGGAGAGGCTCTGCTCTCT 1582
1501 CTTGAACATGTCAGGACATCATTAATTCCTTGTGCGGAGAGGCTCTGCTCTCT 1560
1583 AATCTAGATGATTAAGTGTGATTAAGTGAATAGTCACTTCTTACTTCATGCAAGAGG 1642
1561 AATCTAGATGATTAAGTGTGATTAAGTGAATAGTCACTTCTTACTTCATGCAAGAGG 1620
1643 ACATATGATGATTCATCATCATGAGACAGCAAAATCTAAGTGAATTTGATTA 1702
1621 ACATATGATGATTCATCATCATGAGACAGCAAAATCTAAGTGAATTTGATTA 1680
1703 AGAGTTGATTAATATATATGAATGCAAGACCCAGAGGGAATGTTATGGGACGCT 1762
1681 AGAGTTGATTAATATATATGAATGCAAGACCCAGAGGGAATGTTATGGGACGCT 1740
1763 TGTAAAGCTGGATGTGAAGCAAGGAGGAGACCTCATAGTATCTTATATATATCT 1822
1741 TGTAAAGCTGGATGTGAAGCAAGGAGGAGACCTCATAGTATCTTATATATATCT 1800
1823 CATTTCTATCTATATACATATCAACAGCTTTTACAGAAATTCATGACGACAA 1882
1801 CATTTCTATCTATATACATATCAACAGCTTTTACAGAAATTCATGACGACAA 1860
1883 TCCCAAAAGGTAACTTATCATTTGATGATGAGTGGCTTTGAATTTTGGCAATCA 1942
1861 TCCCAAAAGGTAACTTATCATTTGATGATGAGTGGCTTTGAATTTTGGCAATCA 1920
1943 TACTGTCACTTATCTCAACTTGAATGATGTTGTCTCTTGTAGTTAATGAAAGATA 2002
1921 TACTGTCACTTATCTCAACTTGAATGATGTTGTCTCTTGTAGTTAATGAAAGATA 1980
2003 GGCACATCTTGTGAGCCACTTTAGGTTCACTCCTGGCAATTAAGATTTCAAGA 2059
1981 GGCACATCTTGTGAGCCACTTTAGGTTCACTCCTGGCAATTAAGATTTCAAGA 2037

RESULT 9
BD082483
LOCUS BD082483 1872 bp DNA linear PAT 27-AUG-2002
DEFINITION PCA3, PCA3 genes, and methods of use.
ACCESSION BD082483
VERSION BD082483.1 GI:22628093
KEYWORDS JP 2001522240-A/2.
SOURCE Mastadenovirus
ORGANISM Mastadenovirus
REFERENCE 1 (bases 1 to 1872)
AUTHORS Bussemakers M.J.G.
TITLE PCA3, PCA3 genes, and methods of use
JOURNAL Patent.: JP 2001522240-A 2 13-NOV-2001;
DIAGNOCURE INC
PN JP 2001522240-A/2
PD 13-NOV-2001
PF 09-APR-1998 JP 1998542194
PR 10-APR-1997 US 60/041836
PI MARION J G BUSSEMAKERS
PC C12N15/00, C12N15/12, C12N5/12, C12N1/21, C07K14/47, C07K16/18, PC

CL1201/68,
PC G01N33/577,A61K39/395,A01K67/027
CC Strandedness: Double;
CC Topology: Linear;
FH key Location/Qualifiers.
FEATURES
source 1..1872
/organism="Mastadenovirus"
/mol_type="genomic DNA"
/db_xref="taxon:10509"
BASE COUNT 567 a 389 c 369 g 539 t 8 others
ORIGIN
Query Match 38.2%; Score 1367; DB 6; Length 1872;
Best local similarity 99.5%; Pred. No. 0;
Matches 1767; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
QY 285 GGTGAGAAATGAAGAGGCTGCTGACTTTACCATCTGAGGCCACACATCTGCTGAATGG 344
DB 98 GGTGAGAAATGAAGAGGCTGCTGACTTTACCATCTGAGGCCACACATCTGCTGAATGG 157
QY 345 AGATATTAACATCTAGAAACAGCAAGATGACATATTAATGTCTAATAGTACATGT 404
DB 158 AGATATTAACATCTAGAAACAGCAAGATGACATATTAATGTCTAATAGTACATGT 217
QY 405 TTTTGACATTTCCAGCCCTTTAAATATCCACACACAGAGAGACAAAAGAACAC 464
DB 218 TTTTGACATTTCCAGCCCTTTAAATATCCACACACAGAGAGACAAAAGAACAC 277
QY 465 AGAGATCCCTGGGAGAAATGCCGGCCGACATCTTGGGTGATGATGAGCCCTGCTGT 524
DB 278 AGAGATCCCTGGGAGAAATGCCGGCCGACATCTTGGGTGATGATGAGCCCTGCTGT 337
QY 525 GCCTGGTCCGCTTGGAGGAGAGACATTAGAAATGAATGATGTCTCTTAAAGA 584
DB 338 GCCTGGTCCGCTTGGAGGAGAGACATTAGAAATGAATGATGTCTCTTAAAGA 397
QY 585 TGGGAGAGAAACAGATCCTGTTGTGATTTTATTTGAACGGGATTTACAGATTTGAAAT 644
DB 398 TGGGAGAGAAACAGATCCTGTTGTGATTTTATTTGAACGGGATTTACAGATTTGAAAT 457
QY 645 GAAGTACAAAGTGAACATTTACCAATGAGAGAGAAACAGAGAAATCTTGATGGCTT 704
DB 458 GAAGTACAAAGTGAACATTTACCAATGAGAGAGAAACAGAGAAATCTTGATGGCTT 517
QY 705 CACAAGACATGCAAAACAAATGAATGATGTGATGATGAGGACCAAGCTGGGG 764
DB 518 CACAAGACATGCAAAACAAATGAATGATGTGATGATGAGGACCAAGCTGGGG 577
QY 765 AGGAGATTAACAGGGGAGAGAGGATCTGGCCCTGCTGCTTAACTGTGGCTT 824
DB 578 AGGAGATTAACAGGGGAGAGAGGATCTGGCCCTGCTGCTTAACTGTGGCTT 637
QY 825 ATAACCAATCATTTCAATTTCTTAACTCTCAAAACAAAGCTGTGTGTAATCTGATCTC 884
DB 638 ATAACCAATCATTTCAATTTCTTAACTCTCAAAACAAAGCTGTGTGTAATCTGATCTC 697
QY 885 TACGGTCTCTTGGGGCCCAACATCTCCATATATCCAGCCACACATCTTTTAATATT 944
DB 698 TACGGTCTCTTGGGGCCCAACATCTCCATATATCCAGCCACACATCTTTTAATATT 757
QY 945 AGTCCAGATCTGATGATGACCTTTACACATGAGAAATACATTAATCTATTCTTTGTC 1004
DB 758 AGTCCAGATCTGATGATGACCTTTACACATGAGAAATACATTAATCTATTCTTTGTC 817
QY 1005 AAGAGCCCTGCTGTGCTGCTTAATATGATGATGATGATGATGATGATGATGATGATG 1064
DB 818 AAGAGCCCTGCTGTGCTGCTTAATATGATGATGATGATGATGATGATGATGATGATG 877
QY 1065 GCCCAGGAGATCTGTGAACAGGCTGGGAGCATCTCAAGATCTTCCAGGTTATATCTTA 1124
DB 878 GCCCAGGAGATCTGTGAACAGGCTGGGAGCATCTCAAGATCTTCCAGGTTATATCTTA 937

QY 1125 CTAGCACACAGCATGATCATTTACGAGTGAATTAATCAACATCATCTCAGTGTCT 1184
DB 938 CTAGCACACAGCATGATCATTTACGAGTGAATTAATCAACATCATCTCAGTGTCT 997
QY 1185 TTGGCCATATCTGAATTCATTTTCCACTTTTGGCCCATCTTCAGACCTCAAAATGTCA 1244
DB 998 TTGGCCATATCTGAATTCATTTTCCACTTTTGGCCCATCTTCAGACCTCAAAATGTCA 1057
QY 1245 TTCCATTAATATCAACAGGATTAATCTTTTAACTTTTAACTTTTAACTTTTAACTTTTAA 1304
DB 1058 TTCCATTAATATCAACAGGATTAATCTTTTAACTTTTAACTTTTAACTTTTAACTTTTAA 1117
QY 1305 CAGCTATGGAATTTAATTAATCATATTTTGTTCAGTCAAGATGATGATGATGATGATGATG 1364
DB 1118 CAGCTATGGAATTTAATTAATCATATTTTGTTCAGTCAAGATGATGATGATGATGATGATG 1177
QY 1365 TCCCTCCCTTTGTTGATTTTTCAGTATTAAGTTAAATGCTTACGCTTGTACG 1424
DB 1178 TCCCTCCCTTTGTTGATTTTTCAGTATTAAGTTAAATGCTTACGCTTGTACG 1237
QY 1425 AGGCTGATTAACAGCAGCCTGCCCATGCCCTCCAGCTTATCTGATCAACATCAAC 1484
DB 1238 AGGCTGATTAACAGCAGCCTGCCCATGCCCTCCAGCTTATCTGATCAACATCAAC 1297
QY 1485 CCTCCCATACACACTTAACAAATCTAATCTTGAATCTTGAACATGTCAGACATAC 1544
DB 1298 CCTCCCATACACACTTAACAAATCTAATCTTGAATCTTGAACATGTCAGACATAC 1357
QY 1545 ATTATTCCTTTCGCTGAGAGAGCTCTTCTGCTTAAATCTAGATGATGATGATGATGATG 1604
DB 1358 ATTATTCCTTTCGCTGAGAGAGCTCTTCTGCTTAAATCTAGATGATGATGATGATGATG 1417
QY 1605 TTGAATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1664
DB 1418 TTGAATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1477
QY 1665 CATGAGACAGCAAACTTAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1724
DB 1478 CATGAGACAGCAAACTTAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1537
QY 1725 ATGCAAGAGCCACAGAGGGAATGTTATGAGGACGTTGTAAAGCTGGGATGTAAGCA 1784
DB 1538 ATGCAAGAGCCACAGAGGGAATGTTATGAGGACGTTGTAAAGCTGGGATGTAAGCA 1597
QY 1785 AAGGCGAGAGACCTCATAGATCTTATTAATTAATTAATTAATTAATTAATTAATTAATTA 1844
DB 1598 AAGGCGAGAGACCTCATAGATCTTATTAATTAATTAATTAATTAATTAATTAATTAATTA 1657
QY 1845 TATCAACAAGCTTTTACAGAAATTCATGCAAGTGCATAATCCCAAGGTAACTTTATCC 1904
DB 1658 TATCAACAAGCTTTTACAGAAATTCATGCAAGTGCATAATCCCAAGGTAACTTTATCC 1717
QY 1905 ATTTCATGTTGAGTGGCTTTTGAATTTTGGCAATCATATCTGCTACTTATATCTCAACT 1964
DB 1718 ATTTCATGTTGAGTGGCTTTTGAATTTTGGCAATCATATCTGCTACTTATATCTCAACT 1777
QY 1965 TGAAGTGTGTTGCTCTTGAATTTTGAAGAAATTAAGGACCTTGTGAGCCACTTT 2024
DB 1778 TGAAGTGTGTTGCTCTTGAATTTTGAAGAAATTAAGGACCTTGTGAGCCACTTT 1837
QY 2025 AGGTTACACTCTGCAATTAAGAAATTAAGAA 2059
DB 1838 AGGTTACACTCTGCAATTAAGAAATTAAGAA 1872

RESULT 10
AR261036 3112 bp DNA linear PAT 29-JAN-2003
LOCUS AR261036
DEFINITION Sequence 468 from patent US 6321716.
ACCESSION AR261036
VERSION AR261036.1 GI:28071799
KEYWORDS
SOURCE Unknown.

ORGANISM Unknown.
REFERENCE Unclassified.
AUTHORS 1 (bases 1 to 3112)
TITLE Mashiki,Z. and Harada,J.
JOURNAL Negative pressure control apparatus for engine mounted in vehicle
Patent: US 6321716-A 468 27-NOV-2001.
FEATURES Location/Qualifiers
source 1. 3112
BASE COUNT 975 a 587 c 624 g 926 t
ORIGIN

Query Match 38.1%; Score 1364; DB 6; Length 3112;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1774; Conservative 0; Mismatches 1; Indels 3; Gaps 3;

QY 285 GGTGAATTAAGAAAGCTGCTGACCTTACCATTGTAGGCCACACATCTGCTGAATGG 344
DB 1313 GGTGAATTAAGAAAGCTGCTGACCTTACCATTGTAGGCCACACATCTGCTGAATGG 1372

QY 345 AGATATTACATCACTAGAAACAGCAAGATGACATATTAATGTCTAGTAGTGCATGT 404
DB 1373 AGATATTACATCACTAGAAACAGCAAGATGACATATTAATGTCTAGTAGTGCATGT 1432

QY 405 TTTTGCACATTTCCAGCCCCCTTTAAATATCCACACACAGAGAGACACAAAAGAACAC 464
DB 1433 TTTTGCACATTTCCAGCCCCCTTTAAATATCCACACACAGAGAGACACAAAAGAACAC 1492

QY 465 AGATATCCCTGGAGAAATGCCGCCGCATCTTGGTCAATCGATGAGCCCTGCCCTGT 524
DB 1493 AGATATCCCTGGAGAAATGCCGCCGCATCTTGGTCAATCGATGAGCCCTGCCCTGT 1552

QY 525 GCTGTGTCCTGCTGAGGAGAGACATTAGAAATGAATGTGTTCTTAAAGCA 584
DB 1553 GCTGTGTCCTGCTGAGGAGAGACATTAGAAATGAATGTGTTCTTAAAGCA 1612

QY 585 TGGGAGGAAACAGATCCCTGTGTGATATTATTTGAAGGGATTACATTTGAAT 644
DB 1613 TGGGAGGAAACAGATCCCTGTGTGATATTATTTGAAGGGATTACATTTGAAT 1672

QY 645 GAACTACAAAGTAGAGATTACCAATGAGAGAAACAGAGAAATCTTGAATGCTT 704
DB 1673 GAACTACAAAGTAGAGATTACCAATGAGAGAAACAGAGAAATCTTGAATGCTT 1732

QY 705 CACACACATGCAACAAACAAATGGAATAGTGTGATGACATGAGGACCCAGCTGGG 764
DB 1733 CACACACATGCAACAAACAAATGGAATAGTGTGATGACATGAGGACCCAGCTGGG 1792

QY 765 AGGATATACACAGGGGACAGGGGTGAGATTTCTGGCCCTGCTTAAATGTGCTTC 824
DB 1793 AGGATATACACAGGGGACAGGGGTGAGATTTCTGGCCCTGCTTAAATGTGCTTC 1852

QY 825 ATAACCAATCATTTCAATTTCTAACCCCTCAAAACAAGCTGTTGAATATGATCTC 884
DB 1853 ATAACCAATCATTTCAATTTCTAACCCCTCAAAACAAGCTGTTGAATATGATCTC 1912

QY 885 TAGGGTTCTTTGCGGCCAACATTTCCATATATCCAGCCACACTATTTTAAATTT 944
DB 1913 TAGGGTTCTTTGCGGCCAACATTTCCATATATCCAGCCACACTATTTTAAATTT 1972

QY 945 AGTTCCAGATCTGTACTGTGACCTTCTACAGTGAATTAATATACATATTTGCTC 1004
DB 1973 AGTTCCAGATCTGTACTGTGACCTTCTACAGTGAATTAATATACATATTTGCTC 2032

QY 1005 AAAGACCTTCGTGTGCTGCTTAATATGTAGTACTGTTTCTTAAGAGAGTCTCG 1064
DB 2033 AAAGACCTTCGTGTGCTGCTTAATATGTAGTACTGTTTCTTAAGAGAGTCTCG 2092

QY 1065 GCCCAGGGGATCTGTGAACAGGCTGGAGACATCTCAAGATCTTTCCAGGGTTACTTA 1124
DB 2093 GCCCAGGGGATCTGTGAACAGGCTGGAGACATCTCAAGATCTTTCCAGGGTTACTTA 2152

QY 1125 CTAGCAACACAGCATTTAGGAGTGAATTTATATCAACATCATCTCTAGTGTCT 1184

DB 2153 CTAGCAACACAGCATTTAGGAGTGAATTTATCTATCAACATCATCTCTAGTGTCT 2212

QY 1185 TTGCCCATACGAATTTCAATTTCCACCTTTGTGGCCATTTCTCAGACCTCAAAATGCA 1244
DB 2213 TTGCCCATACGAATTTCAATTTCCACCTTTGTGGCCATTTCTCAGACCTCAAAATGCA 2272

QY 1245 TTCCATATATACAGAGATTACCTTTTTTTTAACTGGAGAAATCAATGTATACATG 1304
DB 2273 TTCCATATATACAGAGATTACCTTTTTTTTAACTGGAGAAATCAATGTATACATG 2332

QY 1305 CAGCTATGGAATTTAATTTACATATTTGTTTCCAGTGAAGATGATAGTCTTTA 1364
DB 2333 CAGCTATGGAATTTAATTTACATATTTGTTTCCAGTGAAGATGATAGTCTTTA 2392

QY 1365 TCCCTCCCTTTGTTGATTTTTTTTCCAGATATAAGTTAAATGCTTAGCTGTACTG 1424
DB 2393 TCCCTCCCTTTGTTGATTTTTTTTCCAGATATAAGTTAAATGCTTAGCTGTACTG 2452

QY 1425 AGGCTATATACAG-CACAGCCTCCGCCATCCCTCCAGCCTTATCTGTCAACACATCA 1483
DB 2453 AGGCTATATACAGCAGCAGCCTCCCTCCATCCCTCCAGCCTTATCTGTCAACATCA 2512

QY 1484 CCCCCTCCATACACCTTAACAAAATCTAATCTGTAATTTCTTGAACATGTACAGACATA 1543
DB 2513 CCCCCTCCAT-CAACCTTAACAAAATCTAATCTGTAATTTCTTGAACATGTACAG-CA 2570

QY 1544 CATTTATCTCTGCTGAGAGGCTCTCTGCTGCTCTTAATCTAGAAATGATGAAT 1603
DB 2571 CATTTATCTCTGCTGAGAGGCTCTCTGCTGCTCTTAATCTAGAAATGATGAAT 2630

QY 1604 TTTGAATTAAGTTGATCTTACTTCAATGCAAGAGGAGACATATGATGATTCATC 1663
DB 2631 TTTGAATTAAGTTGATCTTACTTCAATGCAAGAGGAGACATATGATGATTCATC 2690

QY 1664 ACATGAGACACAAATACTATAAGTGTATTTGATATTAAGTTTATGATTAATATATGA 1723
DB 2691 ACATGAGACACAAATACTATAAGTGTATTTGATTAAGTTTATGATTAATATATGA 2750

QY 1724 AATGCAAGAGCAGAGAGGAATGTTATGGGACAGTTTAAAGCCTGGAGTGAAGC 1783
DB 2751 AATGCAAGAGCAGAGAGGAATGTTATGGGACAGTTTAAAGCCTGGAGTGAAGC 2810

QY 1784 AAAGCAGGAGACCTCATAGTATCTTATATATATCTTCAATTTCTATCTATCA 1843
DB 2811 AAAGCAGGAGACCTCATAGTATCTTATATATATCTTCAATTTCTATCTATCA 2870

QY 1844 ATATCCAAACAGCTTTTACAGAAATCATGCAAGTGAATCCCAAGGTAACTTTATC 1903
DB 2871 ATATCCAAACAGCTTTTACAGAAATCATGCAAGTGAATCCCAAGGTAACTTTATC 2930

QY 1904 CATTTCAATGAGTGGCTTTTGAATTTTGGCAAAATCATCTGCTATCTCAACT 1963
DB 2931 CATTTCAATGAGTGGCTTTTGAATTTTGGCAAAATCATCTGCTATCTCAACT 2990

QY 1964 TTGAGATGTGTTGCTCTTGTATTAATGAAGAAATAGGGACCTGTTGTAGCCACT 2023
DB 2991 TTGAGATGTGTTGCTCTTGTATTAATGAAGAAATAGGGACCTGTTGTAGCCACT 3050

QY 2024 TAGGGTCACTCCGGAATTAAGATTTTCAAGAGC 2061
DB 3051 TAGGGTCACTCCGGAATTAAGATTTTCAAGAGC 3088

RESULT 11
AR278567
LOCUS AR278567 3112 bp DNA linear PAT 10-Apr-2003
DEFINITION Sequence 468 from patent US 6512094.
ACCESSION AR278567
VERSION AR278567.1 GI:29712813
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

Unclassified.
1 (bases 1 to 3112)
REFERENCE Xu, J., Dillon, D.C., Mitcham, J.L., Harlocker, S.L., Jiang, Y.,
AUTHORS Kalos, M.D., Fanger, G.R., Retter, M.W., Stolk, J.A., Day, C.H.,
Vedler, T.S., Carter, D., Li, S.X., Wang, A., Skelly, K.A.W.,
Hepler, M.T., and Henderson, R.A.
TITLE Compositions and methods for the therapy and diagnosis of prostate
cancer
JOURNAL Patent: US 6512094-A 468 28-JAN-2003;
FEATURES Location/Qualifiers
source 1..3112
BASE COUNT 975 a 587 c 624 g 926 t
ORIGIN
Query Match 38.1%; Score 1364; DB 6; Length 3112;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1774; Conservative 0; Mismatches 1; Indels 3; Gaps 3;
QY 285 GGTGAGAAATAGAAAGCGTGCCTTACATCTGAGGCCACACATCTGTAATGG 344
DB 1313 GGTGAGAAATAGAAAGCGTGCCTTACATCTGAGGCCACACATCTGTAATGG 1372
QY 345 AGATAATTAACATCACTAGAAACAGCAGATGACAAATATATGTCTAAGTAGACATGT 404
DB 1373 AGATAATTAACATCACTAGAAACAGCAGATGACAAATATATGTCTAAGTAGACATGT 1432
QY 405 TTTTGACATTTCCAGCCCTTTAAATATCCACACACAGAGAGACAAAAGAACAC 464
DB 1433 TTTTGACATTTCCAGCCCTTTAAATATCCACACACAGAGAGACAAAAGAACAC 1492
QY 465 AGAGATCCCTGGGAGAAATGCCGGCCGATCTTGGTCATGATGACCTCGCCCTGT 524
DB 1493 AGAGATCCCTGGGAGAAATGCCGGCCGATCTTGGTCATGATGACCTCGCCCTGT 1552
QY 525 GCGTGTCCCGCTTGTGAGGAGAGACATTAAGAAATGATGTGTTCTTAAAGA 584
DB 1553 GCGTGTCCCGCTTGTGAGGAGAGACATTAAGAAATGATGTGTTCTTAAAGA 1612
QY 585 TGGGCGAGAAACAGATCTCTGTGTGATATTTATTGAAACGGGATTAAGATTGAAAT 644
DB 1613 TGGGCGAGAAACAGATCTCTGTGTGATATTTATTGAAACGGGATTAAGATTGAAAT 1672
QY 645 GAAGTCACAAAGTGACATTACCAATGAGAGAAACACAGCAGAAATCTTGATGCTT 704
DB 1673 GAAGTCACAAAGTGACATTACCAATGAGAGAAACACAGCAGAAATCTTGATGCTT 1732
QY 705 CACAGACATGCAACAAACAAATGGAATACTGTGATGACATGAGCAGCAAGCTGGGG 764
DB 1733 CACAGACATGCAACAAACAAATGGAATACTGTGATGACATGAGCAGCAAGCTGGGG 1792
QY 765 AGAGATTAACACAGGGGAGAGGGTCAGATTCGTGCTGCTTAAACGTGGCTTC 824
DB 1793 AGAGATTAACACAGGGGAGAGGGTCAGATTCGTGCTGCTTAAACGTGGCTTC 1852
QY 825 ATACCAAAATCAATTTATATTTCTAACCTCAAAACAAAGCTGTGTAATCTGATTC 884
DB 1853 ATACCAAAATCAATTTATATTTCTAACCTCAAAACAAAGCTGTGTAATCTGATTC 1912
QY 885 TAGGTTCTTGGGCCCAACATTCCTCATATATCCAGCAGCACTCATTTTAAATTT 944
DB 1913 TAGGTTCTTGGGCCCAACATTCCTCATATATCCAGCAGCACTCATTTTAAATTT 1972
QY 945 AGTTCCCAATCTGTACTGTGACCTTTTACACATGTAAGTAACATTAATCTGATTC 1004
DB 1973 AGTTCCCAATCTGTACTGTGACCTTTTACACATGTAAGTAACATTAATCTGATTC 2032
QY 1005 AAGAACCCTTGTGTTGCTGCTTAATATAGTGTGCTTTTCTTAAGAGAGTGTCTG 1064
DB 2033 AAGAACCCTTGTGTTGCTGCTTAATATAGTGTGCTTTTCTTAAGAGAGTGTCTG 2092
QY 1065 GCCCAGGAGATCTGTGAACAGGCTGGGAAGATCTCAAGATCTTTCAGAGGTTATCTTA 1124
DB 1124

DB 2093 GCCCAGGAGATCTGTGAACAGGCTGGGAAGCATCTCAAGATCTTTCAGAGTTATCTTA 2152
QY 1125 CTAGCACAGAGATGATTCATTAAGGAGTAATTTATCTAATCAACATCATCTCAGTCCT 1184
DB 2153 CTAGCACAGAGATGATTCATTAAGGAGTAATTTATCTAATCAACATCATCTCAGTCCT 2212
QY 1185 TTGCCCATCTGAAATTCATTTCCGACTTTTGGCCATCTTCAGACCTCAAAATGTCA 1244
DB 2213 TTGCCCATCTGAAATTCATTTCCGACTTTTGGCCATCTTCAGACCTCAAAATGTCA 2272
QY 1245 TTCCATTAATATCACAGATTAATCTTTTAACTGGAAGAAATTAAGTTATCATG 1304
DB 2273 TTCCATTAATATCACAGATTAATCTTTTAACTGGAAGAAATTAAGTTATCATG 2332
QY 1305 CAGCTATGGGAATTAATACATATTTTCCGTCGCAAGAAATGATGATGCTCTTA 1364
DB 2333 CAGCTATGGGAATTAATACATATTTTCCGTCGCAAGAAATGATGATGCTCTTA 2392
QY 1365 TCCCTCCCTTGTGATTTTTCAGATATTAAGTTAAATGCTTAGCCTGTACTG 1424
DB 2393 TCCCTCCCTTGTGATTTTTCAGATATTAAGTTAAATGCTTAGCCTGTACTG 2452
QY 1425 AGGCTGTATACAG-CACAGCCTCTCCCATCCCTCCAGCTTATCTGTATCACATCA 1483
DB 2453 AGGCTGTATACAGCAGCAGCCTCTCCCATCCCTCCAGCTTATCTGTATCACATCA 2512
QY 1484 CCGCTCCCATACCACTTAACAAATCTAATCTGTAATCTTGAACATGTACAGCATTA 1543
DB 2513 CCGCTCCCAT- GACCTTAACAAATCTAATCTGTAATCTTGAACATGTACAG- CATTA 2570
QY 1544 CATATTCCTTGTGCTGAGAAAGCTCTCTGTCTTAAATCTTAAGTAATGTAAT 1603
DB 2571 CATATTCCTTGTGCTGAGAAAGCTCTCTGTCTTAAATCTTAAGTAATGTAAT 2630
QY 1604 TTTGAATTAAGTTGACTTCTTACTTCATGCAAAAGGACACATATGATTCATCATC 1663
DB 2631 TTTGAATTAAGTTGACTTCTTACTTCATGCAAAAGGACACATATGATTCATCATC 2690
QY 1664 ACATGAGACAGCAAACTAAGAGTAAATGATTAATGATTAATGATTAATGATTA 1723
DB 2691 ACATGAGACAGCAAACTAAGAGTAAATGATTAATGATTAATGATTAATGATTA 2750
QY 1724 AATGCAAGACACAGAGGGAATGTTATGAGGACAGTTTGTAAAGCTGGATGTAAGC 1783
DB 2751 AATGCAAGACACAGAGGGAATGTTATGAGGACAGTTTGTAAAGCTGGATGTAAGC 2810
QY 1784 AAAGCAGGGAACCTCATAGTATCTTATATATATATCTTCAATCTCTATCTATCA 1843
DB 2811 AAAGCAGGGAACCTCATAGTATCTTATATATATATCTTCAATCTCTATCTATCA 2870
QY 1844 ATATCCAAACAGCTTTTACAGAAATTCATGCAAGTGAATCCCAAGGTAACCTTATC 1903
DB 2871 ATATCCAAACAGCTTTTACAGAAATTCATGCAAGTGAATCCCAAGGTAACCTTATC 2930
QY 1904 CATTCATGAGTATGCTGCTTGAATTTTGGCAATTCATGCTGACATTAATCTCAAGT 1963
DB 2931 CATTCATGAGTATGCTGCTTGAATTTTGGCAATTCATGCTGACATTAATCTCAAGT 2990
QY 1964 TTGAGATGTGTTGCTCTTGTATTAATTAAGAAATAGGCACTCTTGTAGCCACTT 2023
DB 2991 TTGAGATGTGTTGCTCTTGTATTAATTAAGAAATAGGCACTCTTGTAGCCACTT 3050
QY 2024 TAGGTTCACTCTGTCATTAAGAAATTTACAAAGAGC 2061
DB 3051 TAGGTTCACTCTGTCATTAAGAAATTTACAAAGAGC 3088
RESULT 12
AX106204 3112 bp DNA linear PAT 30-APR-2001
LOCUS AX106204
DEFINITION Sequence 342 from Patent WO0125273.
ACCESSION AX106204
VERSION AX106204.1 GI:13921893

KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
REFERENCE 1
AUTHORS Skelky, Y.A., Xu, J., Cheever, M.A. and Reed, S.G.
TITLE Compositions and methods for wtl specific immunotherapy
JOURNAL Patent: WO 0125273-A 342 12-APR-2001;
CORIXA CORPORATION (US)
FEATURES
Source location/Qualifiers
1. 3112
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
BASE COUNT 975 a 587 c 624 g 926 t
ORIGIN
Query Match 38.1%; Score 1364; DB 6; Length 3112;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1774; Conservative 0; Mismatches 1; Indels 3; Gaps 3;
OY 285 GGTGGAATTAAGAAAGCTGCTGACTTACCATGTGAGGCACACATCTGCTGAATGG 344
DB 1313 GGTGGAATTAAGAAAGCTGCTGACTTACCATGTGAGGCACACATCTGCTGAATGG 1372
OY 345 AGATAATTACATCACTAGAAACACAGATGACATATTAATGTCTAAGTAGTGCATGT 404
DB 1373 AGATAATTACATCACTAGAAACACAGATGACATATTAATGTCTAAGTAGTGCATGT 1432
OY 405 TTTTGACATTTCCAGCCCTTTTAATATCCACACACAGAGACACAAAAGAGAGC 464
DB 1433 TTTTGACATTTCCAGCCCTTTTAATATCCACACACAGAGACACAAAAGAGAGC 1492
OY 465 AGAGATCCCTGGAGAAATGCGCGCGCCCATCTTGGTCATGATGAGCCGCGCTGT 524
DB 1493 AGAGATCCCTGGAGAAATGCGCGCGCCCATCTTGGTCATGATGAGCCGCGCTGT 1552
OY 525 GCGTGTGCGCGCTTGTGAGGAGAGACATTTAGAAATGATGTGTTCTTAAAGA 584
DB 1553 GCGTGTGCGCGCTTGTGAGGAGAGACATTTAGAAATGATGTGTTCTTAAAGA 1612
OY 585 TGGGACAGAAAACAGATCTGTGTGATATTTATTTAAAGGGATTTACAGATTTGAAT 644
DB 1613 TGGGACAGAAAACAGATCTGTGTGATATTTATTTAAAGGGATTTACAGATTTGAAT 1672
OY 645 GAAGCACAAAGTGAATACCAATGAGAGAAAACAGAGAGAAATCTTGATGGCTT 704
DB 1673 GAAGCACAAAGTGAATACCAATGAGAGAAAACAGAGAGAAATCTTGATGGCTT 1732
OY 705 CACAAGACATCAACAAACAAATGGAATGATGTGATGACATGAGGACGCCAAGCTGGGG 764
DB 1733 CACAAGACATCAACAAACAAATGGAATGATGTGATGACATGAGGACGCCAAGCTGGGG 1792
OY 765 AGGAGATACCAACGGGGGAGAGAGGATTTGCGCCCTGCTTAACTGTGCTTC 824
DB 1793 AGGAGATACCAACGGGGGAGAGAGGATTTGCGCCCTGCTTAACTGTGCTTC 1852
OY 825 ATAACCAATCATTTTCAATTTCTAACCCCTCAAAACAAAGCTGTGATATCTGATGTC 884
DB 1853 ATAACCAATCATTTTCAATTTCTAACCCCTCAAAACAAAGCTGTGATATCTGATGTC 1912
OY 885 TAGGGTCTCTTGGGGCCAAATTTCCATATATCCAGCCACACTCTTTTATATATT 944
DB 1913 TAGGGTCTCTTGGGGCCAAATTTCTCCATATATCCAGCCACACTCTTTTATATATT 1972
OY 945 AGTTCCAGATCTGACTGTACCTTTCTACACTGTAGAAATTAACATTTTGTTC 1004
DB 1973 AGTTCCAGATCTGACTGTACCTTTCTACACTGTAGAAATTAACATTTTGTTC 2032
OY 1005 AAAAGCCTTGTGCTGCTAATATATGAGTACAGCTGTTTCTTAAGAGTGTCTG 1064
DB 2033 AAAAGCCTTGTGCTGCTAATATATGAGTACAGCTGTTTCTTAAGAGTGTCTG 2092

OY 1065 GCCCAGGGGATCTGGAACAGGCTGGAGGATCTCAAGATCTTTCCAGGGTATACTTA 1124
DB 2093 GCCCAGGGGATCTGGAACAGGCTGGAGGATCTCAAGATCTTTCCAGGGTATACTTA 2152
OY 1125 CTAGCACACAGCATGATCTTACGAGGAGTAATTTATCAATCAATCATCTCAGTGTCT 1184
DB 2153 CTAGCACACAGCATGATCTTACGAGGAGTAATTTATCAATCAATCATCTCAGTGTCT 2212
OY 1185 TTGCCCATACGAAATTTATTTCCACCTTTTGTGCGCCATTTCTCAAGACCTCAAAATGCA 1244
DB 2213 TTGCCCATACGAAATTTATTTCCACCTTTTGTGCGCCATTTCTCAAGACCTCAAAATGCA 2272
OY 1245 TTCCATTAATATCAAGGATTAACCTTTTATTTTAACTGGAGAAATCAATGTTATAC 1304
DB 2273 TTCCATTAATATCAAGGATTAACCTTTTATTTTAACTGGAGAAATCAATGTTATAC 2332
OY 1305 CAGCTAATGGAATTTAATTAATATTTTGTTCACGTGCAAAAGATGACTAAGTCCTTA 1364
DB 2333 CAGCTAATGGAATTTAATTAATATTTTGTTCACGTGCAAAAGATGACTAAGTCCTTA 2392
OY 1365 TCCCTCCCTTGTGTTGATTTTTCACGATTAAGTTAAATGCTTACGCTGTACTG 1424
DB 2393 TCCCTCCCTTGTGTTGATTTTTCACGATTAAGTTAAATGCTTACGCTGTACTG 2452
OY 1425 AGGCTGTATACAG-CACAGCCTTCCCATCCCTCCACGCTTATCTGTCAACACATCAA 1483
DB 2453 AGGCTGTATACAGCAGCAGCCTTCCCATCCCTCCACGCTTATCTGTCAACACATCAA 2512
OY 1484 CCCCCTCCATACACCTTAACAAATCTAATCTTGAATCTTGTGACATGTGACACATA 1543
DB 2513 CCCCCTCCAT- GCACCTTAACAAATCTAATCTTGAATCTTGTGACATGTGACAG -CATA 2570
OY 1544 CATTAATTCCTGCTGAGAGGCTCTCTGCTGCTTAATCTAGAAATGATGAAT 1603
DB 2571 CATTAATTCCTGCTGAGAGGCTCTCTGCTGCTTAATCTAGAAATGATGAAT 2630
OY 1604 TTTGAATTAAGTTGACTATCTTACTTCAATGCAAAAGGAGACATATGATGATCATC 1663
DB 2631 TTTGAATTAAGTTGACTATCTTACTTCAATGCAAAAGGAGACATATGATGATCATC 2690
OY 1664 ACATGACACACCAATTAATAAGTATTTGATTAATAGAGTTTATGATTAATATATGA 1723
DB 2691 ACATGACACACCAATTAATAAGTATTTGATTAATAGAGTTTATGATTAATATATGA 2750
OY 1724 AATGCAAGGACACAGAGGAATGTTTGGGGACGCTTTTAAAGCCGGATGGAAGC 1783
DB 2751 AATGCAAGGACACAGAGGAATGTTTATGGGGACGCTTTTAAAGCCGGATGGAAGC 2810
OY 1784 AAAGCAGGAACTCATATGATCTTATATATATATCTTATCTATCTATGACA 1843
DB 2811 AAAGCAGGAACTCATATGATCTTATATATATATCTTATCTATCTATGACA 2870.
OY 1844 ATATCCAAACAGCTTTTACAGAAATTCATGCAAGTGCAAATGCCCAAAGTAACTTTATC 1903
DB 2871 ATATCCAAACAGCTTTTACAGAAATTCATGCAAGTGCAAATGCCCAAAGTAACTTTATC 2930
OY 1904 CATTTCAATGAGTGGGCTTTTAAATTTTGGCAAAATCATCTGCTACTTATGCAACT 1963
DB 2931 CATTTCAATGAGTGGGCTTTTAAATTTTGGCAAAATCATCTGCTACTTATGCAACT 2990
OY 1964 TTGAGATGTGTTGTCTTGTAGTAAATTTGAAGAAATAGGCACTCTTGTGAGCACTT 2023
DB 2991 TTGAGATGTGTTGTCTTGTAGTAAATTTGAAGAAATAGGCACTCTTGTGAGCACTT 3050
OY 2024 TAGGGTCACTCTGGCAATTAAGAAATTTACAAAGAGC 2061
DB 3051 TAGGGTCACTCTGGCAATTAAGAAATTTACAAAGAGC 3088
RESULT 13
AX106687
LOCUS AX106687 3112 bp DNA linear PAT 30-APR-2001

DEFINITION Sequence 468 from Patent WO0125272.
ACCESSION AX106687
VERSION AX106687.1 GI:13922352
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
REFERENCE 1
AUTHORS Xu,J., Skeiky,Y.A., Reed,S.G. and Cheever,M.A.
TITLE Compositions and methods for therapy and diagnosis of prostate cancer
JOURNAL Patent: WO 0125272-A 468 12-APR-2001;
CORIXA CORPORATION (US)
FEATURES
Source location/Qualifiers
1..3112
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
BASE COUNT 975 a 587 c 624 g 926 t
ORIGIN
Query Match 38.1%; Score 1364; DB 6; Length 3112;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1774; Conservative 0; Mismatches 1; Indels 3; Gaps 3;
QY 285 GGTGAATAAGAAAGCTGCTGACTTTACCATCTGAGGCCACACATCTGCTGAATAG 344
DB 1313 GGTGAATAAGAAAGCTGCTGACTTTACCATCTGAGGCCACACATCTGCTGAATAG 1372
QY 345 AGATATTTAACTACTAGAACAGACAGATGACAAATATATGTCTAAGTAGTACATGT 404
DB 1373 AGATATTTAACTACTAGAACAGACAGATGACAAATATATGTCTAAGTAGTACATGT 1432
QY 405 TTTTGACATTTCCAGCCCCCTTTAATATATCCACACACAGAGACAAAAGAGACAC 464
DB 1433 TTTTGACATTTCCAGCCCCCTTTAATATATCCACACACAGAGACAAAAGAGACAC 1492
QY 465 AAGAGATCCCTGGGAGAAATGCCGCCGCGCATCTTGGTCATCGATGACCCGCGCTT 524
DB 1493 AAGAGATCCCTGGGAGAAATGCCGCCGCGCATCTTGGTCATCGATGACCCGCGCTT 1552
QY 525 GCGTGGCCCGCTTGGAGGAGAGACATTAAGAAATGAATTGATGTCTTCTTAAGGA 584
DB 1553 GCGTGGCCCGCTTGGAGGAGAGACATTAAGAAATGAATTGATGTCTTCTTAAGGA 1612
QY 585 TGGGAGAGAAACAGATCTGTTGTGATATTTATTGAACGGGATTTACAGATTTGAAT 644
DB 1613 TGGGAGAGAAACAGATCTGTTGTGATATTTATTGAACGGGATTTACAGATTTGAAT 1672
QY 645 GAAGTCACAAAGTGGAGCATTAACCAATGAGAGAAACAGAGAAATCTTGATGGCTT 704
DB 1673 GAAGTCACAAAGTGGAGCATTAACCAATGAGAGAAACAGAGAAATCTTGATGGCTT 1732
QY 705 CACAAGACATGCACAAACAAATGGAATCTGTGATGACATGAGGACCAAGCTGGGG 764
DB 1733 CACAAGACATGCACAAACAAATGGAATCTGTGATGACATGAGGACCAAGCTGGGG 1792
QY 765 AGGAGATTAACACAGGGGAGAGGGTCAGATTCTGGCCCTGCTTAACCTGTGCTTC 824
DB 1793 AGGAGATTAACACAGGGGAGAGGGTCAGATTCTGGCCCTGCTTAACCTGTGCTTC 1852
QY 825 ATTAACCAATCATTTTCTATTTCTAACCTCAAAACAAAGCTGTTGATATCTGATCTC 884
DB 1853 ATTAACCAATCATTTTCTATTTCTAACCTCAAAACAAAGCTGTTGATATCTGATCTC 1912
QY 885 TAGGTTCTTCTGGGCCCAACATTTCTCATATATTCACGACACATCATTTTAAATTT 944
DB 1913 TAGGTTCTTCTGGGCCCAACATTTCTCATATATTCACGACACATCATTTTAAATTT 1972
QY 945 AGTTCCAGATCTGTACTGTGACTTTCATCTGTACACTGTAGATTAACATTAATCTATTGTTTC 1004
DB 1973 AGTTCCAGATCTGTACTGTGACTTTCATCTGTACACTGTAGATTAACATTAATCTATTGTTTC 2032

QY 1005 AAAGACCCCTTGCTGTGCTGCTTAATATGTACTGACTGTTTCTTAAGAGAGTGTCTG 1064
DB 2033 AAAGACCCCTTGCTGTGCTGCTTAATATGTACTGACTGTTTCTTAAGAGAGTGTCTG 2092
QY 1065 GCCCAGGGGATCTGTGAACAGCGTGGGAAGCATCTCAAGATCTTTCCAGGGTATTAATCTTA 1124
DB 2093 GCCCAGGGGATCTGTGAACAGCGTGGGAAGCATCTCAAGATCTTTCCAGGGTATTAATCTTA 2152
QY 1125 CTAGCACACAGATGATCTATTACGAGTGAATATCTAATCAACATCATCTCAGTGTCT 1184
DB 2153 CTAGCACACAGATGATCTATTACGAGTGAATATCTAATCAACATCATCTCAGTGTCT 2212
QY 1185 TTGCCCATCTGAATTCATTTCCACTTTTGCCACTTTCACAGACCTCAAAATGTCA 1244
DB 2213 TTGCCCATCTGAATTCATTTCCACTTTTGCCACTTTCACAGACCTCAAAATGTCA 2272
QY 1245 TTCCATTAATATACAGAGATTAATCTTTTAACTGGAAGAAATTCATATGTTACATG 1304
DB 2273 TTCCATTAATATACAGAGATTAATCTTTTAACTGGAAGAAATTCATATGTTACATG 2332
QY 1305 CAGCTATGGGAATTTATTAATATTTGTTTCCAGTCCAAAGATGACTAAGTCTTTTA 1364
DB 2333 CAGCTATGGGAATTTATTAATATTTGTTTCCAGTCCAAAGATGACTAAGTCTTTTA 2392
QY 1365 TCCCTCCCTTGTGATTTTTCAGATTAATGAATGAATGCTTAGCCCTGTACTG 1424
DB 2393 TCCCTCCCTTGTGATTTTTCAGATTAATGAATGAATGCTTAGCCCTGTACTG 2452
QY 1425 AGGCTGTATACAG-CACAGCCTCTCCCACTCCCTCCAGGCTTATCTCATCACATCA 1483
DB 2453 AGGCTGTATACAGC-CACAGCCTCTCCCACTCCCTCCAGGCTTATCTCATCACATCA 2512
QY 1484 CCCCTCCCTTACACCTTAACAAATCTTAATCTTAATCTTGAACATGTACAGACATA 1543
DB 2513 CCCCTCCCTTACACCTTAACAAATCTTAATCTTGAACATGTACAGACATA 2570
QY 1544 CATTAATCTTCTGCTGCTGAGAGCTCTTCTGCTCTTAATCTGAATGATGATTAAT 1603
DB 2571 CATTAATCTTCTGCTGCTGAGAGCTCTTCTGCTCTTAATCTGAATGATGATTAAT 2630
QY 1604 TTTGAATAAGTTGACTACTTCTTACTCATCAAGAGAGGACATATGAGATTCATCATC 1663
DB 2631 TTTGAATAAGTTGACTACTTCTTACTCATCAAGAGAGGACATATGAGATTCATCATC 2690
QY 1664 ACATGAGACAGCAATATCTAAGAGTAAATTTGATTTATTAAGAGTTTAAATATATGA 1723
DB 2691 ACATGAGACAGCAATATCTAAGAGTAAATTTGATTTATTAAGAGTTTAAATATATGA 2750
QY 1724 AATGCAAGGCCACAGAGGGAATGTTTATGGGGCAGCTTGTGAAGCTGGATGTGAAGC 1783
DB 2751 AATGCAAGGCCACAGAGGGAATGTTTATGGGGCAGCTTGTGAAGCTGGATGTGAAGC 2810
QY 1784 AAAGCAGGGAACCTCATAGTATCTTATTAATATATCTTCAATTTCTATCTATACACA 1843
DB 2811 AAAGCAGGGAACCTCATAGTATCTTATTAATATATCTTCAATTTCTATCTATACACA 2870
QY 1844 ATATCAACAAGCTTTTACAGAAATTCATGCACTGCAATTCGCCAAAGTAACTTTATC 1903
DB 2871 ATATCAACAAGCTTTTACAGAAATTCATGCACTGCAATTCGCCAAAGTAACTTTATC 2930
QY 1904 CATTTTCATGAGTGCCTTTTGAATTTTGAATTTTGAATTTTGAATTTTGAATTTTGAAT 1963
DB 2931 CATTTTCATGAGTGCCTTTTGAATTTTGAATTTTGAATTTTGAATTTTGAATTTTGAAT 2990
QY 1964 TTGAGATGATGTTGCTTGTGATTAATTAAGAAATAGGCACTTGTGAGCCACTT 2023
DB 2991 TTGAGATGATGTTGCTTGTGATTAATTAAGAAATAGGCACTTGTGAGCCACTT 3050
QY 2024 TAGGTTCACTCTCGCATTAAGAAATTTTACAAAGAGC 2061
DB 3051 TAGGTTCACTCTCGCATTAAGAAATTTTACAAAGAGC 3088

RESULT 14	AXI40978	3112 bp	DNA	linear	PAT 31-MAY-2001
LOCUS	AXI40978				
DEFINITION	Sequence 468 from Patent WO0134802.				
ACCESSION	AXI40978				
VERSION	AXI40978.1	GI:14281075			
KEYWORDS					
SOURCE	1				
ORGANISM	Homo sapiens (human)				
REFERENCE	Homo sapiens				
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.				
TITLE	Xu, J., Dillon, D.C., Mitchem, J.L., Harlocker, S.L., Jiang, Y., Reed, S.G., Klotz, M.D., Retter, M.W., Stolk, J.A., Day, C.H., Skeiky, Y.A. and Wang, A.				
JOURNAL	Compositions and methods for the therapy and diagnosis of prostate cancer				
FEATURES	Patent: WO 0134802-A 468 17-MAY-2001; CORIXA CORPORATION (US)				
SOURCE	location/Qualifiers				
	1. 3112				
	/organism="Homo sapiens"				
	/mol_type="genomic DNA"				
	/db_xref="taxon:9606"				
BASE COUNT	975 a 587 c 624 g 926 t				
ORIGIN					
Query Match	38.1%, Score 1364; DB 6; Length 3112;				
Best Local Similarity	99.8%; Pred. No. 0;				
Matches 1774; Conservative	0; Mismatches 1; Indels 3; Gaps 3;				
OY	285 GGTGGAATTAAGAAAGCGCTGCTACCTTACCATCTGAGGCGACACATCGCTGAATAGG	344			
DB	1313 GGTGGAATTAAGAAAGCGCTGCTACCTTACCATCTGAGGCGACACATCGCTGAATAGG	1372			
OY	345 AGATTAATTAACATCTACTGAAACAGCAAGATGACAAATTAATGCTAAGTAGACATGT	404			
DB	1373 AGATTAATTAACATCTACTGAAACAGCAAGATGACAAATTAATGCTAAGTAGACATGT	1432			
OY	405 TTTTGACATTTCCAGCCCTTTTAATATTCACACACACAGAGAACACAAAGAGACAC	464			
DB	1433 TTTTGACATTTCCAGCCCTTTTAATATTCACACACACAGAGAACACAAAGAGACAC	1492			
OY	465 AGAGATCCCTGGGGAATATGCCGGCCGACATCTGGGTCTATGATGAGCCTCGCCCTGT	524			
DB	1493 AGAGATCCCTGGGGAATATGCCGGCCGACATCTGGGTCTATGATGAGCCTCGCCCTGT	1552			
OY	525 GCCTGTCCTGCTGTGAGGGAAGACATTTGAATAATGATGATGCTTCTTAAAGA	584			
DB	1553 GCCTGTCCTGCTGTGAGGGAAGACATTTGAATAATGATGATGCTTCTTAAAGA	1612			
OY	585 TGGGCAGGAAACAGATCTGTGATATTTTGAACGGATTAACAGATTTGAAT	644			
DB	1613 TGGGCAGGAAACAGATCTGTGATATTTTGAACGGATTAACAGATTTGAAT	1672			
OY	645 GAATGTCACAAAGTAGACATTTCCATATGAGAGAAACAGACGAGAAAATCTGATGGCTT	704			
DB	1673 GAATGTCACAAAGTAGACATTTCCATATGAGAGAAACAGACGAGAAAATCTGATGGCTT	1732			
OY	705 CACAAGACATGCAACAAACAAATGGAATCTGATGACATGAGGACAGCCAACTGGGG	764			
DB	1733 CACAAGACATGCAACAAACAAATGGAATCTGATGACATGAGGACAGCCAACTGGGG	1792			
OY	765 AGGAGATTAACACGGGGCAGAGGTCAGAGATTTGGCCCTGCTCTAATGTGCGTTC	824			
DB	1793 AGGAGATTAACACGGGGCAGAGGTCAGAGATTTGGCCCTGCTCTAATGTGCGTTC	1852			
OY	825 ATATCCAAATCATTTCAATTTTCAACCTCAAAACAAAGCTGTGTAATCTGCATCTC	884			
DB	1853 ATATCCAAATCATTTCAATTTTCAACCTCAAAACAAAGCTGTGTAATCTGCATCTC	1912			
OY	885 TACGGTCTCTTCTGGGCCAACATTTCCATATTTCCAGCCACATCATTTTATATTT	944			

D	1913	TACGGTTCCTCTGCGGCCAACATTCCTCATATATCCAGCCACACTATTTTAAATTT	1972
Q	945	AGTTCCAGATCTGTACTGTGACCTTTCTACACTGTAGAATTAACATTACTCATTTTGTTC	1004
D	1973	AGTTCACGATCTGTACTGTGACCTTTCTACACTGTAGAATTAACATTACTCATTTTGTTC	2032
Q	1005	AAAGACCCCTGTGTGCTGCTTAATATGTGCTGACCTGTTTTCCTAAGAGGTCTG	1064
D	2033	AAAGACCCCTGTGTGCTGCTTAATATGTGCTGACCTGTTTTCCTAAGAGGTCTG	2092
Q	1065	GCCGAGGGGATCTGTGAACAGCGTGGGAGAGCATCTCAAGATCTTCCAGGGTTATCTTA	1124
D	2093	GCCGAGGGGATCTGTGAACAGCGTGGGAGAGCATCTCAAGATCTTCCAGGGTTATCTTA	2152
Q	1125	CTAGACACACATGATCATTTAGGAGATTTATCTTAATCAACATCATCTCAGTCTC	1184
D	2153	CTAGACACACATGATCATTTAGGAGATTTATCTTAATCAACATCATCTCAGTCTC	2212
Q	1185	TTGGCCATCTGAAATTCATTTCCACTTTTGTGCCACTTCTCAAGACCTCAAAATGTCA	1244
D	2213	TTGGCCATCTGAAATTCATTTCCACTTTTGTGCCACTTCTCAAGACCTCAAAATGTCA	2272
Q	1245	TTCCATTTAATATCACAGATTAACCTTTTTTTTAACCTGGAAGAATTCATGTTACATG	1304
D	2273	TTCCATTTAATATCACAGATTAACCTTTTTTTTAACCTGGAAGAATTCATGTTACATG	2332
Q	1305	CAGCATATGGAAATTAATTAACATTTTGTTCAGAGCAAGATGACATAGCTCTTA	1364
D	2333	CAGCATATGGAAATTAATTAACATTTTGTTCAGAGCAAGATGACATAGCTCTTA	2392
Q	1365	TCCCTCCCTTTGTTGATTTTTTTTCCAGTATAAGTTAAAGTCTTAAGCCTTGATCTG	1424
D	2393	TCCCTCCCTTTGTTGATTTTTTTTCCAGTATAAGTTAAAGTCTTAAGCCTTGATCTG	2452
Q	1425	AGCGGTATTAAG-CACAGCCTCCGCCACATCCGCCAGCCTTATCTGTCATCACATCAAA	1483
D	2453	AGCGGTATTAAGCAGCAGCCTCCGCCACATCCGCCAGCCTTATCTGTCATCACATCAAA	2512
Q	1484	CCCCCTCCCATACACACTAAACAAATATCACTTTTAATTCCTTGAACATGTACAGACATA	1543
D	2513	CCCCCTCCCATACACACTAAACAAATATCACTTTTAATTCCTTGAACATGTACAGACATA	2570
Q	1544	CATTATTCCTTCTGCTGAGAAAGCTCTTCTTGTCTCTTAATCTACAATGATGTAAAGT	1603
D	2571	CATTATTCCTTCTGCTGAGAAAGCTCTTCTTGTCTCTTAATCTACAATGATGTAAAGT	2630
Q	1604	TTTGAATATGATGACTATCTACCTTCATGCAAAAGAGGACACATATGAGATTCATATC	1663
D	2631	TTTGAATATGATGACTATCTACCTTCATGCAAAAGAGGACACATATGAGATTCATATC	2690
Q	1664	ACATGAGACGCAAAATACTAAAGGTATTAATTTGATTTAAGAGTTTGAATTAATATATGA	1723
D	2691	ACATGAGACGCAAAATACTAAAGGTATTAATTTGATTTAAGAGTTTGAATTAATATATGA	2750
Q	1724	AATGCAAGAGCCACAGAGGGAATTTATATGGGCGACGTTTGTAAAGCCTGGAGATGTAGC	1783
D	2751	AATGCAAGAGCCACAGAGGGAATTTATATGGGCGACGTTTGTAAAGCCTGGAGATGTAGC	2810
Q	1784	AAAGGAGGGAACCTCATATGATCTTATATATATATATATATCTTCTATCTCATATACA	1843
D	2811	AAAGGAGGGAACCTCATATGATCTTATATATATATATATATCTTCTATCTCATATACA	2870
Q	1844	ATATTCACAAGCTTTTTCACAGAAATCATGACAGTGCACAAATCCCAAGAGTAACTTTATC	1903
D	2871	ATATTCACAAGCTTTTTCACAGAAATCATGACAGTGCACAAATCCCAAGAGTAACTTTATC	2930
Q	1904	CATTTCATGATGATGGCTTTAAATTTTGGCAAAATCATACGATGATCAATTCATCAACT	1963
D	2931	CATTTCATGATGATGGCTTTAAATTTTGGCAAAATCATACGATGATCAATTCATCAACT	2990
Q	1964	TTTGAGATGTGTTTCTCTGTAGTAAATTTGAAGAAATAAGGCACTCTTGTGAGCCACTT	2023

Db 2991 TTGAGATGTTGTTGCTGTAGTTAATTGAAGAATAAGGCGACTCTGTGAGCGACTT 3050
QY 2024 TAGGTTCACTCTCTGGCAATTAAGAATTTACAAAGC 2061
Db 3051 TAGGTTCACTCTCTGGCAATTAAGAATTTACAAAGC 3088
RESULT 15
AX200838
LOCUS AX200838 3112 bp DNA linear PAT 29-AUG-2001
DEFINITION Sequence 468 from Patent WO0151633.
ACCESSION AX200838
VERSION AX200838.1 GI:15390741
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y.,
Reed,S.G., Kalos,M.D., Fanger,G.R., Day,C.H., Ketter,M.W.,
Stolk,J.A., Skelky,Y.A., Wang,A. and Meagher,M.J.
TITLE Compositions and methods for the therapy and diagnosis of prostate
cancer
JOURNAL Patent: WO 0151633-A 468 19-JUL-2001;
CORIXA CORPORATION (US)
FEATURES
source location/Qualifiers
1..3112
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
BASE COUNT 975 a 587 c 624 g 926 t
ORIGIN
Query Match 38.1%; Score 1364; DB 6; Length 3112;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1774; Conservative 0; Mismatches 1; Indels 3; Gaps 3;
QY 265 GGTGGAATTAAGAAAGCTGCTGACTTACCATCTGAGGCCACATCTGCTGAATGG 344
Db 1313 GGTGGAATTAAGAAAGCTGCTGACTTACCATCTGAGGCCACATCTGCTGAATGG 1372
QY 345 AGATATTAACTACTAGAAACACAGAGATGACAAATATATGTCTAAGTAGTGCATGT 404
Db 1373 AGATATTAACTACTAGAAACACAGAGATGACAAATATATGTCTAAGTAGTGCATGT 1432
QY 405 TTTTGCACATTTCCAGCCCTTTTAAATATCCACACACAGAGAGACACAAAAGAGCAC 464
Db 1433 TTTTGCACATTTCCAGCCCTTTTAAATATCCACACACAGAGAGACACAAAAGAGCAC 1492
QY 465 AGAGATCCCTGGGAAATATGCCCGCCGCATCTTGGGTCAATGAGCCCTGCCCTGT 524
Db 1493 AGAGATCCCTGGGAAATATGCCCGCCGCATCTTGGGTCAATGAGCCCTGCCCTGT 1552
QY 525 GCTCTGTCCTGCTGTGAGGGAAGACATTAAGAAATGATGTGTTCTTAAAGA 584
Db 1553 GCTCTGTCCTGCTGTGAGGGAAGACATTAAGAAATGATGTGTTCTTAAAGA 1612
QY 585 TGGCGAGGAAAACAGATCCTGTTGTGATATTATTGAACGGGATTCAGATTTGAAT 644
Db 1613 TGGCGAGGAAAACAGATCCTGTTGTGATATTATTGAACGGGATTCAGATTTGAAT 1672
QY 645 GAAGTCACAAAGTGGCATTTCCATGAGAGAAAACAGACAGAAAATCTTGATGGCT 704
Db 1673 GAAGTCACAAAGTGGCATTTCCATGAGAGAAAACAGACAGAAAATCTTGATGGCT 1732
QY 705 CACAAGACATGCAAAACAAATGGAATCTGTATGATGACATGAGAGCCAAAGCTGGGG 764
Db 1733 CACAAGACATGCAAAACAAATGGAATCTGTATGATGACATGAGAGCCAAAGCTGGGG 1792
QY 765 AGGAGATTAACACAGGGGAGAGAGGTCTGAGATTTGCGCCCTGCTTAAACTGTGCTTC 824
Db 1793 AGGAGATTAACACAGGGGAGAGAGGTCTGAGATTTGCGCCCTGCTTAAACTGTGCTTC 1852

QY 825 ATACCAATATCATTTTCATATTTCTAACCTCAAAAACAAAGCTGTGTAATATCTGATCTC 884
Db 1853 ATACCAATATCATTTTCATATTTCTAACCTCAAAAACAAAGCTGTGTAATATCTGATCTC 1912
QY 885 TAGGGTTCTCTGGGGCCCAACATTTCTCATATATCCAGCCACACATTTTAATATTT 944
Db 1913 TAGGGTTCTCTGGGGCCCAACATTTCTCATATATCCAGCCACACATTTTAATATTT 1972
QY 945 AGTTCCAGATCTGATCTGATCTGATCTTTCACACTGTAGAAATACATTTACTATTTGTTTC 1004
Db 1973 AGTTCCAGATCTGATCTGATCTGATCTTTCACACTGTAGAAATACATTTACTATTTGTTTC 2032
QY 1005 AAAAGACCTCTGCTGTGCTGCTTAATATGATGATGATCTGTTTCTTAAGAGGTCTCG 1064
Db 2033 AAAAGACCTCTGCTGTGCTGCTTAATATGATGATGATCTGTTTCTTAAGAGGTCTCG 2092
QY 1065 GCCCAGGGGATGTGAAACAGAGCTGGGAAGCTCTCAAGATCTTCCAGGGTTATACCTTA 1124
Db 2093 GCCCAGGGGATGTGAAACAGAGCTGGGAAGCTCTCAAGATCTTCCAGGGTTATACCTTA 2152
QY 1125 CTAGCACACAGCATGATCATTTAGGAGTAATATCTAATCAACATCATCTCACTGTCT 1184
Db 2153 CTAGCACACAGCATGATCATTTAGGAGTAATATCTAATCAACATCATCTCACTGTCT 2212
QY 1185 TTGCCCCATCTGAATTTCAATTTCCCACTTTTGCCCCATCTCAAGAGCTCAAAATGTCA 1244
Db 2213 TTGCCCCATCTGAATTTCAATTTCCCACTTTTGCCCCATCTCAAGAGCTCAAAATGTCA 2272
QY 1245 TTCCATTAATATCACAGATTAATCTTTTAACTTTTAACTGGAAGATCAATGTTACATG 1304
Db 2273 TTCCATTAATATCACAGATTAATCTTTTAACTTTTAACTGGAAGATCAATGTTACATG 2332
QY 1305 CAGCTATGGGAATTAATTAATCAATATTTGTTTCCAGTGCAAGATGATGATCTCTTA 1364
Db 2333 CAGCTATGGGAATTAATTAATCAATATTTGTTTCCAGTGCAAGATGATGATCTCTTA 2392
QY 1365 TCCCTCCCTCTGTTGATTTTTTTTCCAGTATTAAGTTAAATGCTTATGCTTACTG 1424
Db 2393 TCCCTCCCTCTGTTGATTTTTTTTCCAGTATTAAGTTAAATGCTTATGCTTACTG 2452
QY 1425 AGGCTGTATACAG -CACAGCCTCTCCCATCTCCCTCAGCCTTATCTGATCACCATCA 1483
Db 2453 AGGCTGTATACAGCACAAGCCTCTCCCATCTCCCTCAGCCTTATCTGATCACCATCA 2512
QY 1484 CCCCTCCATACACCTTAACAAATCTAATCTGTAATCTCTTGAACATGTCAGACATA 1543
Db 2513 CCCCTCCAT -GCACCTTAACAAATCTAATCTGTAATCTCTTGAACATGTCAG -CATA 2570
QY 1544 CATTAATCTCTGCTGAGAAAGCTCTCTCTCTCTTAATCTTAAGATGTTGAAGT 1603
Db 2571 CATTAATCTCTGCTGAGAAAGCTCTCTCTCTCTCTTAATCTTAAGATGTTGAAGT 2630
QY 1604 TTTGAATTAAGTGAATCTTACTCATGCAAGAAGGACACATATGATTCATCATC 1663
Db 2631 TTTGAATTAAGTGAATCTTACTCATGCAAGAAGGACACATATGATTCATCATC 2690
QY 1664 ACATGAGACAGCAATACTAAAAGTGTAAATTTGATTAAGAGTTTAAATAATATGA 1723
Db 2691 ACATGAGACAGCAATACTAAAAGTGTAAATTTGATTAAGAGTTTAAATAATATGA 2750
QY 1724 AATGCAAGGCCACAGAGAGGAATGTTTATGGGGCAGTTTGAACCTGGGATGGAAGC 1783
Db 2751 AATGCAAGGCCACAGAGAGGAATGTTTATGGGGCAGTTTGAACCTGGGATGGAAGC 2810
QY 1784 AAAGCAGGGAACCTCATAGTATCTTAATATATATATATATATCTATCTATCTATCA 1843
Db 2811 AAAGCAGGGAACCTCATAGTATCTTAATATATATATATATATCTATCTATCTATCA 2870
QY 1844 ATATCAACAGCTTTTACAGAAATTCATGCAAGTCAAAATCCCAAGGTAACCTTTATC 1903
Db 2871 ATATCAACAGCTTTTACAGAAATTCATGCAAGTCAAAATCCCAAGGTAACCTTTATC 2930

```
QY 1904 CATTTCATGCTGAGTGGGCTTTAGAAATTTGGCAAATCATCTGCTCACTTATCTCAACT 1963
    |||||||
Db 2931 CATTTCATGCTGAGTGGGCTTTAGAAATTTGGCAAATCATCTGCTCACTTATCTCAACT 2990
    |||||||
QY 1964 TTGAGATGCTTTGCTCTTGTAGTTAATTGAAGAAATAGGGCACTTGTGAGGCACTT 2023
    |||||||
Db 2991 TTGAGATGCTTTGCTCTTGTAGTTAATTGAAGAAATAGGGCACTTGTGAGGCACTT 3050
    |||||||
QY 2024 TAGGGTTCACCTCTGGCAATTAAGAATTTACCAAGAGC 2061
    |||||||
Db 3051 TAGGGTTCACCTCTGGCAATTAAGAATTTACCAAGAGC 3088
    |||||||
```

Search completed: September 27, 2003, 06:45:07
Job time : 13041.4 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 26, 2003, 21:40:03 : Search time 116.911 Seconds
(without alignments)
7690.430 Million cell updates/sec

Title: US-09-402-713A-1

Perfect score: 2037
Sequence: 1 agaagcgcgcacagaaaaa.....cataaagaattacaaga 2037

Scoring table:

OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 569978 seqs, 220691566 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

Issued_Patents_NA.*
1: /cgn2.6/ptodata/1/ina/5A.COMB.seq:*
2: /cgn2.6/ptodata/1/ina/5B.COMB.seq:*
3: /cgn2.6/ptodata/1/ina/6A.COMB.seq:*
4: /cgn2.6/ptodata/1/ina/6B.COMB.seq:*
5: /cgn2.6/ptodata/1/ina/PC105.COMB.seq:*
6: /cgn2.6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1154	56.7	2426	US-09-439-313-470	Sequence 470, App
2	1154	56.7	2426	US-09-352-616A-470	Sequence 470, App
3	1154	56.7	3112	US-09-439-313-468	Sequence 468, App
4	1154	56.7	3112	US-09-352-616A-468	Sequence 468, App
5	1033	50.7	2229	US-09-439-313-469	Sequence 469, App
6	1033	50.7	2229	US-09-352-616A-469	Sequence 469, App
7	720	35.3	812	US-09-439-313-471	Sequence 471, App
8	720	35.3	812	US-09-352-616A-471	Sequence 471, App
9	201	9.9	718	US-09-439-313-313	Sequence 313, App
10	201	9.9	718	US-09-352-616A-313	Sequence 313, App
11	201	9.9	718	US-09-232-149A-313	Sequence 313, App
12	179	8.8	301	US-09-439-313-287	Sequence 287, App
13	179	8.8	301	US-09-352-616A-287	Sequence 287, App
14	179	8.8	301	US-09-232-149A-287	Sequence 287, App
15	26	1.3	1379	US-09-620-312D-791	Sequence 791, App
16	26	1.3	1462	US-09-620-312D-788	Sequence 788, App
17	26	1.3	1519	US-09-620-312D-789	Sequence 789, App
18	20	1.0	1664976	US-08-916-421B-1	Sequence 1, Appl
19	19	0.9	161	US-08-450-834-3	Sequence 3, Appl
20	19	0.9	948	US-09-107-532A-2263	Sequence 2263, App
21	19	0.9	98844	US-09-791-211-10	Sequence 10, Appl
22	18	0.9	1324	US-09-599-360B-59	Sequence 59, Appl
23	18	0.9	1735	US-08-102-863-10	Sequence 10, Appl
24	18	0.9	1735	PCR-US92-10885-10	Sequence 10, Appl
25	18	0.9	3645	US-08-663-112-1	Sequence 1, Appl
26	18	0.9	4527	US-08-944-449-8	Sequence 8, Appl
27	18	0.9	4527	US-09-353-362-8	Sequence 8, Appl

28	18	0.9	8930	US-09-077-098A-1	Sequence 1, Appl
29	18	0.9	17000	US-09-679-299A-18	Sequence 18, Appl
30	18	0.9	72604	US-09-268-992-7	Sequence 7, Appl
31	18	0.9	72604	US-09-657-474-7	Sequence 7, Appl
32	18	0.9	99500	US-09-798-096-10	Sequence 10, Appl
33	17	0.8	157	US-08-392-678-11	Sequence 11, Appl
34	17	0.8	157	US-08-457-304A-11	Sequence 11, Appl
35	17	0.8	157	US-08-456-701A-11	Sequence 11, Appl
36	17	0.8	157	US-08-684-932A-11	Sequence 11, Appl
37	17	0.8	426	US-09-328-352-2225	Sequence 2225, App
38	17	0.8	590	US-09-364-206-25	Sequence 25, Appl
39	17	0.8	659	US-08-454-115-1	Sequence 1, Appl
40	17	0.8	831	US-08-450-834-5	Sequence 5, Appl
41	17	0.8	981	US-09-134-001C-982	Sequence 982, App
42	17	0.8	1017	US-09-328-475C-104	Sequence 104, App
43	17	0.8	1242	US-08-454-115-4	Sequence 4, Appl
44	17	0.8	2196	US-08-313-274-1	Sequence 1, Appl
45	17	0.8	2389	US-09-228-986-1	Sequence 1, Appl

ALIGNMENTS

```
RESULT 1
US-09-439-313-470/c
: Sequence 470, Application US/09439313
: Patent No. 6329505
: GENERAL INFORMATION:
: APPLICANT: Xu, Jiangchun
: APPLICANT: Dillon, Davin C.
: APPLICANT: Mitcham, Jennifer L.
: APPLICANT: Harlocker, Susan Louise
: APPLICANT: Jiang Yuxi
: APPLICANT: Reed, Steven G.
: APPLICANT: Kalos, Michael
: APPLICANT: Fanger, Gary
: APPLICANT: Retter, Mark
: APPLICANT: Solt, John
: APPLICANT: Day, Craig
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
: FILE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
: FILE REFERENCE: 210121.427C9
: CURRENT APPLICATION NUMBER: US/09/439,313
: CURRENT FILING DATE: 1999-11-12
: NUMBER OF SEQ ID NOS: 575
: SOFTWARE: FASTSEQ For Windows Version 3.0
: SEQ ID NO: 470
: LENGTH: 2426
: TYPE: DNA
: ORGANISM: Homo sapiens
US-09-439-313-470

Query Match      56.7%; Score 1154; DB 4; Length 2426;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

263 GGTGGAATAAGAAAGCGTGTGACCTTACCATGTGAGCCACACATCTGCTGTAATGG 322
|||||
1769 GGTGGAATAAGAAAGCGTGTGACCTTACCATGTGAGCCACACATCTGCTGTAATGG 1710
|||||
323 AGATATTAACCTCACTGAAACACGAGATGACATTAATGCTAGTGTGACATGT 382
|||||
1709 AGATATTAACCTCACTGAAACACGAGATGACATTAATGCTAGTGTGACATGT 1650
|||||
383 TTTTCACATTTCCAGCCCTTTAAATATCCACACACAGAGAACACAAAAGAACAC 442
|||||
1649 TTTTCACATTTCCAGCCCTTTAAATATCCACACACAGAGAACACAAAAGAACAC 1590
|||||
443 AGAGATCCCTGGGGAATAATGCCCGCCGACATCTTGGGTCAATGAGCCTCCGCTGT 502
|||||
1589 AGAGATCCCTGGGGAATAATGCCCGCCGACATCTTGGGTCAATGAGCCTCCGCTGT 1530
|||||
503 GCCTGCTCCCGCTTGTGAGGAGAACGACATTGAAATGATGCTTCTTAAGGA 562
```

|||||
Db 1529 GCCGTGCCGCTGTGAGGGAAGACATTAGAAAAGATGTGTTCCCTTAAGA 1470
QY 563 TGGGAGGAAAAAGATCTGTGTGATATTTTGAACGGGATTAACGATTGAAT 622
Db 1469 TGGGAGGAAAAAGATCTGTGTGATATTTTGAACGGGATTAACGATTGAAT 1410
QY 623 GAAGTCACAAAGATGAGATTAACCAATGAGAGAAACAGAGAAATCTTGATGCTT 682
Db 1409 GAAGTCACAAAGATGAGATTAACCAATGAGAGAAACAGAGAAATCTTGATGCTT 1350
QY 683 CACAAGCATGCAACAAACAAATGGAATCTGTGATGATGAGGAGCCAGCTGGG 742
Db 1349 CACAAGCATGCAACAAACAAATGGAATCTGTGATGATGAGGAGCCAGCTGGG 1290
QY 743 AGGAGATACACAGGGGAGGAGGATCTGTGAGGAGGAGGAGGAGGAGGAGGAGG 802
Db 1289 AGGAGATACACAGGGGAGGAGGATCTGTGAGGAGGAGGAGGAGGAGGAGGAGG 1230
QY 803 ATAAACCAATCATTTTCAATTTTCTAACCCCTCAAAAACAAAGCTGTGTAATATCTGATCTC 862
Db 1229 ATAAACCAATCATTTTCAATTTTCTAACCCCTCAAAAACAAAGCTGTGTAATATCTGATCTC 1170
QY 863 TAAGGTCCTTCTGGGCGCAACATCTTCCATATATCCAGCCACACTATTATTAATTT 922
Db 1169 TAGGTCCTTCTGGGCGCAACATCTTCCATATATCCAGCCACACTATTATTAATTT 1110
QY 923 AGTTCAGATCTGTACTGTGACCTTCTACACTGTGAAATTAACATTAATCTGATCTTTC 982
Db 1109 AGTTCAGATCTGTACTGTGACCTTCTACACTGTGAAATTAACATTAATCTGATCTTTC 1050
QY 983 AAAGACCTTCGTGTCTCTGCTTAATATGTAAGCTGACTGTTTTTCTTAAGAGTGTCTG 1042
Db 1049 AAAGACCTTCGTGTCTCTGCTTAATATGTAAGCTGACTGTTTTTCTTAAGAGTGTCTG 990
QY 1043 GCCCAGGAGATCTGTGAACAGGCTGGGAGAGCATCTCAAGATCTTCCAGGTTTACTTA 1102
Db 989 GCCCAGGAGATCTGTGAACAGGCTGGGAGAGCATCTCAAGATCTTCCAGGTTTACTTA 930
QY 1103 CTAGACACAGCATGATCATTTAGGAGTGAATTAATCAACATCATCTCAGTGTCT 1162
Db 929 CTAGACACAGCATGATCATTTAGGAGTGAATTAATCAACATCATCTCAGTGTCT 870
QY 1163 TTGGCCCTACTGAATTCATTTCCCACTTTTGTGCCATTTCTCAAGACCTCAAAATGTCA 1222
Db 869 TTGGCCCTACTGAATTCATTTCCCACTTTTGTGCCATTTCTCAAGACCTCAAAATGTCA 810
QY 1223 TTCCATTAATATCAGAGATTAATCTTTTAACTGAGAGATTAATGTTACTAG 1282
Db 809 TTCCATTAATATCAGAGATTAATCTTTTAACTGAGAGATTAATGTTACTAG 750
QY 1283 CAGCTATGGAATTTAATTAATATTTTGTTCAGTGCAGAGATGACTAAGTCTTTA 1342
Db 749 CAGCTATGGAATTTAATTAATATTTTGTTCAGTGCAGAGATGACTAAGTCTTTA 690
QY 1343 TCCCTCCCTTTGTTGATTTTTCCTCAATTAAGTAAATGCTTAAGCTTTAGCTG 1402
Db 689 TCCCTCCCTTTGTTGATTTTTCCTCAATTAAGTAAATGCTTTAGCTTTAGCTG 630
QY 1403 AGGCTGTATACAGC 1416
Db 629 AGGCTGTATACAGC 616

RESULT 2

US-09-352-616a-470/c
; Sequence 470, Application US/09352616a
; Patient No. 6395278
; GENERAL INFORMATION:
; APPLICANT: Dillon, Davin C.
; APPLICANT: Harlocker, Susan Louise
; APPLICANT: Jlang, Yuqul
; APPLICANT: Xu, Jlangchun

APPLICANT: Mitcham, Jennifer Lynn
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
; FILE REFERENCE: 210121.42708
; CURRENT APPLICATION NUMBER: US/09/352,616a
; CURRENT FILING DATE: 1999-07-13
; NUMBER OF SEQ ID NOS: 472
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 470
; LENGTH: 2426
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-352-616a-470
Query Match 56.7%; Score 1154; DB 4; Length 2426;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 263 GGTGAGAAATAGAAAGGCTGTGACTTTTACATCTGAGGCCACACATCTGTGAATGG 322
Db 1769 GGTGAGAAATAGAAAGGCTGTGACTTTTACATCTGAGGCCACACATCTGTGAATGG 1710
QY 323 AGATAATTAATCATCTAGAAACAGCAAGATGACATATATATGTTCTAAGTAGTACATGT 382
Db 1709 AGATAATTAATCATCTAGAAACAGCAAGATGACATATATATGTTCTAAGTAGTACATGT 1650
QY 383 TTTTGACATTTCCAGCCCTTTAAATATTCACACACAGAGCAACAAAGCAAGAC 442
Db 1649 TTTTGACATTTCCAGCCCTTTAAATATTCACACACAGAGCAACAAAGCAAGAC 1590
QY 443 AGAGATCCCTGGGAGAAATGCCGCCGCCATCTTGGGTATCATGATGAGCTGCCCTGT 502
Db 1589 AGAGATCCCTGGGAGAAATGCCGCCGCCATCTTGGGTATCATGATGAGCTGCCCTGT 1530
QY 503 GCCCTGGTCCCGCTTGTGAGGAGAGGACATTAAGAAATGAATGATGTTCTTAAAGGA 562
Db 1529 GCCCTGGTCCCGCTTGTGAGGAGAGGACATTAAGAAATGAATGATGTTCTTAAAGGA 1470
QY 563 TGGGAGGAAAAAGATCTGTGTGATATTTTGAACGGGATTAACGATTGAAT 622
Db 1469 TGGGAGGAAAAAGATCTGTGTGATATTTTGAACGGGATTAACGATTGAAT 1410
QY 623 GAAGTCACAAAGATGAGATTAACCAATGAGAGAAACAGAGAAATCTTGATGCTT 682
Db 1409 GAAGTCACAAAGATGAGATTAACCAATGAGAGAAACAGAGAAATCTTGATGCTT 1350
QY 683 CACAAGCATGCAACAAACAAATGGAATCTGTGATGATGAGGAGCCAGCTGGG 742
Db 1349 CACAAGCATGCAACAAACAAATGGAATCTGTGATGATGAGGAGCCAGCTGGG 1290
QY 743 AGGAGATACACAGGGGAGGAGGATCTGTGAGGAGGAGGAGGAGGAGGAGGAGG 802
Db 1289 AGGAGATACACAGGGGAGGAGGATCTGTGAGGAGGAGGAGGAGGAGGAGGAGG 1230
QY 803 ATAAACCAATCATTTTCAATTTTCTAACCCCTCAAAAACAAAGCTGTGTAATATCTGATCTC 862
Db 1229 ATAAACCAATCATTTTCAATTTTCTAACCCCTCAAAAACAAAGCTGTGTAATATCTGATCTC 1170
QY 863 TAAGGTCCTTCTGGGCGCAACATCTTCCATATATCCAGCCACACTATTATTAATTT 922
Db 1169 TAAGGTCCTTCTGGGCGCAACATCTTCCATATATCCAGCCACACTATTATTAATTT 1110
QY 923 AGTTCAGATCTGTACTGTGACCTTCTACACTGTGAAATTAACATTAATCTGATCTTTC 982
Db 1109 AGTTCAGATCTGTACTGTGACCTTCTACACTGTGAAATTAACATTAATCTGATCTTTC 1050
QY 983 AAAGACCTTCGTGTCTCTGCTTAATATGTAAGCTGACTGTTTTTCTTAAGAGTGTCTG 1042
Db 1049 AAAGACCTTCGTGTCTCTGCTTAATATGTAAGCTGACTGTTTTTCTTAAGAGTGTCTG 990
QY 1043 GCCCAGGAGATCTGTGAACAGGCTGGGAGAGCATCTCAAGATCTTCCAGGTTTACTTA 1102
Db 989 GCCCAGGAGATCTGTGAACAGGCTGGGAGAGCATCTCAAGATCTTCCAGGTTTACTTA 930

443 AGAGATCCCTGGAGAAATGCCGGCCGATCTTGGTCATGATGAGCTCGCCCTGT 502
1595 AAGAGATCCCTGGAGAAATGCCGGCCGATCTTGGTCATGATGAGCTCGCCCTGT 1536
503 GCGTGGTCCCTGTGAGGGAAGACATTTAGAAAATGAATGATGTCTTCTTAAGGA 562
1535 GCGTGGTCCCTGTGAGGGAAGACATTTAGAAAATGAATGATGTCTTCTTAAGGA 1476
563 TGGGAGGAAAAACATCTCTGTGTGATATTTATTGACGGGATTTACAGTTTGAAT 622
1475 TGGGAGGAAAAACATCTCTGTGTGATATTTATTGACGGGATTTACAGTTTGAAT 1416
623 GAAGTCACAAATGAGCATTTACCAATGAGGAAAAACAGAGAAATCTGATGGCT 682
1415 GAAGTCACAAATGAGCATTTACCAATGAGGAAAAACAGAGAAATCTGATGGCT 1356
683 CACAAGACATGCAACAAACAAATGGAATCTGTATGACATGAGGCAAGCTGGGG 742
1355 CACAAGACATGCAACAAACAAATGGAATCTGTATGACATGAGGCAAGCTGGGG 1296
743 AGGATATACCAACGGGGCAGAGGGTCAGGATTTGCGCTGCTTAACCTGTGCTTC 802
1295 AGGATATACCAACGGGGCAGAGGGTCAGGATTTGCGCTGCTTAACCTGTGCTTC 1236
803 ATACCAATCATTTCTATTTCTAACCTCAAAACAAAGCTGTGATATCTGATCTC 862
1235 ATACCAATCATTTCTATTTCTAACCTCAAAACAAAGCTGTGATATCTGATCTC 1176
863 TACGGTCTCTTGGGCCCAACATTTCTCAATATTCAGCCACACTCATTTTAAATTT 922
1175 TACGGTCTCTTGGGCCCAACATTTCTCAATATTCAGCCACACTCATTTTAAATTT 1116
923 AGTTCACAGATGTGACGTGACCTTTCTACACTGTAGAAATACATTTACTCTTTGTC 982
1115 AGTTCACAGATGTGACGTGACCTTTCTACACTGTAGAAATACATTTACTCTTTGTC 1056
983 AAGAGACCTTCTGTGCTGCTTAATATGATGATGATGATGATGATGATGATGATG 1042
1055 AAGAGACCTTCTGTGCTGCTTAATATGATGATGATGATGATGATGATGATGATG 996
1043 GCCCAGGGGANTGTGAACAGGCTGGGAAGCATCTCAAGATCTTTCAGGGTTATCTTA 1102
995 GCCCAGGGGANTGTGAACAGGCTGGGAAGCATCTCAAGATCTTTCAGGGTTATCTTA 936
1103 CTAGACACAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1162
935 CTAGACACAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 876
1163 TTGGCCATACGAAATTCATTTCCACTTTTGTGCCCATTTCTCAAGACCTCAAAATGTCA 1222
875 TTGGCCATACGAAATTCATTTCCACTTTTGTGCCCATTTCTCAAGACCTCAAAATGTCA 816
1223 TTCCATTAATATCAGAGATTAATCTTTTAACTGGAAGATTCATGTTACATG 1282
815 TTCCATTAATATCAGAGATTAATCTTTTAACTGGAAGATTCATGTTACATG 757
1283 CAGCATATGGGATTTAATTTACATTTTGTTCAGTGCAAGATGACTAGTCTTTA 1342
756 CAGCATATGGGATTTAATTTACATTTTGTTCAGTGCAAGATGACTAGTCTTTA 697
1343 TCCCTCCCTTGTGATTTTTCAGTATTAAGTTAAATGCTTGGCTTGTACTG 1402
696 TCCCTCCCTTGTGATTTTTCAGTATTAAGTTAAATGCTTGGCTTGTACTG 637
1403 AGGCTGTATACAGC 1416
636 AGGCTGTATACAGC 623

RESULT 6
US-09-352-616A-469/c
; Sequence 469, Application US/09352616A

Patent No. 6395278
GENERAL INFORMATION:
APPLICANT: Dillon, Davin C.
APPLICANT: Harlocker, Susan Louise
APPLICANT: Jiang, Yugu
APPLICANT: Xu, Jiangchun
APPLICANT: Mitcham, Jennifer Lynn
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
FILE REFERENCE: 210121.42708
CURRENT FILING DATE: 1999-07-13
NUMBER OF SEQ ID NOS: 472
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 469
LENGTH: 2229
TYPE: DNA
ORGANISM: Homo sapiens
US-09-352-616A-469

Query Match 50.7%; Score 1033; DB 4; Length 2229;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1153; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

263 GGTGAGAAATTAAGAAAGGCTGCTGACTTACCATCTGAGGCCACACATGCTGAAATG 322
1775 GGTGAGAAATTAAGAAAGGCTGCTGACTTACCATCTGAGGCCACACATGCTGAAATG 1716
323 AGATTAATTAACATCTAGAAACAGCAGATGACATATATATGTTAAGTATGACATGT 382
1715 AGATTAATTAACATCTAGAAACAGCAGATGACATATATATGTTAAGTATGACATGT 1656
383 TTTTGCACATTTCCAGCCCTTTAATATCCACACACAGAGAACACAAAAGAACAC 442
1655 TTTTGCACATTTCCAGCCCTTTAATATCCACACACAGAGAACACAAAAGAACAC 1596
443 AGAGATCCCTGGGAGAAATGCCGGCCGATCTTGGGTCATGATGATGATGATGATG 502
1595 AGAGATCCCTGGGAGAAATGCCGGCCGATCTTGGGTCATGATGATGATGATGATG 1536
503 GCGTGGTCCCTGTGAGGGAAGACATTTAGAAATGATGATGATGATGATGATGATG 562
1535 GCGTGGTCCCTGTGAGGGAAGACATTTAGAAATGATGATGATGATGATGATGATG 1476
563 TGGGAGGAAAAACATCTCTGTGATGATTTATTTGAAGGGATTCAGATTTGAAT 622
1475 TGGGAGGAAAAACATCTCTGTGATGATTTATTTTGAAGGGATTTACAGATTTGAAT 1416
623 GAAGTCACAAATGAGCATTTACCAATGAGGAAAAACAGAGAAATCTTGTATGCTTC 682
1415 GAAGTCACAAATGAGCATTTACCAATGAGGAAAAACAGAGAAATCTTGTATGCTTC 1356
683 CACAAGACATGCAACAAACAAATGGAATCTGTATGACATGAGGCAAGCTGGGG 742
1355 CACAAGACATGCAACAAACAAATGGAATCTGTATGACATGAGGCAAGCTGGGG 1296
743 AGGATATACCAACGGGGCAGAGGGTCAGGATTTGCGCTGCTTAACCTGCTTC 802
1295 AGGATATACCAACGGGGCAGAGGGTCAGGATTTGCGCTGCTTAACCTGCTTC 1236
803 ATACCAATCATTTCTATTTCTAACCTCAAAACAAAGCTGTGATATCTGATCTC 862
1235 ATACCAATCATTTCTATTTCTAACCTCAAAACAAAGCTGTGATATCTGATCTC 1176
863 TACGGTCTCTTGGGCCCAACATTTCTCAATATTCAGCCACACTCATTTTAAATTT 922
1175 TACGGTCTCTTGGGCCCAACATTTCTCAATATTCAGCCACACTCATTTTAAATTT 1116
923 AGTTCACAGATGTGACGTGACCTTTCTACACTGTAGAAATACATTTACTCTTTGTC 982
1115 AGTTCACAGATGTGACGTGACCTTTCTACACTGTAGAAATACATTTACTCTTTGTC 1056
983 AAGAGACCTTCTGTGCTGCTTAATATGATGATGATGATGATGATGATGATGATG 1042

Db	1055	AAAGACCCTTGCTGTGCTGCTAATATGTAAGCTGCTGTTTCTCTAAGGAGTGTCTG	996
OY	1043	GCCCCAGGGAGTCTGTGAAACAGGCTGGGAGAGCATCTCAAGATCTTTCACGGTTATACTTA	11020
Db	995	GCCCCAGGGAGTCTGTGAAACAGGCTGGGAGAGCATCTCAAGATCTTTCACGGTTATACTTA	936
OY	1103	CTAGCACACAGCATGATCATTACGGAGTGAATATCTAATCAACATCATCTCCAGTGTCT	1162
Db	935	CTAGCACACAGCATGATCATTACGGAGTGAATATCTAATCAACATCATCTCCAGTGTCT	876
OY	1163	TTGCCCATCTACGAAATTCATTTCCCACTTTTGTGCCCACTTCTCAAGACCTCAAAATGTCA	12222
Db	875	TTGCCCATCTACGAAATTCATTTCCCACTTTTGTGCCCACTTCTCAAGACCTCAAAATGTCA	816
OY	1223	TTCCATTAAATTCACAGGATTAACCTTTTTTTTAACTGGAAGAATTCATGTTACATG	1282
Db	815	TTCCATTAAATTCACAGGATTAAC-TTTTTTTTTAACTGGAAGAATTCATGTTACATG	757
OY	1283	CAGCTATGAGGAATTTAATTAACATATTTTGGTTTCCAGTGCAGGAAGTAGCTAAGCTCTTA	1342
Db	756	CAGCTATGAGGAATTTAATTAACATATTTTGGTTTCCAGTGCAGGAAGTAGCTAAGCTCTTA	697
OY	1343	TCCCTCCCTTTGGTTGATTTTTTTTCCAGATATAAGTTAAAGTCTTAGCCTGTACTG	1402
Db	696	TCCCTCCCTTTGGTTGATTTTTTTTCCAGATATAAGTTAAAGTCTTAGCCTGTACTG	637
OY	1403	AGGCTGTATACAGC 1416	
Db	636	AGGCTGTATACAGC 623	

RESULT 7

```

US-09-439-313-471/c
: Sequence 471, Application US/09439313
: Patent No. 6329505
: GENERAL INFORMATION:
: APPLICANT: Xu, Jiangchun
: APPLICANT: Dillon, David C.
: APPLICANT: Mitcham, Jennifer L.
: APPLICANT: Harlocker, Susan Louise
: APPLICANT: Jiang Yuqul
: APPLICANT: Reed, Steven G.
: APPLICANT: Kalos, Michael
: APPLICANT: Fanger, Gary
: APPLICANT: Retter, Mark
: APPLICANT: Solk, John
: APPLICANT: Day, Craig
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
: TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
: FILE REFERENCE: 210121.427C9
: CURRENT APPLICATION NUMBER: US/09/439, 313
: CURRENT FILING DATE: 1999-11-12
: NUMBER OF SEQ ID NOS: 575
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 471
: LENGTH: 812
: TYPE: DNA
: ORGANISM: Homo sapiens
US-09-439-313-471

```

Query Match	35.3%;	Score 720;	DB 4;	Length 812;
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches 720;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

QY	263	GGTGAGAAATTAAGAAAGCGCTGCTACTTTACCATCTGAGGCGACACATCTGCTGAAATGG	322
Db	720	GGTGAGAAATTAAGAAAGCGCTGCTACTTTACCATCTGAGGCGACACATCTGCTGAAATGG	661
QY	323	AGATAATTAACATCTACTGAAACAGCAGCATGACATATTAATGTGTAAGTAGTGCATGT	382
Db	660	AGATAATTAACATCTACTGAAACAGCAGCATGACATATTAATGTGTAAGTAGTGCATGT	601

QY	383	TTTTGCACATTTCCAGCCCTTTAAATATCCACACACACAGAGACACAAAAAGACAC	442
Db	600	TTTTGGCATTTCACCCCTTTAAATATCCACACACAGAGAAACAAAAAGAACAC	541
OY	443	AGAGATCCCGGGGAAATGCCCCGGCCATCTTGGGGTCATTCGATGAGCCCTGCCTGT	502
Db	540	AGAGATCCCTGGGAGAAATGCCCCGGCCATCTTGGGTCAATCGATGAGCCTGCCCTGT	481
OY	503	GCCGTGTCGCCCTTGTGAGGGAGAGACATTAGAAAATGAATTGATGTTCCTTTAAAGA	562
Db	480	GCCGTGTCGCCCTTGTGAGGGAGAGACATTAGAAAATGAATTGATGTTCCTTTAAAGA	421
OY	563	TGGGCAGAAAACACAGTCTGTGTGTGATATTATTAGACGGCATTCAGATTTGAAT	622
Db	420	TGGGCAGAAAACAGATCCTGTGTGTGATATTATTAGACGGCATTCAGATTTGAAT	361
OY	623	GAAGTCACAAAGTACATTTACCAATGAGAGAAAACAGAGAAATCTTGATGGCTT	682
Db	360	GAAGTCACAAAGTACATTTACCAATGAGAGAAAACAGAGAAATCTTGATGGCTT	301
OY	683	CACAGACATGCAACCAACAAAATGGAAATCTGTGATGACATGAGGCGCCCAAGCTGGG	742
Db	300	CACAGACATGCAACCAACAAAATGGAAATCTGTGATGACATGAGGCGCCCAAGCTGGG	241
OY	743	AGGAGATTAACACGGGGCAGAGGGTCAAGATTTCTGGCCTGCTGCTTAACGTGTGCTTC	802
Db	240	AGGAGATTAACACGGGGCAGAGGGTCAAGATTTCTGGCCTGCTGCTTAACGTGTGCTTC	181
OY	803	ATTAAACAAATCATTTATATTTCTTAACCTCAAAACAAAGCGTGTGAATTCGATCTC	862
Db	180	ATTAAACAAATCATTTATATTTCTTAACCTCAAAACAAAGCGTGTGTGAATTCGATCTC	121
OY	863	TAGGTTCTCTTGGGCCCAACATTTCTCATATTAACGACACACTATTTTAAATTTT	922
Db	120	TAGGTTCTCTTGGGCCCAACATTTCTCATATTAACGACACACTATTTTAAATTTT	61
OY	923	AGTTCCACAGATCTGTACTGTGACCTTTCTACACTGTAGAAATTAACATTAATCTATTTGTTC	982
Db	60	AGTTCCACAGATCTGTACTGTGACCTTTCTACACTGTAGAAATTAACATTAATCTATTTGTTC	1

RESULT 8

```

US-09-352-616A-471/c
: Sequence 471, Application US/09352616A
: Patent No. 6395278
:
: GENERAL INFORMATION:
: APPLICANT: Dillon, Davin C.
: APPLICANT: Harlocker, Susan Louise
: APPLICANT: Jiang, Yugu
: APPLICANT: Xu, Jiangchun
: APPLICANT: Mitcham, Jennifer Lynn
:
: TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
:
: TITLE OF INVENTION: OF PROSTATE CANCER AND METHODS FOR THEIR USE
:
: FILE REFERENCE: 210121.427C8
:
: CURRENT APPLICATION NUMBER: US/09/352,616A
:
: NUMBER OF SEQ ID NOS: 472
:
: SOFTWARE: FastSeq for Windows Version 3.0
:
: SEQ ID NO 471
:
: LENGTH: 812
:
: TYPE: DNA
:
: ORGANISM: Homo sapiens
:
: US-09-352-616A-471

```

Query Match	35.3%	Score 720;	DB 4;	Length 812;
Best Local Similarity	100.0%	Pred. No. 0;		
Matches 720;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0

QY	Db	OY
263	GGTGGAATTAAGAAAGCGCTGCTGACTTTTACCATGTGAGGCCACACATCTGCTGAATATGG	322
720	GGTGGAATTAAGAAAGCGCTGCTGACTTTTACCATGTGAGGCCACACATCTGCTGAATATGG	661
323	AGATAATTTAACCATCTACTAGAAACAGCAGATGACCAATATTAATGTCCTAAGTAGTGCATGAT	382


```

Db 660 AGATATTACATCTCTGAAACACAGATGACATATTAATGTTAGTGTGACATGT 601
|
|
|
Oy 383 TTTTGACATTTCCAGCCCTTTTAAATATCCACACACAGAGACACAAAAGAGACAC 442
|
|
|
Db 600 TTTTTCACATTTCCAGCCCTTTTAAATATCCACACACAGAGACACAAAAGAGACAC 541
|
|
|
Oy 443 AGAGATCCCTGGGAGAAATGCCCCGCCCATCTTGGGTCAATGAGCCCTGCCCTGT 502
|
|
|
Db 540 AGAGATCCCTGGGAGAAATGCCCCGCCCATCTTGGGTCAATGAGCCCTGCCCTGT 481
|
|
|
Oy 503 GCTGTGTCCTGCTGTGAGGAGAGACATTTAGAAATGAATTGATGTTCTTCTTAAAGA 562
|
|
|
Db 480 GCTGTGTCCTGCTGTGAGGAGAGACATTTAGAAATGAATTGATGTTCTTCTTAAAGA 421
|
|
|
Oy 563 TGGGAGAGAAACAGATCTGTGTGATATTTTGAACGGGATTAACAGATTTGAAT 622
|
|
|
Db 420 TGGGAGAGAAACAGATCTGTGTGATATTTTGAACGGGATTAACAGATTTGAAT 361
|
|
|
Oy 623 GAAGTCAAAAGTGAAGCATTTACCAATGAGAGAAACAGAGAAATCTTGATGGCTT 682
|
|
|
Db 360 GAAGTCAAAAGTGAAGCATTTACCAATGAGAGAAACAGAGAAATCTTGATGGCTT 301
|
|
|
Oy 683 CACAAGACATGCAACAAACAAATGGAATGATGATGATGATGATGATGATGATGATG 742
|
|
|
Db 300 CACAAGACATGCAACAAACAAATGGAATGATGATGATGATGATGATGATGATGATG 241
|
|
|
Oy 743 AGGAGATRACACAGGGGAGAGGATGAGATTTGGCCCTGCTGCTTAACTGTGCGTTC 802
|
|
|
Db 240 AGGAGATRACACAGGGGAGAGGATGAGATTTGGCCCTGCTGCTTAACTGTGCGTTC 181
|
|
|
Oy 803 ATACCAAAATCATTTTCAATTTTCAACCTCAAAACAAAGCTGTTGATATTCGATCTC 862
|
|
|
Db 180 ATACCAAAATCATTTTCAATTTTCAACCTCAAAACAAAGCTGTTGATATTCGATCTC 121
|
|
|
Oy 863 TAGGTTCTCTTGGGCCCAACATTTCTCCATATATCCAGCACACTCTTTTAAATATT 922
|
|
|
Db 120 TAGGTTCTCTTGGGCCCAACATTTCTCCATATATCCAGCACACTCTTTTAAATATT 61
|
|
|
Oy 923 AGTTCGCCGATCTGTACTGTGACCTTTTACACGTGAGAAATACATTTCTCTATTTGTTTC 982
|
|
|
Db 60 AGTTCGCCGATCTGTACTGTGACCTTTTACACGTGAGAAATACATTTCTCTATTTGTTTC 1
|
|
|

```

RESULT 9

```

US-09-439-313-313
; Sequence 313, Application US/09439313
; Patent No. 6329505
; GENERAL INFORMATION:
; APPLICANT: Dillon, Davin C.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan Louise
; APPLICANT: Jiang Yugu
; APPLICANT: Reed, Steven G.
; APPLICANT: Kalos, Michael
; APPLICANT: Fanger, Gary
; APPLICANT: Retter, Mark
; APPLICANT: Solk, John
; APPLICANT: Day, Craig
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
; FILE REFERENCE: 210121.427C9
; CURRENT FILING DATE: 1999-11-12
; CURRENT APPLICATION NUMBER: US/09/439,313
; NUMBER OF SEQ ID NOS: 575
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 313
; LENGTH: 718
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc_feature

```

```

; LOCATION: (1)...(718)
; OTHER INFORMATION: n = A,T,C or G
US-09-439-313-313

```

```

Query Match
Best Local Similarity 9.9%; Score 201; DB 4; Length 718;
Matches 301; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```

```

Oy 263 GGTGAGAAATAGAAAGGCTGCTGACTTTTACATCTGAGGCCACACATCTGCTGAATGG 322
|
|
|
Db 73 GGTGAGAAATAGAAAGGCTGCTGACTTTTACATCTGAGGCCACACATCTGCTGAATGG 132
|
|
|
Oy 323 AGATATTACATCTCTGAAACACAGATGACATATTAATGTTAGTGTGACATGT 382
|
|
|
Db 133 AGATATTACATCTCTGAAACACAGATGACATATTAATGTTAGTGTGACATGT 192
|
|
|
Oy 383 TTTTGACATTTCCAGCCCTTTTAAATATCCACACACAGAGACACAAAAGAGACAC 442
|
|
|
Db 193 TTTTGACATTTCCAGCCCTTTTAAATATCCACACACAGAGACACAAAAGAGACAC 252
|
|
|
Oy 443 AGAGATCCCTGGGAGAAATGCCCGGCCCATCTTGGGTCAATGATGATGATGATGATG 502
|
|
|
Db 253 AGAGATCCCTGGGAGAAATGCCCGGCCCATCTTGGGTCAATGATGATGATGATGATG 312
|
|
|
Oy 503 GCTGTGTCCTGCTGTGAGGAGAGACATTTAGAAATGAATTGATGTTCTTCTTAAAGA 562
|
|
|
Db 313 GCTGTGTCCTGCTGTGAGGAGAGACATTTAGAAATGAATTGATGTTCTTCTTAAAGA 372
|
|
|
Oy 563 TGG 565
|
|
|
Db 373 TGG 375
|
|
|

```

RESULT 10

```

US-09-352-616A-313
; Sequence 313, Application US/09352616A
; Patent No. 6395278
; GENERAL INFORMATION:
; APPLICANT: Dillon, Davin C.
; APPLICANT: Harlocker, Susan Louise
; APPLICANT: Jiang, Yugu
; APPLICANT: Xu, Jiangchun
; APPLICANT: Mitcham, Jennifer Lynn
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
; FILE REFERENCE: 210121.427C8
; CURRENT FILING DATE: 1999-07-13
; NUMBER OF SEQ ID NOS: 472
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 313
; LENGTH: 718
; TYPE: DNA
; ORGANISM: Homo sapien
; NAME/KEY: misc_feature
; LOCATION: (1)...(718)
; OTHER INFORMATION: n = A,T,C or G
US-09-352-616A-313

```

```

Query Match
Best Local Similarity 9.9%; Score 201; DB 4; Length 718;
Matches 301; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```

```

Oy 263 GGTGAGAAATAGAAAGGCTGCTGACTTTTACATCTGAGGCCACACATCTGCTGAATGG 322
|
|
|
Db 73 GGTGAGAAATAGAAAGGCTGCTGACTTTTACATCTGAGGCCACACATCTGCTGAATGG 132
|
|
|
Oy 323 AGATATTACATCTCTGAAACACAGATGACATATTAATGTTAGTGTGACATGT 382
|
|
|
Db 133 AGATATTACATCTCTGAAACACAGATGACATATTAATGTTAGTGTGACATGT 192
|
|
|
Oy 383 TTTTGACATTTCCAGCCCTTTTAAATATCCACACACAGAGACACAAAAGAGACAC 442
|
|
|

```

|||||
Db 193 TTTTGCATTTCCAGCCCTTTTAAATATCCACACACAGGAGCAAAAGGAACAC 252
QY 443 AGAGATCCCTGGAGAAATCCCGGCCCATCTTGGTATCGATGAGCCTGCCCTGT 502
Db 253 AGAGATCCCTGGAGAAATCCCGGCCCATCTTGGTATCGATGAGCCTGCCCTGT 312
QY 503 GCCTGGTCCCGCTTGTGAGGAAAGACATTAGAAAATGAATGTGTTCTTAAAGA 562
Db 313 GCCTGGTCCCGCTTGTGAGGAAAGACATTAGAAAATGAATGTGTTCTTAAAGA 372
QY 563 TGG 565
Db 373 TGG 375

RESULT 11
US-09-232-149A-313
Sequence 313, Application US/09232149A
Patent No. 6465611
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer Lynn
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE
FILE REFERENCE: 210121.427C6
CURRENT APPLICATION NUMBER: US/09/232,149A
CURRENT FILING DATE: 1999-01-15
NUMBER OF SEQ ID NOS: 338
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 313
LENGTH: 718
TYPE: DNA
ORGANISM: Homo sapien
FEATURE:
NAME/KEY: misc_feature
LOCATION: (11)...(718)
OTHER INFORMATION: n = A,T,C or G
US-09-232-149A-313

Query Match 9.9%; Score 201; DB 4; Length 718;
Best Local Similarity 99.3%; Pred. No. 6.1e-88;
Matches 301; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 263 GGTGAGAAATAGAAAGGCTGCTACCTTACATCTGAGGCCACACATCTGCTGAATGG 322
Db 73 GGTGAGAAATAGAAAGGCTGCTACCTTACATCTGAGGCCACACATCTGCTGAATGG 132
QY 323 AGTAAATTAACATCACTAGAAACAGCAAGATGACATATATGTCTTAAGTAGACATGT 382
Db 133 AGTAAATTAACATCACTAGAAACAGCAAGATGACATATATGTCTTAAGTAGACATGT 192
QY 383 TTTTGCATTTCCAGCCCTTTTAAATATCCACACACAGGAGCAAAAGGAACAC 442
Db 193 TTTTGCATTTCCAGCCCTTTTAAATATCCACACACAGGAGCAAAAGGAACAC 252
QY 443 AGAGATCCCTGGAGAAATCCCGGCCCATCTTGGTATCGATGAGCCTGCCCTGT 502
Db 253 AGAGATCCCTGGAGAAATCCCGGCCCATCTTGGTATCGATGAGCCTGCCCTGT 312
QY 503 GCCTGGTCCCGCTTGTGAGGAAAGACATTAGAAAATGAATGTGTTCTTAAAGA 562
Db 313 GCCTGGTCCCGCTTGTGAGGAAAGACATTAGAAAATGAATGTGTTCTTAAAGA 372
QY 563 TGG 565
Db 373 TGG 375

RESULT 12
US-09-439-313-287/C
Sequence 287, Application US/09439313

Patent No. 6329505
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan Louise
APPLICANT: Jiang Yuqi
APPLICANT: Reed, Steven G.
APPLICANT: Kalos, Michael
APPLICANT: Fanger, Gary
APPLICANT: Retter, Mark
APPLICANT: Solt, John
APPLICANT: Day, Craig
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
FILE REFERENCE: 210121.427C9
CURRENT APPLICATION NUMBER: US/09/439,313
CURRENT FILING DATE: 1999-11-12
NUMBER OF SEQ ID NOS: 575
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 287
LENGTH: 301
TYPE: DNA
ORGANISM: Homo sapien
US-09-439-313-287

Query Match 8.8%; Score 179; DB 4; Length 301;
Best Local Similarity 99.6%; Pred. No. 3e-77;
Matches 229; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 637 AGCATTAACATGAGGAAAGGAGGAAATCTTGTGCTTACACAGCATGCA 696
Db 301 AGCATTAACATGAGGAAAGGAGGAAATCTTGTGCTTACACAGCATGCA 242
QY 697 CAACAAAATGGAATCTGTGATGACATGAGGAGGAGGAGGAGATACACG 756
Db 241 CAACAAAATGGAATCTGTGATGACATGAGGAGGAGGAGGAGATACACG 182
QY 757 GGGCAGAGGCTCAGGATTTGGCCCTGCTCTAACTGCTTCAATACCAATCAT 816
Db 181 GGGCAGAGGCTCAGGATTTGGCCCTGCTCTAACTGCTTCAATACCAATCAT 122
QY 817 TCATATTTCACCCCTCAAAAGAGCTGTTGATATCTGATCTACG 866
Db 121 TCATATTTCACCCCTCAAAAGAGCTGTTGATATCTGATCTACG 72

RESULT 13
US-09-352-616A-287/C
Sequence 287, Application US/09352616A
Patent No. 6395278
GENERAL INFORMATION:
APPLICANT: Dillon, Davin C.
APPLICANT: Harlocker, Susan Louise
APPLICANT: Jiang Yuqi
APPLICANT: Xu, Jiangchun
APPLICANT: Mitcham, Jennifer Lynn
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
FILE REFERENCE: 210121.427C8
CURRENT APPLICATION NUMBER: US/09/352,616A
CURRENT FILING DATE: 1999-07-13
NUMBER OF SEQ ID NOS: 472
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 287
LENGTH: 301
TYPE: DNA
ORGANISM: Homo sapien
US-09-352-616A-287

Query Match 8.8%; Score 179; DB 4; Length 301;
Best Local Similarity 99.6%; Pred. No. 3e-77;
Matches 229; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

QY 637 AGCATTTACCAATGAGAGGAAAAACAGAGGAAATCTTGATGGCTTCAAGACATGCAA 696
    |||||||
DB 301 AGCATTTACCAATGAGAGGAAAAACAGAGGAAATCTTGATGGCTTCAAGACATGCAA 242
QY 697 CAACCAAAATGGAATACTGTGTATGATGAGGACAGCCAAAGCTGGGAGAGATAACACAG 756
    |||||||
DB 241 CAACCAAAATGGAATACTGTGTATGATGAGGACAGCCAAAGCTGGGAGAGATAACACAG 182
QY 757 GGGCAGAGGCTCAGAGATTCTGGCCCTGCTTAACCTGTGCTTCATTAACCAATCAT 816
    |||||||
DB 181 GGGCAGAGGCTCAGAGATTCTGGCCCTGCTTAACCTGTGCTTCATTAACCAATCAT 122
QY 817 TCATATTTCTAACCTCAAAACAAAGCTGTGTAATATCTATCTCTACG 866
    |||||||
DB 121 TCATATTTCTAACCTCAAAACAAAGCTGTGTAATATCTATCTCTACG 72

```

RESULT 14

```

US-09-232-149A-287/C
; Sequence 287, Application US/09232149A
; Patent No. 6465611
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Jennifer Lynn
; APPLICANT: Mitcham, Jennifer Lynn
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE
; FILE REFERENCE: 210121.427C6
; CURRENT APPLICATION NUMBER: US/09/232.149A
; CURRENT FILING DATE: 1999-01-15
; NUMBER OF SEQ ID NOS: 338
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 287
; LENGTH: 301
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-232-149A-287

```

```

Query Match      8.8%; Score 179; DB 4; Length 301;
Best Local Similarity 99.6%; Pred. No. 3e-77;
Matches 229; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

QY 637 AGCATTTACCAATGAGAGGAAAAACAGAGGAAATCTTGATGGCTTCAAGACATGCAA 696
    |||||||
DB 301 AGCATTTACCAATGAGAGGAAAAACAGAGGAAATCTTGATGGCTTCAAGACATGCAA 242
QY 697 CAACCAAAATGGAATACTGTGTATGATGAGGACAGCCAAAGCTGGGAGAGATAACACAG 756
    |||||||
DB 241 CAACCAAAATGGAATACTGTGTATGATGAGGACAGCCAAAGCTGGGAGAGATAACACAG 182
QY 757 GGGCAGAGGCTCAGAGATTCTGGCCCTGCTTAACCTGTGCTTCATTAACCAATCAT 816
    |||||||
DB 181 GGGCAGAGGCTCAGAGATTCTGGCCCTGCTTAACCTGTGCTTCATTAACCAATCAT 122
QY 817 TCATATTTCTAACCTCAAAACAAAGCTGTGTAATATCTATCTCTACG 866
    |||||||
DB 121 TCATATTTCTAACCTCAAAACAAAGCTGTGTAATATCTATCTCTACG 72

```

RESULT 15

```

US-09-620-312D-791
; Sequence 791, Application US/09620312D
; Patent No. 6569662
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Zhang, Jie
; APPLICANT: Ren, Feiyan
; APPLICANT: Chen, Rui-hong
; APPLICANT: Zhao, Qing A.
; APPLICANT: Wehrman, Tom

```

```

; APPLICANT: Xue, Aidong J.
; APPLICANT: Yang, Yonghong
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Zhou, Ping
; APPLICANT: Ma, Yundong
; APPLICANT: Wang, Duntui
; APPLICANT: Wang, Zhiwei
; APPLICANT: John Tillinghast
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: No. 6569662e1 Nucleic Acids and
; FILE REFERENCE: Polypeptides
; FILE REFERENCE: 784CIP2B
; CURRENT APPLICATION NUMBER: US/09/620.312D
; CURRENT FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: 09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/488,725
; PRIOR FILING DATE: 2000-01-21
; NUMBER OF SEQ ID NOS: 1105
; SOFTWARE: PL_FL_genes Version 1.0
; SEQ ID NO 791
; LENGTH: 1379
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (109)..(789)
US-09-620-312D-791

```

```

Query Match      1.3%; Score 26; DB 4; Length 1379;
Best Local Similarity 100.0%; Pred. No. 0.0065;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1142 TCACATCATCTCTCAGTGTCTTGGC 1167
    |||||||
DB 335 TCACATCATCTCTCAGTGTCTTGGC 360

```

```

Search completed: September 27, 2003, 11:43:49
Job time : 120.911 secs

```

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: September 26, 2003, 19:58:56 ; Search time 69 Seconds
(without alignments)
326.240 Million cell updates/sec

Title: US-09-402-713A-2

Perfect score: 51

Sequence: 1 MFLHISPFKPHPTQEAQKE.....HLGSSMLALCLVPLVREGH 51

Scoring table:

	OLIGO
Xgapop 60.0 ,	Xgapext 60.0
Ygapop 60.0 ,	Ygapext 60.0
Fgapop 6.0 ,	Fgapext 7.0
Delop 6.0 ,	Delext 7.0

Searched: 569978 seqs, 220691566 residues

Word size: 1

Total number of hits satisfying chosen parameters: 1135271

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: listing first 45 summaries

Command line parameters:

-MODEL=frame+p2n model -DEV=xlh
-O=/cgn2.1/USPTO/US09402713/runat_26092003_143100_16996/app.query.fasta.1.199
-DB=Issued_Patents_NA -QEXT=fastap -SUFFIX=olig.rni -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=oligo -TRANS=human40.cdi
-LIST=45 -DOCCALIGN=200 -THR_SCORE=quality -THR_MIN=1 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09402713.ecgn.1.1.56.0runat_26092003_143100_16996 -NCPU=6 -ICPU=3
-NO_MMAPP -LARGEOUTERY -NEG_SCORES=0 -WAIT -DSPELOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7

Database :

- 1: Issued Patents NA:*
- 2: /cgn2.6/ptodata/1/ina/5A.COMB.seq:*
- 3: /cgn2.6/ptodata/1/ina/5B.COMB.seq:*
- 4: /cgn2.6/ptodata/1/ina/6A.COMB.seq:*
- 5: /cgn2.6/ptodata/1/ina/6B.COMB.seq:*
- 6: /cgn2.6/ptodata/1/ina/Backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	51	100.0	812	4	US-09-439-313-471
C 2	51	100.0	812	4	US-09-352-616A-471
C 3	51	100.0	2229	4	US-09-439-313-469
C 4	51	100.0	2229	4	US-09-352-616A-469
C 5	51	100.0	2426	4	US-09-439-313-470
C 6	51	100.0	2426	4	US-09-352-616A-470
C 7	51	100.0	3112	4	US-09-439-313-468
C 8	51	100.0	3112	4	US-09-352-616A-468
C 9	43	84.3	718	4	US-09-439-313-313
C 10	43	84.3	718	4	US-09-352-616A-313
C 11	43	84.3	718	4	US-09-232-149A-313
C 12	8	15.7	30001	1	US-08-125-468-1

C 13	8	15.7	30001	2	US-08-474-933-1	Sequence 1, Appl1
C 14	7	13.7	540	4	US-09-495-050A-219	Sequence 219, App
C 15	7	13.7	497	4	US-09-702-705-65	Sequence 65, Appl
C 16	7	13.7	547	4	US-09-736-457-65	Sequence 65, Appl
C 17	7	13.7	588	3	US-09-129-030-27	Sequence 27, Appl
C 18	7	13.7	745	4	US-09-581-001B-20	Sequence 20, Appl
C 19	7	13.7	1335	4	US-09-107-533A-298	Sequence 298, App
C 20	7	13.7	1376	2	US-08-868-288A-2	Sequence 2, Appl1
C 21	7	13.7	1376	3	US-09-235-373-2	Sequence 2, Appl1
C 22	7	13.7	1376	3	US-09-388-993-2	Sequence 2, Appl1
C 23	7	13.7	1467	3	US-09-252-991A-1331	Sequence 1331, Ap
C 24	7	13.7	1578	3	US-09-044-904A-1	Sequence 1, Appl1
C 25	7	13.7	1578	4	US-09-586-924-1	Sequence 1, Appl1
C 26	7	13.7	1621	4	US-09-996-243-147	Sequence 147, App
C 27	7	13.7	2163	4	US-09-328-352-639	Sequence 639, App
C 28	7	13.7	2268	4	US-09-620-312D-909	Sequence 909, App
C 29	7	13.7	2329	4	US-09-411-977-1	Sequence 1, Appl1
C 30	7	13.7	2437	1	US-07-795-859B-5	Sequence 5, Appl1
C 31	7	13.7	2437	1	US-08-457-616-5	Sequence 5, Appl1
C 32	7	13.7	2437	4	US-09-235-538-1	Sequence 1, Appl1
C 33	7	13.7	2538	4	US-09-252-991A-1285	Sequence 1285, Ap
C 34	7	13.7	2571	4	US-09-252-991A-1279	Sequence 1279, Ap
C 35	7	13.7	2600	1	US-08-147-949A-1	Sequence 1, Appl1
C 36	7	13.7	2798	4	US-09-484-970B-90	Sequence 90, Appl1
C 37	7	13.7	3023	4	US-09-203-453-4	Sequence 4, Appl1
C 38	7	13.7	3023	4	US-09-900-236-4	Sequence 4, Appl1
C 39	7	13.7	3066	3	US-09-086-912-1	Sequence 1, Appl1
C 40	7	13.7	3066	4	US-09-203-453-1	Sequence 1, Appl1
C 41	7	13.7	3066	4	US-09-900-236-1	Sequence 1, Appl1
C 42	7	13.7	3218	4	US-09-221-017B-255	Sequence 255, App
C 43	7	13.7	13188	4	US-08-961-527-70	Sequence 70, Appl
C 44	7	13.7	31328	4	US-09-215-694-19	Sequence 19, Appl
C 45	7	13.7	36651	4	US-09-738-894A-3	Sequence 3, Appl1

ALIGNMENTS

RESULT 1
US-09-439-313-471/C
Sequence 471, Application US/09439313
Patent No. 6329505
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan Louise
APPLICANT: Jiang Yugu
APPLICANT: Reed, Steven G.
APPLICANT: Kalos, Michael
APPLICANT: Rafter, Gary
APPLICANT: Retter, Mark
APPLICANT: Solk, John
APPLICANT: Day, Craig
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
FILE REFERENCE: 210121.427C9
CURRENT APPLICATION NUMBER: US/09/439,313
CURRENT FILING DATE: 1999-11-12
NUMBER OF SEQ ID NOS: 575
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 471
LENGTH: 812
TYPE: DNA
ORGANISM: Homo sapiens
US-09-439-313-471

Alignment Scores:
Pred. No.: 1.59e-44
Score: 51.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Length: 812
Matches: 51
Conservative: 0
Mismatch: 0
Indels: 0
Gaps: 0
DB: 4

```
US-09-402-713a-2 (1-51) x US-09-439-313-471 (1-812)
QY 1 MetPheLeuHisIleSerSerProPheLysTYrProHisThrGlnGluAlaGlnLysGlu 20
Db 604 ATGTTTGGACATTTCCAGCCCTTTAAATATCCACACACAGGAGCAAAAGGAA 545
QY 21 AlaGlnArgSerLeuGlyGluMetProGlyArgHisLeuGlySerSerMetSerLeuAla 40
Db 544 GCACAGAGATCCCTGGGAGAAATGCCGCCGCATCTTGATCATGATGAGCCCTGCC 485
QY 41 LeuCysLeuValProLeuValArgGluGlyHis 51
Db 484 CTGTGCTGTGCTCCGCTTGAGGAGGAGACAT 452

RESULT 2
US-09-352-616a-471/c
; Sequence 471, Application US/09352616a
; GENERAL INFORMATION:
; APPLICANT: Dillon, Davin C.
; APPLICANT: Harlocker, Susan Louise
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Xu, Jiangchun
; APPLICANT: Mitcham, Jennifer Lynn
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
; FILE REFERENCE: 210121.427C8
; CURRENT APPLICATION NUMBER: US/09/352,616a
; NUMBER OF SEQ ID NOS: 1999-07-13
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 471
; LENGTH: 812
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-352-616a-471

Alignment Scores:
Pred. No.: 1.59e-44 Length: 812
Score: 51.00 Matches: 51
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 0

US-09-402-713a-2 (1-51) x US-09-352-616a-471 (1-812)
QY 1 MetPheLeuHisIleSerSerProPheLysTYrProHisThrGlnGluAlaGlnLysGlu 20
Db 604 ATGTTTGGACATTTCCAGCCCTTTAAATATCCACACACAGGAGCAAAAGGAA 545
QY 21 AlaGlnArgSerLeuGlyGluMetProGlyArgHisLeuGlySerSerMetSerLeuAla 40
Db 544 GCACAGAGATCCCTGGGAGAAATGCCGCCGCATCTTGATCATGATGAGCCCTGCC 485
QY 41 LeuCysLeuValProLeuValArgGluGlyHis 51
Db 484 CTGTGCTGTGCTCCGCTTGAGGAGGAGACAT 452

RESULT 3
US-09-439-313-469/c
; Sequence 469, Application US/09439313
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan Louise
; APPLICANT: Jiang Yuqiu
; APPLICANT: Reed, Steven G.
; APPLICANT: Kalos, Michael
; APPLICANT: Fanger, Gary
```

```
; APPLICANT: Retter, Mark
; APPLICANT: Solk, John
; APPLICANT: Day, Craig
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C9
; CURRENT APPLICATION NUMBER: US/09/439,313
; NUMBER OF SEQ ID NOS: 575
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 469
; LENGTH: 2229
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-439-313-469

Alignment Scores:
Pred. No.: 4.16e-44 Length: 2229
Score: 51.00 Matches: 51
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 0

US-09-402-713a-2 (1-51) x US-09-439-313-469 (1-2229)
QY 1 MetPheLeuHisIleSerSerProPheLysTYrProHisThrGlnGluAlaGlnLysGlu 20
Db 1659 ATGTTTGGACATTTCCAGCCCTTTAAATATCCACACACAGGAGCAAAAGGAA 1600
QY 21 AlaGlnArgSerLeuGlyGluMetProGlyArgHisLeuGlySerSerMetSerLeuAla 40
Db 1599 GCACAGAGATCCCTGGGAGAAATGCCGCCGCATCTTGATCATGATGAGCCCTGCC 1540
QY 41 LeuCysLeuValProLeuValArgGluGlyHis 51
Db 1539 CTGTGCTGTGCTCCGCTTGAGGAGGAGACAT 1507

RESULT 4
US-09-352-616a-469/c
; Sequence 469, Application US/09352616a
; GENERAL INFORMATION:
; APPLICANT: Dillon, Davin C.
; APPLICANT: Harlocker, Susan Louise
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Xu, Jiangchun
; APPLICANT: Mitcham, Jennifer Lynn
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
; FILE REFERENCE: 210121.427C8
; CURRENT APPLICATION NUMBER: US/09/352,616a
; NUMBER OF SEQ ID NOS: 472
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 469
; LENGTH: 2229
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-352-616a-469

Alignment Scores:
Pred. No.: 4.16e-44 Length: 2229
Score: 51.00 Matches: 51
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 0

US-09-402-713a-2 (1-51) x US-09-352-616a-469 (1-2229)
QY 1 MetPheLeuHisIleSerSerProPheLysTYrProHisThrGlnGluAlaGlnLysGlu 20
|||||
```

```
Db      1659 ATGTTTTGCACATTTCCAGCCCTTTAAATATCCACACACAGGAAGCAAAAAGGAA 1600
Oy      21 AlAGlnArSerLeuGluMetProGlyArGHisLeuGlySerSerMetSerLeuA 40
        |||||||
Db      1599 GCACAGAGATCCCTGGGAGAAATCCCGGCCCATCTTGGTCAATGATGAGCTCGCC 1540
Oy      41 LeuCysLeuValProLeuValArgGluGlyHis 51
        |||||||
Db      1539 CTGTGCTGTGTCGCCGCTTGTGAGGGAAGACAT 1507

RESULT 5
US-09-439-313-470/c
; Sequence 470, Application US/09439313
; Patent No. 6329505
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan Louise
; APPLICANT: Jiang Yuqiu
; APPLICANT: Reed, Steven G.
; APPLICANT: Kalos, Michael
; APPLICANT: Fanger, Gary
; APPLICANT: Retter, Mark
; APPLICANT: Solk, John
; APPLICANT: Day, Craig
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
; FILE REFERENCE: 210121.427C9
; CURRENT FILING DATE: US/09/439, 313
; NUMBER OF SEQ ID NOS: 575
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 470
; LENGTH: 2426
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-439-313-470

Alignment Scores:
Pred. No.:      4,5e-44      Length:      2426
Score:          51.00      Matches:      51
Percent Similarity: 100.00%  Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match:    100.00%      Indels:      0
DB:             4           Gaps:      0

US-09-402-713A-2 (1-51) x US-09-439-313-470 (1-2426)
Oy      1 MetPheLeuHisIleSerSerProPheLysTyrProHisThrGlnGluAlaGlnLysGlu 20
        |||||||
Db      1653 ATGTTTTGCACATTTCCAGCCCTTTAAATATCCACACACAGGAAGCAAAAAGGAA 1594
Oy      21 AlAGlnArSerLeuGluMetProGlyArGHisLeuGlySerSerMetSerLeuA 40
        |||||||
Db      1593 GCACAGAGATCCCTGGGAGAAATCCCGGCCCATCTTGGTCAATGATGAGCTCGCC 1534
Oy      41 LeuCysLeuValProLeuValArgGluGlyHis 51
        |||||||
Db      1533 CTGTGCTGTGTCGCCGCTTGTGAGGGAAGACAT 1501

RESULT 6
US-09-352-616A-470/c
; Sequence 470, Application US/09352616A
; Patent No. 6395278
; GENERAL INFORMATION:
; APPLICANT: Dillon, Davin C.
; APPLICANT: Harlocker, Susan Louise
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Xu, Jiangchun
; APPLICANT: Mitcham, Jennifer Lynn
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
; TITLE OF INVENTION: OF PROSTATE CANCER AND METHODS FOR THEIR USE
```

```
; FILE REFERENCE: 210121.427C8
; CURRENT APPLICATION NUMBER: US/09/352, 616A
; CURRENT FILING DATE: 1999-07-13
; NUMBER OF SEQ ID NOS: 472
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 470
; LENGTH: 2426
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-352-616A-470

Alignment Scores:
Pred. No.:      4,5e-44      Length:      2426
Score:          51.00      Matches:      51
Percent Similarity: 100.00%  Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match:    100.00%      Indels:      0
DB:             4           Gaps:      0

US-09-402-713A-2 (1-51) x US-09-352-616A-470 (1-2426)
Oy      1 MetPheLeuHisIleSerSerProPheLysTyrProHisThrGlnGluAlaGlnLysGlu 20
        |||||||
Db      1653 ATGTTTTGCACATTTCCAGCCCTTTAAATATCCACACACAGGAAGCAAAAAGGAA 1594
Oy      21 AlAGlnArSerLeuGluMetProGlyArGHisLeuGlySerSerMetSerLeuA 40
        |||||||
Db      1593 GCACAGAGATCCCTGGGAGAAATCCCGGCCCATCTTGGTCAATGATGAGCTCGCC 1534
Oy      41 LeuCysLeuValProLeuValArgGluGlyHis 51
        |||||||
Db      1533 CTGTGCTGTGTCGCCGCTTGTGAGGGAAGACAT 1501

RESULT 7
US-09-439-313-468
; Sequence 468, Application US/09439313
; Patent No. 6329505
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan Louise
; APPLICANT: Jiang Yuqiu
; APPLICANT: Reed, Steven G.
; APPLICANT: Kalos, Michael
; APPLICANT: Fanger, Gary
; APPLICANT: Retter, Mark
; APPLICANT: Solk, John
; APPLICANT: Day, Craig
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
; FILE REFERENCE: 210121.427C9
; CURRENT FILING DATE: US/09/439, 313
; NUMBER OF SEQ ID NOS: 575
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 468
; LENGTH: 3112
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-439-313-468

Alignment Scores:
Pred. No.:      5,71e-44      Length:      3112
Score:          51.00      Matches:      51
Percent Similarity: 100.00%  Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match:    100.00%      Indels:      0
DB:             4           Gaps:      0

US-09-402-713A-2 (1-51) x US-09-439-313-468 (1-3112)
Oy      1 MetPheLeuHisIleSerSerProPheLysTyrProHisThrGlnGluAlaGlnLysGlu 20
```

```
Db      1429 ATGTTTTGCACATTTCCACCCCTTTAAATATCCACACACAGGAGCAAAAGGAA 1488
Qy      21 AlaglnArgSerLeuGlyMetProGlyArgHisLeuGlySerMetSerLeuAla 40
Db      1489 GCACAGAGATCCCTGGGAGAAATGCCGCGCCCACTTGGGTATCATGATGAGCCTCGCC 1548
Qy      41 LeuCysLeuValProLeuValArgGluGlyHis 51
Db      1549 CTGTGCTGTGCTCCGCTTGTGAGGAGGAGACAT 1581

RESULT 8
US-09-352-616A-468
; Sequence 468, Application US/09352616A
; Patent No. 6395278
; GENERAL INFORMATION:
; APPLICANT: Dillon, Davin C.
; APPLICANT: Harlocker, Susan Louise
; APPLICANT: Jiang, Yugu
; APPLICANT: Xu, Jiangchun
; APPLICANT: Mitcham, Jennifer Lynn
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
; TITLE OF INVENTION: OF PROSTATE CANCER AND METHODS FOR THEIR USE
; FILE REFERENCE: 210121.427C8
; CURRENT APPLICATION NUMBER: US/09/352,616A
; CURRENT FILING DATE: 1999-07-13
; NUMBER OF SEQ ID NOS: 472
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 468
; LENGTH: 3112
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-352-616A-468

Alignment Scores:
Pred. No.:      5 718-44      Length:      3112
Score:          51.00      Matches:      31
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches: 0
Query Match:    100.00%      Indels:    0
DB:             4          Gaps:          0

US-09-402-713A-2 (1-51) x US-09-352-616A-468 (1-3112)
Qy      1 MetPheLeuHisIleSerSerProPheIleTYRProHisThrGlnGluAlaGlnGlyGlu 20
Db      1429 ATGTTTTCACATTTCCAGCCCTTTAAATATCCACACACAGGAGCAAAAGGAA 1488
Qy      21 AlaglnArgSerLeuGlyMetProGlyArgHisLeuGlySerMetSerLeuAla 40
Db      1489 GCACAGAGATCCCTGGGAGAAATGCCGCGCCCACTTGGGTATCATGATGAGCCTCGCC 1548
Qy      41 LeuCysLeuValProLeuValArgGluGlyHis 51
Db      1549 CTGTGCTGTGCTCCGCTTGTGAGGAGGAGACAT 1581

RESULT 9
US-09-439-313-313
; Sequence 313, Application US/09439313
; Patent No. 6329505
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan Louise
; APPLICANT: Jiang Yugu
; APPLICANT: Reed, Steven G.
; APPLICANT: Kalos, Michael
; APPLICANT: Fanger, Gary
; APPLICANT: Retter, Mark
; APPLICANT: Solk, John
; APPLICANT: Day, Craig
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
```

```
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C9
; CURRENT APPLICATION NUMBER: US/09/439,313
; CURRENT FILING DATE: 1999-11-12
; NUMBER OF SEQ ID NOS: 575
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 313
; LENGTH: 718
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(718)
; OTHER INFORMATION: n = A,T,C or G
US-09-439-313-313

Alignment Scores:
Pred. No.:      3 066-36      Length:      718
Score:          43.00      Matches:      43
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches: 0
Query Match:    84.31%      Indels:    0
DB:             4          Gaps:          0

US-09-402-713A-2 (1-51) x US-09-439-313-313 (1-718)
Qy      1 MetPheLeuHisIleSerSerProPheIleTYRProHisThrGlnGluAlaGlnGlyGlu 20
Db      189 ATGTTTTCACATTTCCAGCCCTTTAAATATCCACACACAGGAGCAAAAGGAA 248
Qy      21 AlaglnArgSerLeuGlyMetProGlyArgHisLeuGlySerMetSerLeuAla 40
Db      249 GCACAGAGATCCCTGGGAGAAATGCCGCGCCCACTTGGGTATCATGATGAGCCTCGCC 308
Qy      41 LeuCysLeu 43
Db      309 CTGTGCTGTG 317

RESULT 10
US-09-352-616A-313
; Sequence 313, Application US/09352616A
; Patent No. 6395278
; GENERAL INFORMATION:
; APPLICANT: Dillon, Davin C.
; APPLICANT: Harlocker, Susan Louise
; APPLICANT: Jiang, Yugu
; APPLICANT: Xu, Jiangchun
; APPLICANT: Mitcham, Jennifer Lynn
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
; TITLE OF INVENTION: OF PROSTATE CANCER AND METHODS FOR THEIR USE
; FILE REFERENCE: 210121.427C8
; CURRENT APPLICATION NUMBER: US/09/352,616A
; CURRENT FILING DATE: 1999-07-13
; NUMBER OF SEQ ID NOS: 472
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 313
; LENGTH: 718
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(718)
; OTHER INFORMATION: n = A,T,C or G
US-09-352-616A-313

Alignment Scores:
Pred. No.:      3 066-36      Length:      718
Score:          43.00      Matches:      43
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches: 0
Query Match:    84.31%      Indels:    0
DB:             4          Gaps:          0
```



```
US-09-402-713A-2 (1-51) x US-09-352-616A-313 (1-718)
QY 1 MetpHeuHsIleSerSerProPhelyTyrProHsIstHngIngluAlaGlnyGlu 20
   ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 189 ATGTTTTCACATTTCAGCCCTTTTAATATCCACACACAGAAACAAAAGAA 248
QY 21 AlaGlnArSerLeuGlyGluMetProGlyArGHisLeuGlySerMetSerLeuAla 40
   ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 249 GCACAGAGATCCCTCGGGAGAAATGCGCCGCCCATCTTGGGTATCATGAGCTCGCC 308
QY 41 LeuGlySer 43
   ||||||||
Db 309 CTGTGCTG 317

RESULT 11
US-09-232-149A-313
; Sequence 313, Application US/09232149A
; Patent No. 6465611
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE
; FILE REFERENCE: 210121.427C6
; CURRENT APPLICATION NUMBER: US/09/232,149A
; NUMBER OF SEQ ID NOS: 338
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 313
; LENGTH: 718
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1) .. (718)
; OTHER INFORMATION: n = A,T,C or G
US-09-232-149A-313

Alignment Scores:
Pred. No.: 3,06e-36 Length: 718
Score: 43.00 Matches: 43
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 84.31% Indels: 0
DB: 4 Gaps: 0

US-09-402-713A-2 (1-51) x US-09-232-149A-313 (1-718)
QY 1 MetpHeuHsIleSerSerProPhelyTyrProHsIstHngIngluAlaGlnyGlu 20
   ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 189 ATGTTTTCACATTTCAGCCCTTTTAATATCCACACACAGAAACAAAAGAA 248
QY 21 AlaGlnArSerLeuGlyGluMetProGlyArGHisLeuGlySerMetSerLeuAla 40
   ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 249 GCACAGAGATCCCTCGGGAGAAATGCGCCGCCCATCTTGGGTATCATGAGCTCGCC 308
QY 41 LeuGlySer 43
   ||||||||
Db 309 CTGTGCTG 317

RESULT 12
US-08-125-468-1/C
; Sequence 1, Application US/08125468
; Patent No. 5589385
; GENERAL INFORMATION:
; APPLICANT: Ryan, Michael J.
; APPLICANT: Lotvin, Jason A.
; APPLICANT: Strachy, Nancy
; APPLICANT: Pantlin, Susan E.
; TITLE OF INVENTION: Cloning of the biosynthetic pathway for
; TITLE OF INVENTION: chlorotetracycline and tetracycline formation and cosmid
; TITLE OF INVENTION: useful therein
```

```
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESS: American Cyanamid Company
STREET: One Cyanamid Plaza
CITY: Wayne
STATE: New Jersey
COUNTRY: USA
ZIP: 07470
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/125,468
FILING DATE: 22-SEP-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Tsevdos, Estelle J
REGISTRATION NUMBER: 31,145
REFERENCE/DOCKET NUMBER: 31,255-02
TELEPHONE: (201)831-3241
TELEFAX: (201)831-3305
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 30001 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-125-468-1

Alignment Scores:
Pred. No.: 316 Length: 30001
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 15.69% Indels: 0
DB: 1 Gaps: 0

US-09-402-713A-2 (1-51) x US-08-125-468-1 (1-30001)
QY 39 LeuAlaLeuGlySerLeuAlaProLeu 46
   ||||||||||||||||||||||||||||
Db 19783 CTGGCGCTGTGCTGTGCTGCTG 19760

RESULT 13
US-08-474-993-1/C
; Sequence 1, Application US/08474993
; Patent No. 5866410
; GENERAL INFORMATION:
; APPLICANT: Ryan, Michael J.
; APPLICANT: Lotvin, Jason A.
; APPLICANT: Strachy, Nancy
; APPLICANT: Pantlin, Susan E.
; TITLE OF INVENTION: Cloning of the biosynthetic pathway for
; TITLE OF INVENTION: chlorotetracycline and tetracycline formation and cosmid
; TITLE OF INVENTION: useful therein
; NUMBER OF SEQUENCES: 1
; CORRESPONDENCE ADDRESS:
; ADDRESS: American Cyanamid Company
; STREET: One Cyanamid Plaza
; CITY: Wayne
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07470
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
```

APPLICATION NUMBER: US/08/474,933
 FILING DATE:
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/125,468
 FILING DATE: 22-SEP-1993
 ATTORNEY/AGENT INFORMATION:
 NAME: Tsevdos, Estelle J
 REGISTRATION NUMBER: 31,145
 REFERENCE/DOCKET NUMBER: 31,255-02
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (201)831-3241
 TELEFAX: (201)831-3305
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 30001 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 US-08-474-933-1

Alignment Scores:
 Pred. No.: 316 Length: 30001
 Score: 8.00 Matches: 8
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 15.69% Indels: 0
 DB: 2 Gaps: 0

US-09-402-713A-2 (1-51) x US-08-474-933-1 (1-30001)

QY 39 LeuAlaLeuCysLeuValProLeu 46
 DB 19783 CTGGCGCTCTGCTGCTGCTGCGCGCTG 19760

RESULT 14
 US-09-495-050A-219/C
 Sequence 219, Application US/09495050A
 Patent No. 6492505
 GENERAL INFORMATION:
 APPLICANT: Roopa, Reddy
 APPLICANT: Guegler, Karl, J.
 APPLICANT: Au-Young, Janice
 TITLE OF INVENTION: COMPOSITION FOR DETECTION OF GENES ENCODING MEMBRANE-ASSOCIATED P
 FILE REFERENCE: PA-0013 US
 CURRENT APPLICATION NUMBER: US/09/495,050A
 CURRENT FILING DATE: 2000-01-31
 PRIOR APPLICATION NUMBER: 60/118,318
 PRIOR FILING DATE: February 1, 1999
 NUMBER OF SEQ ID NOS: 305
 SOFTWARE: PERL Program
 SEQ ID NO 219
 LENGTH: 490
 TYPE: DNA
 ORGANISM: Homo sapiens
 FEATURE:
 NAME/KEY: misc_feature
 OTHER INFORMATION: Incyte ID No. 6492505 2553280CT1
 US-09-495-050A-219

Alignment Scores:
 Pred. No.: 69.2 Length: 490
 Score: 7.00 Matches: 7
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 13.73% Indels: 0
 DB: 4 Gaps: 0

US-09-402-713A-2 (1-51) x US-09-495-050A-219 (1-490)

QY 3 LeuHisIleSer*SerProPhe 9
 |||||||||||||||||||F||

DB 346 TTACAAATTTCTTCTCTTTT 326

RESULT 15
 US-09-702-705-65/C
 Sequence 65, Application US/09702705
 Patent No. 6504010
 GENERAL INFORMATION:
 APPLICANT: Wang, Tonglong
 APPLICANT: Bangur, Chaitanya S.
 APPLICANT: Iodes, Michael A.
 APPLICANT: Panger, Gary
 APPLICANT: Vedvick, Tom
 APPLICANT: Carter, Darrick
 APPLICANT: Retter, Marc
 APPLICANT: Mannion, Jane
 APPLICANT: Pan, Liqun
 TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
 FILE REFERENCE: 210121.478C14
 CURRENT APPLICATION NUMBER: US/09/702,705
 CURRENT FILING DATE: 2000-10-30
 NUMBER OF SEQ ID NOS: 1833
 SOFTWARE: FastSeq for Windows Version 3.0
 SEQ ID NO 65
 LENGTH: 547
 TYPE: DNA
 ORGANISM: Homo sapien
 FEATURE:
 NAME/KEY: misc_feature
 LOCATION: (1)...(547)
 OTHER INFORMATION: n = A,T,C or G
 US-09-702-705-65

Alignment Scores:
 Pred. No.: 76.9 Length: 547
 Score: 7.00 Matches: 7
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 13.73% Indels: 0
 DB: 4 Gaps: 0

US-09-402-713A-2 (1-51) x US-09-702-705-65 (1-547)

QY 5 IleSerSerProPheIleTyr 11
 DB 164 ATTCTCTCTCTTCAATAT 144

Search completed: September 26, 2003, 21:39:29
 Job time: 76 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 26, 2003, 21:01:08 : Search time 7412.95 Seconds
(without alignments)
11241.524 Million cell updates/sec

Title: US-09-402-713A-1

Perfect score: 2037
Sequence: 1 agaagctgcacacgaaaaa.....caataagaattacaaaga 2037

Scoring table:

OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 2888711 seqs, 2045481386 residues

Word size : 0

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

GenEmbl:*
1: gb_ba:*
2: gb_hg:*
3: gb_in:*
4: gb_cm:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vl:*
15: em_da:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
21: em_or:*
22: em_ov:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sts:*
28: em_un:*
29: em_vl:*
30: em_hg_hum:*
31: em_hg_inv:*
32: em_hg_other:*
33: em_hg_mus:*
34: em_hg_pln:*
35: em_hg_rtd:*
36: em_hg_mam:*
37: em_hg_vrt:*
38: em_sy:*
39: em_hg_hum:*
40: em_hggo_mus:*
41: em_hggo_other:*

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	2037	100.0	2037	6	BD082482	BD082482 PCA3, PCA
2	1775	87.1	1872	6	BD082483	BD082483 PCA3, PCA
3	1629	80.0	3582	6	BD082485	BD082485 PCA3, PCA
4	1629	80.0	3923	6	AR261166	AR261166 Sequence
5	1629	80.0	3923	6	AR278697	AR278697 Sequence
6	1629	80.0	3923	6	AX200988	AX200988 Sequence
7	1629	80.0	3923	6	AX267716	AX267716 Sequence
8	1629	80.0	3923	6	AF103907	AF103907 Homo sapi
9	1185	58.2	5435	9	AF103908	AF103908 Homo sapi
10	1154	56.7	2426	6	AR261038	AR261038 Sequence
11	1154	56.7	2426	6	AR278569	AR278569 Sequence
12	1154	56.7	2426	6	AX106206	AX106206 Sequence
13	1154	56.7	2426	6	AX106689	AX106689 Sequence
14	1154	56.7	2426	6	AX140980	AX140980 Sequence
15	1154	56.7	2426	6	AX200840	AX200840 Sequence
16	1154	56.7	2426	6	AX267496	AX267496 Sequence
17	1154	56.7	3112	6	AR261036	AR261036 Sequence
18	1154	56.7	3112	6	AR278567	AR278567 Sequence
19	1154	56.7	3112	6	AX106204	AX106204 Sequence
20	1154	56.7	3112	6	AX106687	AX106687 Sequence
21	1154	56.7	3112	6	AX140978	AX140978 Sequence
22	1154	56.7	3112	6	AX200838	AX200838 Sequence
23	1154	56.7	3112	6	AX267494	AX267494 Sequence
24	1033	50.7	2229	6	AR261037	AR261037 Sequence
25	1033	50.7	2229	6	AR278568	AR278568 Sequence
26	1033	50.7	2229	6	AX106205	AX106205 Sequence
27	1033	50.7	2229	6	AX106688	AX106688 Sequence
28	1033	50.7	2229	6	AX140979	AX140979 Sequence
29	1033	50.7	2229	6	AX200839	AX200839 Sequence
30	1033	50.7	2229	6	AX267495	AX267495 Sequence
31	972	47.7	128480	9	AL359314	AL359314 Human DNA
32	723	35.5	820	6	BD082484	BD082484 PCA3, PCA
33	720	35.3	812	6	AR261039	AR261039 Sequence
34	720	35.3	812	6	AR278570	AR278570 Sequence
35	720	35.3	812	6	AX106207	AX106207 Sequence
36	720	35.3	812	6	AX106690	AX106690 Sequence
37	720	35.3	812	6	AX140981	AX140981 Sequence
38	720	35.3	812	6	AX200841	AX200841 Sequence
39	720	35.3	812	6	AX267497	AX267497 Sequence
40	473	23.2	597	6	BD078456	BD078456 101 human
41	276	13.5	129109	9	AL390239	AL390239 Human DNA
42	241	11.8	481	6	BD119166	BD119166 EST and e
43	233	11.4	359	6	AX018075	AX018075 Sequence
44	233	11.4	359	6	BD134961	BD134961 Human nuc
45	210	10.3	278	6	AX107858	AX107858 Sequence

ALIGNMENTS

RESULT 1
BD082482
LOCUS BD082482 2037 bp. DNA linear PART 27-AUG-2002
DEFINITION PCA3, PCA3 genes, and methods of use.
ACCESSION BD082482.1 GI:22628092
VERSION JP 2001522240-A/1.
KEYWORDS Mastadenovirus
SOURCE Mastadenovirus
ORGANISM Viruses; deDNA viruses, no RNA stage; Adenoviridae.
REFERENCE 1 (bases 1 to 2037)
AUTHORS Bussemakers, M.J.G.
TITLE PCA3, PCA3 genes, and methods of use
JOURNAL Patent: JP 2001522240-A 1 13-NOV-2001;
DIAGNOCURE INC SECRETARY OF THE DEPARTMENT OF HEALTH HUMAN SERVICES

COMMENT PN JP 2001522240-A/1
PD 13-NOV-2001
PE 09-APR-1998 JP 1998542194
PR 10-APR-1997 US 60/041836
PI MARION J G BUSSEMAKERS
PC C12N15/00,C12N15/12,C12N5/12,C12N1/21,C07K14/47,C07K16/18, PC
C12Q1/68,
PC G01N33/577,A61K39/395,A01K67/027
CC Strandedness: Double;
CC Topology: Linear;
FH Key Location/Qualifiers
FT CDS 379..531.
Location/Qualifiers
1..2037
/organism="Mastadenovirus"
/mol_type="genomic DNA"
/db_xref="taxon:10509"

BASE COUNT 622 a 426 c 406 g 575 t 8 others

ORIGIN

Query Match 100.0%; Score 2037; DB 6; Length 2037;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2037; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGAAGCTGGCATCGAAGAAACAGAGGGGAGATTTGTGGCTGCAGCCGAGGGAGACCAG 60
DB 1 AGAAGCTGGCATCGAAGAAACAGAGGGGAGATTTGTGGCTGCAGCCGAGGGAGACCAG 60
QY 61 GAAGATCGCATGGTGGGAAGGAGACCTGATGATACAGAGAAATTCACACATATATCTTAG 120
DB 61 GAAGATCGCATGGTGGGAAGGAGACCTGATGATACAGAGAAATTCACACATATATCTTAG 120
QY 121 TGTTCATGACACCAAGATTAATTAAGTGAAGAGCTAGTCCGTGTGAGTCTTCCTCAGT 180
DB 121 TGTTCATGACACCAAGATTAATTAAGTGAAGAGCTAGTCCGTGTGAGTCTTCCTCAGT 180
QY 181 GACACAGGGGTGATCGACATCGAGGCGACCTTCTGTACTCTCAGCAGCAAGAAAGA 240
DB 181 GACACAGGGGTGATCGACATCGAGGCGACCTTCTGTACTCTCAGCAGCAAGAAAGA 240
QY 241 CTACAGACATCTCAATGGCAGGGGTGAGAAATAAGAAAGGCTGCTGACTTTACCATCTGA 300
DB 241 CTACAGACATCTCAATGGCAGGGGTGAGAAATAAGAAAGGCTGCTGACTTTACCATCTGA 300
QY 301 GGGCAGCATCTGCTGAATGGAGATTAATTAACATCTAGAAACACCAAGATGACATA 360
DB 301 GGGCAGCATCTGCTGAATGGAGATTAATTAACATCTAGAAACACCAAGATGACATA 360
QY 361 TAAATGCTAGTAGTGACATGTTTTGACATTTCCAGCCCTTTAATATCCACACACA 420
DB 361 TAAATGCTAGTAGTGACATGTTTTGACATTTCCAGCCCTTTAATATCCACACACA 420
QY 421 CAGGAAGCAGAAAAGGAAGCAGAGATCCCTGGGAGAAATGCCCGGCCCATCTTGGG 480
DB 421 CAGGAAGCAGAAAAGGAAGCAGAGATCCCTGGGAGAAATGCCCGGCCCATCTTGGG 480
QY 481 TCATTCATGAGCTCGCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 540
DB 481 TCATTCATGAGCTCGCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 540
QY 541 AATTCATGCTGCTTAAAGATGGGAGAAACAGATCCTGCTGCTGCTGCTGCTGCTGCTG 600
DB 541 AATTCATGCTGCTTAAAGATGGGAGAAACAGATCCTGCTGCTGCTGCTGCTGCTGCTG 600
QY 601 AACGGATTTACAGATTTGAAATGAAGTCACAAAGTGAGATTAACATGAGAGAAACA 660
DB 601 AACGGATTTACAGATTTGAAATGAAGTCACAAAGTGAGATTAACATGAGAGAAACA 660
QY 661 GAGGAGAAATCTTGATGGCTTCAACAAGACATGCACAAACAAATGGAATACTGATG 720
DB 661 GAGGAGAAATCTTGATGGCTTCAACAAGACATGCACAAACAAATGGAATACTGATG 720
QY 721 ACATGAGGAGCAAGCTGGGAGGAGATTAACACGGGGGCAAGGGCTCAGGATTTGCGC 780

DB 721 ACATGAGGAGCAAGCTGGGAGGAGATTAACACGGGGGCAAGGGCTCAGGATTTGCGC 780
QY 781 CTGCTGGCTAAAGCTGGGCTGCATACCAAAATCTTTCATATTTCTTAACCTGAAACAA 840
DB 781 CTGCTGGCTAAAGCTGGGCTGCATACCAAAATCTTTCATATTTCTTAACCTGAAACAA 840
QY 841 AGCTGTTGAATATCTGATGCTGACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 900
DB 841 AGCTGTTGAATATCTGATGCTGACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 900
QY 901 GCCACACTCATTTTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 960
DB 901 GCCACACTCATTTTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 960
QY 961 AATTAACATTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1020
DB 961 AATTAACATTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1020
QY 1021 GTTTTTCCTAAGAGAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1080
DB 1021 GTTTTTCCTAAGAGAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1080
QY 1081 GATCTTTCAGAGGTTATCTTACTAGCACACAGCATATATTAACGAGTGAATTAATCTA 1140
DB 1081 GATCTTTCAGAGGTTATCTTACTAGCACACAGCATATATTAACGAGTGAATTAATCTA 1140
QY 1141 ATCAACATCAATCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1200
DB 1141 ATCAACATCAATCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1200
QY 1201 TTCTCAAGACCTCAAAATGCTCATTCATTAATATCACAGATTAATCTTTTCTTAAAC 1260
DB 1201 TTCTCAAGACCTCAAAATGCTCATTCATTAATATCACAGATTAATCTTTTCTTAAAC 1260
QY 1261 TGGAGAAATTCATGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1320
DB 1261 TGGAGAAATTCATGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1320
QY 1321 GCAAAAGTGAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1380
DB 1321 GCAAAAGTGAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1380
QY 1381 TAAATGCTTAAAGCTTGTACTGAGGCTGTATACAGACACCTCCCTCCCTCAGC 1440
DB 1381 TAAATGCTTAAAGCTTGTACTGAGGCTGTATACAGACACCTCCCTCCCTCAGC 1440
QY 1441 CTTATCTGATACCATCAACCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCT 1500
DB 1441 CTTATCTGATACCATCAACCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCT 1500
QY 1501 CCTTGAACATGTCAGGNCATATCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1560
DB 1501 CCTTGAACATGTCAGGNCATATCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1560
QY 1561 AANTCTGATGATGATTAAGTTTGAATTAAGTTGACTATCTTCTTATGCAAGAAAGG 1620
DB 1561 AANTCTGATGATGATTAAGTTTGAATTAAGTTGACTATCTTCTTATGCAAGAAAGG 1620
QY 1621 ACACATATGAGATTCATCATCATGAGCAGCAAGAAATTAAGTGAATTAATTAATTA 1680
DB 1621 ACACATATGAGATTCATCATCATGAGCAGCAAGAAATTAAGTGAATTAATTAATTA 1680
QY 1681 AGAGTTTGAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1740
DB 1681 AGAGTTTGAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1740
QY 1741 TGTAAAGCTGGGATGTAAGAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1800
DB 1741 TGTAAAGCTGGGATGTAAGAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1800
QY 1801 CATTCCTATCTCTTCAACATATCAACCAACCTTTTACAGAAATTCATGAGTGCACAA 1860

Db 1801 CATTTCTATCTATCTATCAACAATATCCAAACAGCTTTTCACAGATTCATGACGTCAAA 1860
OY 1861 TCCCCAAAGTAACCTTTATCCATTTTCATGAGTGCCTTTAGAAATTTGGCAATCA 1920
Db 1861 TCCCCAAAGTAACCTTTATCCATTTTCATGAGTGCCTTTAGAAATTTGGCAATCA 1920
OY 1921 TACTGTGCTATCTACATCTTGAGATGTTTGTGCTTGTAGTAATTTGAAGAATA 1980
Db 1921 TACTGTGCTATCTACATCTTGAGATGTTTGTGCTTGTAGTAATTTGAAGAATA 1980
OY 1981 GGGCAGCTTGTGAGCCACTTTAGGCTTCACTCTCGCAATAAAGAAATTTTACAAAGA 2037
Db 1981 GGGCAGCTTGTGAGCCACTTTAGGCTTCACTCTCGCAATAAAGAAATTTTACAAAGA 2037

RESULT 2
BD082483 1872 bp DNA linear PAT 27-AUG-2002
LOCUS BD082483
DEFINITION PC3, PC43 genes, and methods of use.
ACCESSION BD082483
VERSION BD082483.1 GI:22628093
KEYWORDS JP 2001522240-A/2.
SOURCE Mastadenovirus
ORGANISM Mastadenovirus
Virus; dsDNA viruses, no RNA stage; Adenoviridae.
REFERENCE 1 (bases 1 to 1872)
AUTHORS Bussemakers,M.J.G.
TITLE PC3, PC43 genes, and methods of use
JOURNAL Patent: JP 2001522240-A 2 13-NOV-2001.
DIAGNOCURE INC
PN JP 2001522240-A/2
PD 13-NOV-2001
PF 09-APR-1998 JP 1998542194
PR 10-APR-1997 US 60/041836
PI MARION J G BUSSEMAKERS
PC C12N15/00,C12N15/12,C12N15/21,C07K14/47,C07K16/18, PC
C12Q1/68,
PC GOIN13/577,A61K39/395,A01K67/027
CC Strandedness: Double;
CC Topology: Linear;
FH Key Location/Qualifiers.

FEATURES
source 1..1872 Location/Qualifiers
1..1872
/organism="Mastadenovirus"
/mol_type="genomic DNA"
/db_xref="taxon:10509"

BASE COUNT 567 a 389 c 369 g 539 t 8 others
ORIGIN

Query Match 87.1%; Score 1775; DB 6; Length 1872;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1775; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 263 GGTGGAATAAAGAGGCTGCTGACTTACCATCTGAGCCACACATCTGCTGAATG 322
Db 98 GGTGGAATAAAGAGGCTGCTGACTTACCATCTGAGCCACACATCTGCTGAATG 157
OY 323 AGATTAATTAACATCTAGAAAACAGACATGACATTAATATGTCTAAGTAGTACATG 382
Db 158 AGATTAATTAACATCTAGAAAACAGACATGACATTAATATGTCTAAGTAGTACATG 217
OY 383 TTTTGCACATTTCCAGCCCTTTAAATATCCACACACACAGAGAAGACAAAAGAGAC 442
Db 218 TTTTGCACATTTCCAGCCCTTTAAATATCCACACACACAGAGAAGACAAAAGAGAC 277
OY 443 AGAGATCCCTGGAGAAATGCCGGCCGACATCTTGATCATGATGAGCTGCGCCGT 502
Db 278 AGAGATCCCTGGAGAAATGCCGGCCGACATCTTGATCATGATGAGCTGCGCCGT 337
OY 503 GCCTGCTCCCTTGTGAGGAGAGACATTAAGAAATGAATGATGTCTTCTTAAGAA 562
Db 338 GCCTGCTCCCTTGTGAGGAGAGACATTAAGAAATGAATGATGTCTTCTTAAGAA 397

OY 563 TGGGAGAAAACAGATCCGTTGTGGATATTTATTTGAACGGGATTACAGATTTGAAT 622
Db 398 TGGGAGAAAACAGATCCGTTGTGGATATTTATTTGAACGGGATTACAGATTTGAAT 457
OY 623 GAAGTCACAAAGTAGACATTATCCAAATAGAGAGAAAACAGACAGAAAATCTTGATGCTT 682
Db 458 GAAGTCACAAAGTAGACATTATCCAAATAGAGAGAAAACAGACAGAAAATCTTGATGCTT 517
OY 683 CACAGACATGACAAACAAATGAATATCTGTATGACATGAGCCAGCCAAAGTGGGG 742
Db 518 CACAAACATGACAAACAAATGAATATCTGTATGACATGAGCCAGCCAAAGTGGGG 577
OY 743 AGGAGATTAACACAGGGGACAGGGTCAAGATTTGAGCTGCTGCTAAACCTGCGCTTC 802
Db 578 AGGAGATTAACACAGGGGACAGGGTCAAGATTTGAGCTGCTGCTGCTGCTGCTGCTGCT 637
OY 803 ATACCAAAATCATTTATATTTTACACCCCAAAACAAAGCTTTTAAATATCTGATCTC 862
Db 638 ATACCAAAATCATTTATATTTTACACCCCAAAACAAAGCTTTTAAATATCTGATCTC 697
OY 863 TACGTTCTCTTGGGCCCAACATCTCCATATATCCAGCCACATCATTTTAAATATTT 922
Db 698 TACGTTCTCTTGGGCCCAACATCTCCATATATCCAGCCACATCATTTTAAATATTT 757
OY 923 AGTTCCAGATCTGTACTGTGACCTTCTACACTGTAGATAATACATTTACTTGTTC 982
Db 758 AGTTCCAGATCTGTACTGTGACCTTCTACACTGTAGATAATACATTTACTTGTTC 817
OY 983 AAAGACCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1042
Db 818 AAAGACCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 877
OY 1043 GCCCAGGGATCTGTAACAGGCTGGAGACATCTCAAGATCTTCCAGGGTTATCTTA 1102
Db 878 GCCCAGGGATCTGTAACAGGCTGGAGACATCTCAAGATCTTCCAGGGTTATCTTA 937
OY 1103 CTAGCACACAGCATGATCATTTACGAGTGAATATCTAATCAACATCATCTCAGTGTCT 1162
Db 938 CTAGCACACAGCATGATCATTTACGAGTGAATATCTAATCAACATCATCTCAGTGTCT 997
OY 1163 TTGCCCATCTGAAATTTCAATTTCCACTTTGTGCCATCTCCAGACCTCAAAATGTCA 1222
Db 998 TTGCCCATCTGAAATTTCAATTTCCACTTTGTGCCATCTCCAGACCTCAAAATGTCA 1057
OY 1223 TTGCATTAATATACAGGATTAATCTTTTAACTTTTAACTTTTAACTTTTAACTTTTAA 1282
Db 1058 TTGCATTAATATACAGGATTAATCTTTTAACTTTTAACTTTTAACTTTTAACTTTTAA 1117
OY 1283 CAGCTATGGGAATTTAATACATATTTGTTTCCAGTCAAGAGATGACTAAGTCCCTTA 1342
Db 1118 CAGCTATGGGAATTTAATACATATTTGTTTCCAGTCAAGAGATGACTAAGTCCCTTA 1177
OY 1178 TCCCTCCCTTTGTTGATTTTTCAGATTAAGATTAAGATTAAGATTAAGATTAAGATTA 1237
OY 1403 AGGCTATATACAGACAGGCTCTCCCATCCCTCCAGCTTATCTGTCAATCACATCAAC 1462
Db 1238 AGGCTATATACAGACAGGCTCTCCCATCCCTCCAGCTTATCTGTCAATCACATCAAC 1297
OY 1463 CCCTCCCATATNSACTAATAAATCTAATCTTAACTTTTAACTTTTAACTTTTAACTTTTAA 1522
Db 1298 CCCTCCCATATNSACTAATAAATCTAATCTTAACTTTTAACTTTTAACTTTTAACTTTTAA 1357
OY 1523 ATTATTCCTTTCCTGAGAAAGCTTCTCTGTCTTAANTCTAGAAATGATGTAAGTT 1582
Db 1358 ATTATTCCTTTCCTGAGAAAGCTTCTCTGTCTTAANTCTAGAAATGATGTAAGTT 1417
OY 1583 TTGAATTAAGTGAATCTTCTTACTTATGCAAAAGAGACATATGATATCATCATCA 1642
Db 1418 TTGAATTAAGTGAATCTTCTTACTTATGCAAAAGAGACATATGATATCATCATCA 1477
OY 1643 CATGACACAGCAAAATCTAAAGTGAATTTGATTTAAGAGTTTGAATTAATATATGAA 1702

Db	1478	CATGAGACAGAAATACTAAAGAGTAAATTGATTATTAAGAGTTAGATAAATATATACAA	1537
OY	1703	ATGCAAGAKCCACAGAGGGAATGTTTATGGGGCACGTTTGTAAAGCTGGGATGTGAAGMA	1762
Db	1538	ATGGAAGKCCACAGAGGGAATGTTTATGGGGCACGTTTGTAAAGCTGGGATGTGAAGMA	1597
OY	1763	AAGCAGAGGAACTCATAGTATCTTATATATATACCTCATTTGCTATATCCATACACAA	1822
Db	1598	AAGCAGAGGAACTCATATAGTATCTTATATATATACCTCATTTGCTATATCCATATACAA	1657
OY	1823	TATCCAAACAGCTTTTCACAGATTCATGCAGTGCAAATCCCAAGTAACCTTTATCC	1882
Db	1658	TATCCAAACAGCTTTTCACAGATTCATGCAGTGCAAATCCCAAGTAACCTTTATCC	1717
OY	1883	ATTTCATGTCAGAGGCCCTTTAGAAATTTTGGCAATCATACTGGTCACTTATCTCAACTT	1942
Db	1718	ATTTCATGTCAGAGGCCCTTTAGAAATTTTGGCAATCATACTGGTCACTTATCTCAACTT	1777
OY	1943	TGAGATGTGTTTGTCTCTGTAGTAATTTGGAAGAAATAGGGCACTCTTGTGAGGCACCTT	2002
Db	1778	TGAGATGTGTTTGTCTCTGTAGTAATTTGGAAGAAATAGGGCACTCTTGTGAGGCACCTT	1837
OY	2003	AGGCTTCACTCTGGCAATAAAGATTTTACAAAGA	2037
Db	1838	AGGCTTCACTCTGGCAATAAAGATTTTACAAAGA	1872

RESULT 3				
BD082485	BD082485	3582 bp	DNA	Linear
LOCUS	PCA3, PCA3 genes, and methods of use.			PAT 27-AUG-2002
DEFINITION	BD082485			
ACCESSION	BD082485.1	GI:22628095		
VERSION	JP 2001522240-A/4.			
KEYWORDS	Mastadenovirus			
SOURCE	Mastadenovirus			
ORGANISM	Viruses; dsDNA viruses, no RNA stage: Adenoviridae.			
REFERENCE	1 (bases 1 to 3582)			
AUTHORS	Bussemakers,M.J.G.			
TITLE	PCA3, PCA3 genes, and methods of use			
JOURNAL	Patent: JP 2001522240-A 4 13-NOV-2001;			

COMMENT	DIAGNOCURE INC
PN JP 2001522240-A/4	
PD 13-NOV-2001	
PE 09-APR-1998 JP 1998542194	
PR 10-APR-1997 US 60/041836	
PI MARRON J G. BUSSEMAKERS	
PC C12N15/00, C12N15/12, C12N5/12, C12N1/21, C07K14/47, C07K16/18, PC	
C12Q1/68,	
PC G01N33/577, A61K39/395, A01K67/027	
CC Strandedness: Double;	
CC Topology: Linear;	
CC Key	
FT Location/Qualifiers	
FT CDS	
location/Qualifiers	
1..3582	
/organism="Mastadenovirus"	
/mol_type="genomic DNA"	
/db_xref="taxon:10509"	
1052 a 787 c 680 g 1063 t	
BASE COUNT	
ORIGIN	

	Query Match	80.0%	Score 1629	DB 6	Length 3582
	Best Local Similarity	99.6%	Pred. No. 0		
	Matches 2029	Conservative	0	Mismatches 8	Indels 0
Qy	1	AGAAGTCGGCATCGAAAAACAGAGGGAGATTGTGTGGCTCGACCCGAGGAGACCCAG	60		
Db	23	AGAAAGTCGGCATCGAAAAACAGAGGGAGATTGTGTGGCTCGACCCGAGGAGACCCAG	82		
Qy	61	GAAATCTGCATGTGGGAGACCTGATGTACAGAGAAATTACACATATATCTTAA	120		

Db	83	GAAGATCTGCATGCTGGGGAAGGACCTGATGATACAGAGGAATTTACACATATATCTTAG	142
QY	121	TGTTTCATATGAACACCAAGATTAATTAAGTGAAGAGACTAGTCCGGCTGTGAGTCTCTCACT	180
Db	143	TGTTTCATATGAACACCAAGATTAATTAATTAAGTGAAGAGACTAGTCCGGCTGTGAGTCTCTCACT	202
QY	181	GACACAGAGGCTGAGTACCATTCGACGGGACTTTTCTGACTTACTCATCTGACAGCAAAAGAA	240
Db	203	GACACAGAGGCTGAGTACCATTCGACGGGACTTTTCTGACTTACTCATCTGACAGCAAAAGAA	262
QY	241	CTACAGACATCTCAATGGCGAGGGGTGAGAAATAGAAAGGCTGCTGACTTTACATCTGA	300
Db	263	CTACAGACATCTCAATGGCGAGGGGTGAGAAATAGAAAGGCTGCTGACTTTACATCTGA	322
QY	301	GGCCACACATCTGCGTGAATGGAGTAATTTAAATCATTACATAGAAAGCAAGATGTGACATA	360
Db	323	GGCCACACATCTGCGTGAATGGAGTAATTTAACTATCATCTAGAAACAGAAAGTACATTA	382
QY	361	TAAATGCTAAAGTAGTACATGTTTTTGGACATTTTCAGCCCTTTTAAATATCCACACACA	420
Db	383	TAAATGCTAAAGTAGTACATGTTTTTGGACATTTTCAGCCCTTTTAAATATCCACACACA	442
QY	421	CAGGAAGCACAAAAGGAAGCACAGATATCCCTGGGAGAAATGGCCGGCGCATCTTGGG	480
Db	443	CAGGAAGCACAAAAGGAAGCACAGATATCCCTGGGAGAAATGGCCGGCGCATCTTGGG	502
QY	481	TCATTCGATGAGCCCTGCGCCCTGTGCTCCCGCTTGTGAGGAGAAAGACATTAGAAAATG	540
Db	503	TCATTCGATGAGCCCTGCGCCCTGTGCTCCCGCTTGTGAGGAGAAAGACATTAGAAAATG	562
QY	541	AATTCGATGCTTCTCTTAAAGATGGGCGAGAAAACAGATCCTGTTGTGATATTTATTTG	600
Db	563	AATTCGATGCTTCTCTTAAAGATGGGCGAGAAAACAGATCCTGTTGTGATATTTATTTG	622
QY	601	AACGGGATTAACAGATTTTGAATGAAGTACACAAAGTACATTACCAATGAGAGGAAACA	660
Db	623	AACGGGATTAACAGATTTTGAATGAAGTACACAAAGTACATTACCAATGAGAGGAAACA	682
QY	661	GACGAGAAAATCTTGATGCTTCACACAGACATGCACAAACAAAATGGGAATACGTGTATG	720
Db	683	GACGAGAAAATCTTGATGCTTCACACAGACATGCACAAACAAAATGGGAATACGTGTATG	742
QY	721	ACATGAGGACCCCAAGCTGGGGAGAGATTAACACAGGGGCGAGAGGTGAGGATTTCTGGCC	780
Db	743	ACATGAGGACCCCAAGCTGGGGAGAGATTAACACAGGGGCGAGAGGTGAGGATTTCTGGCC	802
QY	781	CTGCTGCCTTAAACTGTGGCTCATPACCAATCATTTTCATATTTCTTCAACCTCCAAAACAA	840
Db	803	CTGCTGCCTTAAACTGTGGCTCATPACCAATCATTTTCATATTTCTTCAACCTCCAAAACAA	862
QY	841	AGCTGTTGTAATATCTGATCTCTACGGTCTTCTGGGCCCCAACATTTCTCATATATCCA	900
Db	863	AGCTGTTGTAATATCTGATCTCTACGGTCTTCTGGGCCCCAACATTTCTCATATATCCA	922
QY	901	GCCACACATCTTTTAAATATTTAACTTCCCAATCTGTACTGTGACCTTTCAACACTGAG	960
Db	923	GCCACACATCTTTTAAATATTTAACTTCCCAATCTGTACTGTGACCTTTCAACACTGAG	982
QY	961	AATPACATTTACTCATTTTGTTCAAAGACCTTTCGTGTTCTGCTGCTAATATATGCTGACT	1020
Db	983	AATPACATTTACTCATTTTGTTCAAAGACCTTTCGTGTTCTGCTGCTAATATATGCTGACT	1042
QY	1021	GTTTTTCCTAAGAGGTGTTTGGGCCAGGGGATCTGTGAACAAGGCTGGGAAGCATCTCAA	1080
Db	1043	GTTTTTCCTAAGAGGTGTTTGGGCCAGGGGATCTGTGAACAAGGCTGGGAAGCATCTCAA	1102
QY	1081	GATCTTTCCAGAGGTATTAATCTTACAGACACAGATGATCATTAACGAGAGTAATATATCTA	1140
Db	1103	GATCTTTCCAGAGGTATTAATCTTACAGACACAGATGATCATTAACGAGAGTAATATATCTA	1162
QY	1141	ATCAACATCATCTTCAGTGTCTTTGGCCATATCTGAATTCATTTTCCACTTTTGTCCCA	1200
Db	1163	ATCAACATCATCTTCAGTGTCTTTGGCCATATCTGAATTCATTTTCCACTTTTGTCCCA	1222

1201 TTCTCAGACCTCAAAATGTCATTCATTAATATACAGAGATTAACTTTTTTTTAAACC 1260
1223 TTCTCAGACCTCAAAATGTCATTCATTAATATACAGAGATTAACTTTTTTTTAAACC 1282
1261 TGGGAAGATTCATGTTACATGACAGCTATGGAATTTAATACATATTTGTTTCCAGT 1320
1283 TGGGAAGATTCATGTTACATGACAGCTATGGAATTTAATACATATTTGTTTCCAGT 1342
1321 GCAAGAGTACATAGTCCCTTTATCCCTCTTTGTTGATTTTTTTTCCAGTAAAGT 1380
1343 GCAAGAGTACATAGTCCCTTTATCCCTCTTTGTTGATTTTTTTTCCAGTAAAGT 1402
1381 TAAATGCTTACCTTTGATGAGGCTGATACAGACAGCCTCCGCCATCCCTCCAGC 1440
1403 TAAATGCTTACCTTTGATGAGGCTGATACAGACAGCCTCCGCCATCCCTCCAGC 1462
1441 CTATATCTGATCACCATCAACCCCTCCCATNYSACCTAAACAAAATCTAAGTTGAAT 1500
1463 CTATATCTGATCACCATCAACCCCTCCCATNYSACCTAAACAAAATCTAAGTTGAAT 1522
1501 CCTTGAACATGTCAGACATCAATATRTTCTCTGCTGAGAGAGCTCTCTGCTCTT 1560
1523 CCTTGAACATGTCAGACATCAATATRTTCTCTGCTGAGAGAGCTCTCTGCTCTT 1582
1561 AATCTAGATGATGTTAAAGTTTGAATGATGATCTTACTTATCATGCAAGAGAGG 1620
1583 AATCTAGATGATGTTAAAGTTTGAATGATGATCTTACTTATCATGCAAGAGAGG 1642
1621 ACACATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1680
1643 ACACATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1702
1681 AGAGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1740
1703 AGAGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1762
1741 TGTAAAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1800
1763 TGTAAAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1822
1801 CATTTCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTAT 1860
1823 CATTTCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTAT 1882
1861 TCCCAAGAGTAACTTTTCAATTCATGATGATGATGATGATGATGATGATGATGATGAT 1920
1883 TCCCAAGAGTAACTTTTCAATTCATGATGATGATGATGATGATGATGATGATGATGAT 1942
1921 TACTGTCATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTAT 1980
1943 TACTGTCATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTAT 2002
1981 GGGCAGCTCTTGTGAGGCACTTTAGGCTTCACTCTGCGCAATAAAGAAATTTACAAAGA 2037
2003 GGGCAGCTCTTGTGAGGCACTTTAGGCTTCACTCTGCGCAATAAAGAAATTTACAAAGA 2059

RESULT 4
AR261166 3923 bp DNA 1linear PAT 29-JAN-2003
LOCUS AR261166
DEFINITION Sequence 690 from patent US 6321716.
ACCESSION AR261166
VERSION AR261166.1 GI:28071929
KEYWORDS
SOURCE
ORGANISM
Unknown.
Unclassified.
1 (bases 1 to 3923)
AUTHORS Mashiki,Z. and Harada,J.
TITLE Negative pressure control apparatus for engine mounted in vehicle
JOURNAL Patent: us 6321716-A 690 27-NOV-2001;
FEATURES Location/Qualifiers

source 1..3923 /organism="unknown"
BASE COUNT 1157 a 840 c 740 g 1186 t
ORIGIN
Query Match 80.0%; Score 1629; DB 6; Length 3923;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 2029; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
1 AGAAGCTGCGATCAGAAAAACAGAGGGGAGATTTGTGTGGCTGACGCCAGAGACCGAG 60
23 AGAAGCTGCGATCAGAAAAACAGAGGGGAGATTTGTGTGGCTGACGCCAGAGACCGAG 82
61 GAAGATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 120
83 GAGATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 142
121 TGTTCATATGAACACCAAGATTAATTAAGTGAAGAGCTAGTCCGCTGATGATCTCTCAGT 180
143 TGTTCATATGAACACCAAGATTAATTAAGTGAAGAGCTAGTCCGCTGATGATCTCTCAGT 202
181 GACACAGGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 240
203 GACACAGGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 262
241 CTACAGACATCTCAATGCGAGGGGTGAGAAATTAAGAAAGGCTGATGATGATGATGATGAT 300
263 CTACAGACATCTCAATGCGAGGGGTGAGAAATTAAGAAAGGCTGATGATGATGATGATGAT 322
301 GGCACACATCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 360
323 GGCACACATCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 382
361 TATGCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 420
383 TATGCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 442
421 CAGGAGCAGCAAAAGAGAGACACAGAGATCCCTGGGAGAAATGCCGGCCCATCTTGGG 480
443 CAGGAGCAGCAAAAGAGAGACACAGAGATCCCTGGGAGAAATGCCGGCCCATCTTGGG 502
481 TCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 540
503 TCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 562
541 AATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 600
563 AATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 622
601 AACGGATTAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 660
623 AACGGATTAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 682
661 GACGAGAAATCTTGTATGCTTCAACAAGATGCAACAACAACAACAACAACAACAACAACA 720
683 GACGAGAAATCTTGTATGCTTCAACAAGATGCAACAACAACAACAACAACAACAACAACA 742
721 ACATGAGCAGCAACCTGGGAGAGATTAACACGCGGCAAGAGGTCAAGATCTTGGCC 780
743 ACATGAGCAGCAACCTGGGAGAGATTAACACGCGGCAAGAGGTCAAGATCTTGGCC 802
781 CTGCTGCTTAACCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 840
803 CTGCTGCTTAACCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 862
841 AGCTGTTGTAATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 900
863 AGCTGTTGTAATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 922
901 GCCACATCTATTTTAAATATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAAT 960
923 GCCACATCTATTTTAAATATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAAT 982

QY 961 AATAACATTTACTATTTTGTTCAAAGACCTTCGTGTCGTCCATAATATAGTACT 1020
| | | | |
Db 983 AATAACATTTACTATTTTGTTCAAAGACCTTCGTGTCGTCCATAATATAGTACT 1042
| | | | |
QY 1021 GTTTTCTTGAAGAGTGTTCGCGCCAGGAGATCTGTACACAGGCTGGGAACATCTCA 1080
| | | | |
Db 1043 GTTTTCTTGAAGAGTGTTCGCGCCAGGAGATCTGTACACAGGCTGGGAACATCTCA 1102
| | | | |
QY 1081 GATCTTTCAGGAGTTATCTACTAGCACAGCATGATCATTTACGGAGTGAATATCTA 1140
| | | | |
Db 1103 GATCTTTCAGGAGTTATCTACTAGCACAGCATGATCATTTACGGAGTGAATATCTA 1162
| | | | |
QY 1141 ATCAACATCATCTCAGTGTCTTCCCATCTGAAATTCATTTCCACTTTTGTGCCA 1200
| | | | |
Db 1163 ATCAACATCATCTCAGTGTCTTCCCATCTGAAATTCATTTCCACTTTTGTGCCA 1222
| | | | |
QY 1201 TTTCAGACCTCAAAATGTCTATTCATTAATATCACAGGTTAACTTTTGTAAAC 1260
| | | | |
Db 1223 TTTCAGACCTCAAAATGTCTATTCATTAATATCACAGGTTAACTTTTGTAAAC 1282
| | | | |
QY 1261 TCGAAGATTCATAGTTACATGACGCTATGGGAATTTATACATTTTGTTCAGT 1320
| | | | |
Db 1283 TCGAAGATTCATAGTTACATGACGCTATGGGAATTTATACATTTTGTTCAGT 1342
| | | | |
QY 1321 GCAAAGATGACTAAGTCTTTATCCCTCCCTCTGTTGATTTTTCAGTAAAGT 1380
| | | | |
Db 1343 GCAAAGATGACTAAGTCTTTATCCCTCTGTTGATTTTTCAGTAAAGT 1402
| | | | |
QY 1381 TAAATGCTTAGCTTGACTGAGGCTGTATACAGCAGCCTCCCATCCCTCCAGC 1440
| | | | |
Db 1403 TAAATGCTTAGCTTGACTGAGGCTGTATACAGCAGCCTCCCATCCCTCCAGC 1462
| | | | |
QY 1441 CTATCTGTCTACCACTCAACCCCTCCCATNATTCATTAACAAATCTACTGTAAT 1500
| | | | |
Db 1463 CTATCTGTCTACCACTCAACCCCTCCCATNATTCATTAACAAATCTACTGTAAT 1522
| | | | |
QY 1501 CCTTGAACATGTCTGAGCATCATCTTTCTTCTGCTGAGAGCTCTCTCTCTCT 1560
| | | | |
Db 1523 CCTTGAACATGTCTGAGCATCATCTTTCTTCTGCTGAGAGCTCTCTCTCTCT 1582
| | | | |
QY 1561 AANTCTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1620
| | | | |
Db 1583 AANTCTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1642
| | | | |
QY 1621 ACACATATGAGATTCATCATCATGAGACAGCAAAATCTTAAAGTGAATTTGATTATA 1680
| | | | |
Db 1643 ACACATATGAGATTCATCATCATGAGACAGCAAAATCTTAAAGTGAATTTGATTATA 1702
| | | | |
QY 1681 AGAGTTAGATTAATATATGAAATGCAAGACCCACAGAGGAATGTTATGGGCGAGTT 1740
| | | | |
Db 1703 AGAGTTAGATTAATATATGAAATGCAAGACCCACAGAGGAATGTTATGGGCGAGTT 1762
| | | | |
QY 1741 TGTAAAGCTGGAGTGAAGAAAGGAGGAACTCATAGTATCTATATATATATCTT 1800
| | | | |
Db 1763 TGTAAAGCTGGAGTGAAGAAAGGAGGAACTCATAGTATCTATATATATATCTT 1822
| | | | |
QY 1801 CATTTCTATCTCTATACAAATATCCAAAGCTTTTCAAGAAATTCATGACAGTGCATA 1860
| | | | |
Db 1823 CATTTCTATCTCTATACAAATATCCAAAGCTTTTCAAGAAATTCATGACAGTGCATA 1882
| | | | |
QY 1861 TCCCAAGGTAACCTTTATCCATTTATGATGATGATGATGATGATGATGATGATGAT 1920
| | | | |
Db 1883 TCCCAAGGTAACCTTTATCCATTTATGATGATGATGATGATGATGATGATGATGAT 1942
| | | | |
QY 1921 TACTGATCATTTATCTAAGTGTGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1980
| | | | |
Db 1943 TACTGATCATTTATCTAAGTGTGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2002
| | | | |
QY 1981 GGGGACTCTTGTAGGACCTTTAGGTTACTCTCTGCAATTAAGAAATTTACAAGA 2037
| | | | |
Db 2003 GGGGACTCTTGTAGGACCTTTAGGTTACTCTCTGCAATTAAGAAATTTACAAGA 2059
| | | | |

RESULT 5
AR278697
LOCUS AR278697 3923 bp DNA linear PAT 10-APR-2003
DEFINITION Sequence 690 from patent US 6512094.
ACCESSION AR278697
VERSION AR278697.1 GI:29712943
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 3923)
AUTHORS Xu,J., Dillon,D.C., Mitchem,J.L., Harlocker,S.L., Jiang,Y.,
Kalos,M.D., Fanger,G.R., Retter,M.W., Stolk,J.A., Day,C.H.,
Vedrick,T.S., Carter,D., Li,S.X., Wang,A., Skelky,Y.A.W.,
Hepler,W.T. and Henderson,R.A.
TITLE Compositions and methods for the therapy and diagnosis of prostate
cancer
JOURNAL Patent: US 6512094-A 690 28-JAN-2003;
FEATURES
source Location/Qualifiers
BASE COUNT 1157 a 840 c 740 g 1186 t
ORIGIN

Query Match 80.0%; Score 1629; DB 6; Length 3923;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 2029; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 AGAAGCTGCGATCGAAAAACAGAGGGAGATTGTGTGCTGACGCCGAGGAGACCAG 60
| | | | |
Db 23 AGAAGCTGCGATCGAAAAACAGAGGGAGATTGTGTGCTGACGCCGAGGAGACCAG 82
| | | | |
QY 61 GAATGTCGATGGTGGGAAGGACCTGATGATACAGAGGAATTCACACATATACCTAG 120
| | | | |
Db 83 GAATGTCGATGGTGGGAAGGACCTGATGATACAGAGGAATTCACACATATACCTAG 142
| | | | |
QY 121 TGTTCATGAACACCAAGATTAATGAAGTGAAGCTAGTCCGCTGTGAGTCTTCAGT 180
| | | | |
Db 143 TGTTCATGAACACCAAGATTAATGAAGTGAAGCTAGTCCGCTGTGAGTCTTCAGT 202
| | | | |
QY 181 GACACAGGCTGGATTCACCATCCGACGACCTTTGTGATCTCAGTGCAGAAAGAGA 240
| | | | |
Db 203 GACACAGGCTGGATTCACCATCCGACGACCTTTGTGATCTCAGTGCAGAAAGAGA 262
| | | | |
QY 241 CTACAGACATCTCAATGGCAGGAGTGAATAATGAAGAGCTGCTGACTTACCATCTGA 300
| | | | |
Db 263 CTACAGACATCTCAATGGCAGGAGTGAATAATGAAGAGCTGCTGACTTACCATCTGA 322
| | | | |
QY 301 GGGCACACATCTGCTGAATGAGATTAATTAACATCACTAGAAACAGCAAGATGACATA 360
| | | | |
Db 323 GGGCACACATCTGCTGAATGAGATTAATTAACATCACTAGAAACAGCAAGATGACATA 382
| | | | |
QY 361 TAAATCTAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 420
| | | | |
Db 383 TAAATCTAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 442
| | | | |
QY 421 CAGGAACACAAAAAGGAAGCAGAGATCCCTGGGAAATAATGCCGCCGCCCATCTGGG 480
| | | | |
Db 443 CAGGAACACAAAAAGGAAGCAGAGATCCCTGGGAAATAATGCCGCCGCCCATCTGGG 502
| | | | |
QY 481 TCATCATGAGCTCGCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540
| | | | |
Db 503 TCATCATGAGCTCGCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 562
| | | | |
QY 541 AATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 600
| | | | |
Db 563 AATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 622
| | | | |
QY 601 AACGGATTCAGATTTGAATGAATGACCAAAAGTGAAGCTTACCAATGAGAGGAACA 660
| | | | |
Db 623 AACGGATTCAGATTTGAATGAATGACCAAAAGTGAAGCTTACCAATGAGAGGAACA 682
| | | | |
QY 661 GACGAGAAATCTTGTATGGCTTCACAAAGACATGCACAAACAAATGGAATCTGTGATG 720
| | | | |

[illegible]

QY	361	TAATGCTAAAGTAGACATGTTTTGGACATTTCCAGCCCTTTAAATATCCACACACA	420
Db	383	TAATGCTAAAGTAGACATGTTTTGGACATTTCCAGCCCTTTAAATATCCACACACA	442
QY	421	CAGAAAGCAGAAAAGGAAGCAGAGATCCCTGGGAGAAATCCCGCGCCGCACTTGGG	480
Db	443	CAGAAAGCAGAAAAGGAAGCAGAGATCCCTGGGAGAAATCCCGCGCCGCACTTGGG	502
QY	481	TCATCGATGAGGCTTCGCCCTGTGCTGCCGCTTGTGAGGGAAGACATTTAGAAATG	540
Db	503	TCATCGATGAGGCTTCGCCCTGTGCTGCCGCTTGTGAGGGAAGACATTTAGAAATG	562
QY	541	AATTGATGTGTCCTTAAAGATGGGCGAGAAAACAGATCCGTGTGATATTTAATTG	600
Db	563	AATTGATGTGTCCTTAAAGATGGGCGAGAAAACAGATCCGTGTGATATTTAATTG	622
QY	601	AACGGGATTTACAGATTTGAAATGAAGTCACAAAGTAGACATTTACCAATGAGAGAAACA	660
Db	623	AACGGGATTTACAGATTTGAAATGAAGTCACAAAGTAGACATTTACCAATGAGAGAAACA	682
QY	661	GACGAGAAATCTTGATGGCTTCACAAACATGCAACCAACCAAAATGGAATATCTGATG	720
Db	683	GACGAGAAATCTTGATGGCTTCACAAACATGCAACCAACCAAAATGGAATATCTGATG	742
QY	721	ACATGAGGACCCAAAGCTGGGAGAGATTAACACAGGGGCGAGAGGGTCAGGATTTGGCC	780
Db	743	ACATGAGGACCCAAAGCTGGGAGAGATTAACACAGGGGCGAGAGGGTCAGGATTTGGCC	802
QY	781	CTGGCGCCTTAAAGCTGGCTCATPACCAAAATCTTATATTTCTAACCCCTCAAAACAA	840
Db	803	CTGGCGCCTTAAAGCTGGCTCATPACCAAAATCTTATATTTCTAACCCCTCAAAACAA	862
QY	841	AGCTGTGTAATATCTGATCTCTACGGTTCCTCTGGGCCCAACATTCCTCATATATCCA	900
Db	863	AGCTGTGTAATATCTGATCTCTACGGTTCCTCTGGGCCCAACATTCCTCATATATCCA	922
QY	901	GCCACACTCAATTTTAAATATTTAGTGTCCCAATCTGTACTGTGACCTTTTACACTGTAG	960
Db	923	GCCACACTCAATTTTAAATATTTAGTGTCCCAATCTGTACTGTGACCTTTTACACTGTAG	982
QY	961	AATAACATTTACTATTTTGTTCAAAAGACCTTCGTGCTGCTGACCTTAATATGATGACT	1020
Db	983	AATAACATTTACTATTTTGTTCAAAAGACCTTCGTGCTGCTGACCTTAATATGATGACT	1042
QY	1021	GTTTTTCTTAAGAGAGTGTTCGGGCCAGGGGATCTGTAAACAGGCTGGGAAGCATCTCA	1080
Db	1043	GTTTTTCTTAAGAGAGTGTTCGGGCCAGGGGATCTGTAAACAGGCTGGGAAGCATCTCA	1102
QY	1081	GATCTTTCAGAGGTTATCTACTACTAGACACAGACATGATCTATACGAGATGAATATCTA	1140
Db	1103	GATCTTTCAGAGGTTATCTACTACTAGACACAGACATGATCTATACGAGATGAATATCTA	1162
QY	1141	ATCAACATCATCTCAGTGTCTTGGCCATACGTGAATTCATTTCCACTTTGTGCCCA	1200
Db	1163	ATCAACATCATCTCAGTGTCTTGGCCATACGTGAATTCATTTCCACTTTGTGCCCA	1222
QY	1201	TTTCCAAACCTCAAAATGTCATTCOCATTAATATACAGGATTAACCTTTTAAAAAC	1260
Db	1223	TTTCCAAACCTCAAAATGTCATTCOCATTAATATACAGGATTAACCTTTTAAAAAC	1282
QY	1261	TGGAAGAATTCATGTTATCATGACAGCTATGGGAATTTAATATACATATTTGTTCACAGT	1320
Db	1283	TGGAAGAATTCATGTTATCATGACAGCTATGGGAATTTAATATACATATTTGTTCACAGT	1342
QY	1321	GCAAAAGATGACTAAGTCTTATATCCCTCCCTTTGTTGATTTTTTTTCCAGTATAAAGT	1380
Db	1343	GCAAAAGATGACTAAGTCTTATATCCCTCCCTTTGTTGATTTTTTTTCCAGTATAAAGT	1402
QY	1381	TAAATATGCTTATGAGTGTGAGAGCTTATATACAGACAGGCTCCGCCCATCTCCACAGC	1440
Db	1403	TAAATATGCTTATGAGTGTGAGAGCTTATATACAGACAGGCTCCGCCCATCTCCACAGC	1462

QY	1441	TTTATCTGTCAACACATCAACCCCTCCCATNTSACCTAAACAAATCTACTGTAT	1500
Db	1463	-CTTATCTGTCAACACATCAACCCCTCCCATACCACTAAACAAATCTAACTGTAT	1522
OY	1501	CCTGAACATCTCAGNCACTCATTTTCCTCTGCGCTGAGAACCTCTCTCTCT	1560
Db	1523	CCTGAACATCTCAGNCACTCATTTTCCTCTGCGCTGAGAACCTCTCTCTCT	1582
OY	1561	AANTCTAGAAATGATGTAAGTTTGAATTAAGTTGACTATCTTACTCATGCAAGAAAGG	1620
Db	1583	AAATCTAGAAATGATGTAAGTTTGAATTAAGTTGACTATCTTACTCATGCAAGAAAGG	1642
OY	1621	ACAATATGAAATTCATCATCTACACTGAGACAGCAAACTACTAAAGTGAATTTGATTA	1680
Db	1643	ACAATATGAAATTCATCATCTACACTGAGACAGCAAACTACTAAAGTGAATTTGATTA	1702
OY	1681	AGAGTTTGAATTAATGATGTAAGTTTGAATTAAGTTTGAATTTGATTTATGAGGACGTT	1740
Db	1703	AGAGTTTGAATTAATGATGTAAGTTTGAATTAAGTTTGAATTTGATTTATGAGGACGTT	1762
OY	1741	TGTAAGCCTGGATGTGAAGMAAGGAGGAACTCATAGTATCTTATAATAATACT	1800
Db	1763	TGTAAGCCTGGATGTGAAGMAAGGAGGAACTCATAGTATCTTATAATAATACT	1822
OY	1801	CATTTCCTCATCTCTATCACAAATTCACAACAGTTTTCACAGAAATCATGCACTGCAA	1860
Db	1823	CATTTCCTCATCTCTATCACAAATTCACAACAGTTTTCACAGAAATCATGCACTGCAA	1882
OY	1861	TCCCAAGAGTAACCTTTATCATCTTATGAGTGAGTGCAGTTTGAATTTGGCAATCA	1920
Db	1883	TCCCAAGAGTAACCTTTATCATCTTATGAGTGAGTGCAGTTTGAATTTGGCAATCA	1942
OY	1921	TACTGGTCACTTATCTCAACTTTGAGATGTGTGTGCTGTAGTAAATGAAAGAAATA	1980
Db	1943	TACTGGTCACTTATCTCAACTTTGAGATGTGTGTGCTGTAGTAAATGAAAGAAATA	2002
OY	1981	GGGACACTTGTGAGCCACTTTAGGTTCACTCTGCGCAATTAAGAAATTTACAAAGA	2037
Db	2003	GGGACACTTGTGAGCCACTTTAGGTTCACTCTGCGCAATTAAGAAATTTACAAAGA	2059

RESULT 7			
AX267716			
LOCUS	AX267716	3923 bp	DNA
DEFINITION	Sequence 690 from Patent WO0173032.		linear
ACCESSION	AX267716		
VERSION	AX267716.1	GI:16516388	
KEYWORDS			
SOURCE	Homo sapiens (human)		

REFERENCE
1 Eukaryota: Metazoa; Chordata; Craniata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.

AUTHORS
 Au, D., Dillon, D. C., Micham, J. L., Harlocker, S. L., Jiang, Y.,
 Katos, M. D., Fanger, G. R., Retter, M. W., Stolk, J. A., Day, C. H.,
 Vetschik, T. S., Carter, D., Li, S. X., Wang, A., Skelky, Y. A., Hepler, W. T.
 and Henderson, R. A.

TITLE
Compositions and methods for the therapy and diagnosis of prostate cancer
Patent: WO 0173032-A 690 04-OCT-2001;
JOURNAL

FEATURES	CORIXA CORPORATION (US)
source	Location/Qualifiers
	1. .3923

```

/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

```

BASE COUNT	1157 a	840 c	740 g	1186 t
ORIGIN				

Query Match	80.0%	Score 1629;	DB 6;	Length 3923;
Best Local Similarity	99.6%;	Pred. No. 0;		
Matches 2029; Conservative	0;	Mismatches 8;	Indels 0;	Gaps 0;

QY 1 AGAAGCTGGCATCAGAAAAACAGAGGGAGATTTGTGTGCTGCAGCCGAGGAGACCGAG 60
DB 23 AGAAGCTGGCATCAGAAAAACAGAGGGAGATTTGTGTGCTGCAGCCGAGGAGACCGAG 82
QY 61 GAAAGTCTGCATGTGTGGGAGAGACCTGATGATACAGAGGATTTACAACACATATKCTTAG 120
DB 83 GAAAGTCTGCATGTGTGGGAGAGACCTGATGATACAGAGGATTTACAACACATATKCTTAG 142
QY 121 TGTTCATGGAACACCAAGATTAATTAAGTGAAGACCTGTGCTGTGCTGTGCTGTGCTGTG 180
DB 143 TGTTCATGGAACACCAAGATTAATTAAGTGAAGACCTGTGCTGTGCTGTGCTGTGCTGTG 202
QY 181 GACACAGGGCTGTGATCACCATCGACGGCACTTTCAGTACTCAGTGCAGCAAGAAAGA 240
DB 203 GACACAGGGCTGTGATCACCATCGACGGCACTTTCAGTACTCAGTGCAGCAAGAAAGA 262
QY 241 CTACAGACATCTCAATGCGAGGGGTGAGAAATTAAGAAAGCTGCTGACTTTACCATCTGA 300
DB 263 CTACAGACATCTCAATGCGAGGGGTGAGAAATTAAGAAAGCTGCTGACTTTACCATCTGA 322
QY 301 GGCCACACATCTGCTGAATGGAGTAAATTAACATCAGTAAAGACGCAAGATGACATTA 360
DB 323 GGCCACACATCTGCTGAATGGAGTAAATTAACATCAGTAAAGACGCAAGATGACATTA 382
QY 361 TAATGCTTAAGTAGTACATGTTTTTGCACATTTTCAGCCCTTTAAATATCCACACACA 420
DB 383 TAATGCTTAAGTAGTACATGTTTTTGCACATTTTCAGCCCTTTAAATATCCACACACA 442
QY 421 CAGGAGCACAAGAGAAAGACACAGATCCTGCGAGAAATGCCGGCCGACATCTTGGG 480
DB 443 CAGGAGCACAAGAGAAAGACACAGATCCTGCGAGAAATGCCGGCCGACATCTTGGG 502
QY 481 TCATGATGAGCGCTGCGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTG 540
DB 503 TCATGATGAGCGCTGCGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTG 562
QY 541 AATTGATGCTGCTTAAAGATGGGAGGAAACAGATCCTGTTGTGATATTTATTTG 600
DB 563 AATTGATGCTGCTTAAAGATGGGAGGAAACAGATCCTGTTGTGATATTTATTTG 622
QY 601 AAGCGGATTTACGATTTGAAATGAATGACCAAAAGTGAGCATTTACCAATGAGAGAAACA 660
DB 623 AAGCGGATTTACGATTTGAAATGAATGACCAAAAGTGAGCATTTACCAATGAGAGAAACA 682
QY 661 GACGAGAAATCTTATGCTTCACAGACATGCAAAACAAATTTGAAATCTGTGATG 720
DB 683 GACGAGAAATCTTATGCTTCACAGACATGCAAAACAAATTTGAAATCTGTGATG 742
QY 721 ACATGAGGACGCAAGCTGTGGGAGAGATTAACACGCGGGCAGAGGGTCAAGATTTGCGCC 780
DB 743 ACATGAGGACGCAAGCTGTGGGAGAGATTAACACGCGGGCAGAGGGTCAAGATTTGCGCC 802
QY 781 CTGCTGCTTAAAGCTGTGCTTCATTAACCAATCATTTTCAATTTTCAACCTTCAAAACA 840
DB 803 CTGCTGCTTAAAGCTGTGCTTCATTAACCAATCATTTTCAATTTTCAACCTTCAAAACA 862
QY 841 AGCTTTGTAATATGATGCTGTAGGCTTCTGTGGGCCCAACATTTCCATATATCA 900
DB 863 AGCTTTGTAATATGATGCTGTAGGCTTCTGTGGGCCCAACATTTCCATATATCA 922
QY 901 GGCACACATCTTAAATATTAATTAAGTCCAGATCTGTACTGTGACCTTCTCACTGTAG 960
DB 923 GGCACACATCTTAAATATTAATTAAGTCCAGATCTGTACTGTGACCTTCTCACTGTAG 982
QY 961 AATAACATTTACTATTTTGTTCAAAGACCTTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTG 1020
DB 983 AATAACATTTACTATTTTGTTCAAAGACCTTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTG 1042
QY 1021 GTTTTCTTAAGAGATGTTCTGCGCCAGGGATCTGTGAACAGGGTGGGAACATCTCA 1080
DB 1043 GTTTTCTTAAGAGATGTTCTGCGCCAGGGATCTGTGAACAGGGTGGGAACATCTCA 1102
QY 1081 GATCTTCCAGGTTATACTTACTAGCACACAGCATGATCATTTACGAGATGAATTATCTA 1140

DB 1103 GATCTTCCAGGTTATACTTACTAGCACACAGCATGATCATTTAGGATGAATTATCTA 1162
QY 1141 ATCAACATCATTCCTAGAGTCTTTGGCCCATACTGAAATTCATTTCCACTTTTGGCCCA 1200
DB 1163 ATCAACATCATTCCTAGAGTCTTTGGCCCATACTGAAATTCATTTCCACTTTTGGCCCA 1222
QY 1201 TTCCTAAGACCTCAAAATGCTCATTTCCATTAATATACAGGATTTAACTTTTAAACC 1260
DB 1223 TTCCTAAGACCTCAAAATGCTCATTTCCATTAATATACAGGATTTAACTTTTAAACC 1282
QY 1261 TGGAAATTCATGTTTACATGACAGCTATGGAATTTAAATACATATTTTGTTCACGT 1320
DB 1283 TGGAAATTCATGTTTACATGACAGCTATGGAATTTAAATACATATTTTGTTCACGT 1342
QY 1321 GCAAAAGTACATAAGCTTTTATCCCTCCCTTTTGTATATTTTTCACATATAAAT 1380
DB 1343 GCAAAAGTACATAAGCTTTTATCCCTCCCTTTTGTATATTTTTCACATATAAAT 1402
QY 1381 TAAATATGCTTACCTTGTACTAGGCTGTATACAGACAGCCCTCCCATCCCTCCAC 1440
DB 1403 TAAATATGCTTACCTTGTACTAGGCTGTATACAGACAGCCCTCCCATCCCTCCAC 1462
QY 1441 CTTATCTGTCAATCACCATCAACCCCTCCCATATVSAACCTAAACAAATCTAATCTTAAT 1500
DB 1463 CTTATCTGTCAATCACCATCAACCCCTCCCATACACACTTAACAAATCTAATCTTAAT 1522
QY 1501 CCTTAACATGTCAGGNCATACATTTTCTCTGCTGTGAGAGCTCTTCTGCTCTT 1560
DB 1523 CCTTAACATGTCAGGNCATACATTTTCTCTGCTGTGAGAGCTCTTCTGCTCTT 1582
QY 1561 AANTCTAGATGATGTAAGTTTGAATTAAGTTGACTATCTTACATGCAAGAAAGG 1620
DB 1583 AANTCTAGATGATGTAAGTTTGAATTAAGTTGACTATCTTACATGCAAGAAAGG 1642
QY 1621 ACACATATGATGATGATCATCATGATGAGACAGCAAAATTAAGTGAATTTGATTTA 1680
DB 1643 ACACATATGATGATGATCATCATGATGAGACAGCAAAATTAAGTGAATTTGATTTA 1702
QY 1681 AGAGTTTATGATTAATATATGAAATGACAGACACAGAGGAAATTTTATGGGACAGTT 1740
DB 1703 AGAGTTTATGATTAATATATGAAATGACAGACACAGAGGAAATTTTATGGGACAGTT 1762
QY 1741 TGTAAAGCTGGGATGTAAGGAAAGGACAGGAAACCTCATGATATCTATATATATCTT 1800
DB 1763 TGTAAAGCTGGGATGTAAGGAAAGGACAGGAAACCTCATGATATCTATATATATCTT 1822
QY 1801 CATTTCTATCTATCATCAATATTCACAAAGCTTTTCACAGAAATTCAGAGTGCANA 1860
DB 1823 CATTTCTATCTATCATCAATATTCACAAAGCTTTTCACAGAAATTCAGAGTGCANA 1882
QY 1861 TCCCCAAAGGTAACCTTATTCATTTGATGATGATGCGCTTTAAGAAATTTGGCAATTA 1920
DB 1883 TCCCCAAAGGTAACCTTATTCATTTGATGATGATGCGCTTTAAGAAATTTGGCAATTA 1942
QY 1921 TACTGTGACTATATCTCAACTTTGAGATGATGTTTCTCTGTAGTAAATTTGAAGAAATA 1980
DB 1943 TACTGTGACTATATCTCAACTTTGAGATGATGTTTCTCTGTAGTAAATTTGAAGAAATA 2002
QY 1981 GGGCACTCTTGTGACCCACTTTTAAAGGTTTCACTCTGCGCAATTAAGAAATTTACAAAGA 2037
DB 2003 GGGCACTCTTGTGACCCACTTTTAAAGGTTTCACTCTGCGCAATTAAGAAATTTACAAAGA 2059

RESULT 8
AF103907 3923 bp mRNA linear PRI 14-AUG-2000
LOCUS AF103907 Homo sapiens non-coding RNA D33 sequence.
DEFINITION AF103907
ACCESSION AF103907
VERSION AF103907.1 GI:6165973
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
1 (bases 1 to 3923)
Bussemakers,M.J., Van Bokhoven,A., Verhaegh,G.W., Smit,F.P.,
Karthus,H.F., Schalken,J.A., Debruyne,F.M., Ru,N. and Isaacs,W.B.
DD3: a new prostate-specific gene, highly overexpressed in prostate
cancer
JOURNAL Cancer Res. 59 (23), 5975-5979 (1999)
MEDLINE 20072260
PUBMED 10606244
2 (bases 1 to 3923)
Bussemakers,M.J.G., Van Bokhoven,A., Verhaegh,G.W., Smit,F.P.,
Karthus,H.F.M., Schalken,J.A., Debruyne,F.M.J., Ru,N. and
Isaacs,W.B.
Direct Submission
Submitted (28-OCT-1998) Urology Research Laboratory, University
Hospital Nijmegen, P.O. Box 9101, Nijmegen 6500 HB, Netherlands
FEATURES
source
1..3923
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/chromosome="9"
/map="9q21-q22"
/tissue_type="prostate"
/note="non-coding RNA DD3"
3756..3911
/note="LINE"
/rpt_family="L1"
/rpt_type="dispersed"
3923
polysite
BASE COUNT 1157 a 840 c 740 g 1186 t
ORIGIN
Query Match 80.0%; Score 1629; DB 9; Length 3923;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 202; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
QY 1 AGAAGCTGGCATCAGAAAAACAGAGGGAGATTGTGTGCTGCAGCCGAGGAGACAG 60
DB 23 AGAAGCTGGCATCAGAAAAACAGAGGGAGATTGTGTGCTGCAGCCGAGGAGACAG 82
QY 61 GAAGATCTGATGGTGGGAAGGACCTGATGATACAGAGAAATTACACATATATCTTAG 120
DB 83 GAAGATCTGATGGTGGGAAGGACCTGATGATACAGAGAAATTACACATATATCTTAG 142
QY 121 TGTTCATGATACCAAGATTAATTAAGTGAAGCTAGTCCGCTGAGTCTCTCAGT 180
DB 143 TGTTCATGATACCAAGATTAATTAAGTGAAGCTAGTCCGCTGAGTCTCTCAGT 202
QY 181 GACACAGGGCTGATCCATCGACGCACTTCTGATCTCACTAGTCAGCAAAAGAGA 240
DB 203 GACACAGGGCTGATCCATCGACGCACTTCTGATCTCACTAGTCAGCAAAAGAGA 262
QY 241 CTACAGCATCTCAATGGCAGGGGTGAAATAAGAAAGCTGCTGACTTTACCATCTGA 300
DB 263 CTACAGCATCTCAATGGCAGGGGTGAAATAAGAAAGCTGCTGACTTTACCATCTGA 322
QY 301 GGCACACATCTGCTGAAATGGAATTAATTAACATCTAGAAACCAAGATGACATA 360
DB 323 GGCACACATCTGCTGAAATGGAATTAATTAACATCTAGAAACCAAGATGACATA 382
QY 361 TAATGCTAAGTAGTGCATGTTTGGACATTTCCAGCCCTTTAAATATCCACACACA 420
DB 383 TAATGCTAAGTAGTGCATGTTTGGACATTTCCAGCCCTTTAAATATCCACACACA 442
QY 421 CAGGAAGCAGAAAGAGACAGAGATCCCTGGAGAAATGCCGGCCCATCTTGGG 480
DB 443 CAGGAAGCAGAAAGAGACAGAGATCCCTGGAGAAATGCCGGCCCATCTTGGG 502
QY 481 TCATCGATGAGCTCGCCCTGTGCTGCTGCTGCTGCTGAGGAGACATTTAGAAATG 540
DB 503 TCATCGATGAGCTCGCCCTGTGCTGCTGCTGCTGCTGAGGAGACATTTAGAAATG 562

QY 541 AATTGATGCTGCTCTTAAGAGTGGCAGGAAAAACAGATCCTGTTGTGATATTTATTTG 600
DB 563 AATTGATGCTGCTCTTAAGAGTGGCAGGAAAAACAGATCCTGTTGTGATATTTATTTG 622
QY 601 AACGGATTACAGATTTGAAATGAAGTCACAAAGTGCATTTACCAATGAGAGGAAAA 660
DB 623 AACGGATTACAGATTTGAAATGAAGTCACAAAGTGCATTTACCAATGAGAGGAAAA 682
QY 661 GAGGAGAAATCTGATGGCTTCACAGACATGCAACAAATGAATGATGATG 720
DB 683 GAGGAGAAATCTGATGGCTTCACAGACATGCAACAAATGAATGATGATG 742
QY 721 ACATGAGGAGCCAGAGCTGGGAGAGATTAACCAAGGGGAGAGGCTCAGATTTGGCC 780
DB 743 ACATGAGGAGCCAGAGCTGGGAGAGATTAACCAAGGGGAGAGGCTCAGATTTGGCC 802
QY 781 CTGCTGCTTAACCTGTGCTTCATTAACCAATCATTTCTATTTCTAACCTCAAAACA 840
DB 803 CTGCTGCTTAACCTGTGCTTCATTAACCAATCATTTCTATTTCTAACCTCAAAACA 862
QY 841 AGCTGTGTAATCTGATGCTCTACGGTTCCTTGGGCCAATCTCATATATCA 900
DB 863 AGCTGTGTAATCTGATGCTCTACGGTTCCTTGGGCCAATCTCATATATCA 922
QY 901 GCCACACTCAATTTTAATTAATTAATTCACAGATCTGATGCTGCTTCTACACTAG 960
DB 923 GCCACACTCAATTTTAATTAATTAATTCACAGATCTGATGCTGCTTCTACACTAG 982
QY 961 AATTAACATTTACTATTTTGTTCAAAGACCTTGTGCTGCTCAATATATGATGACT 1020
DB 983 AATTAACATTTACTATTTTGTTCAAAGACCTTGTGCTGCTCAATATATGATGACT 1042
QY 1021 GTTTTCTTAAGGAGTGTGCTGCGCCAGGGAGATGTGAACAGGCTGGAGATCTCA 1080
DB 1043 GTTTTCTTAAGGAGTGTGCTGCGCCAGGGAGATGTGAACAGGCTGGAGATCTCA 1102
QY 1081 GATCTTTCAGAGGTTTATCTTACTAGCACACAGCATGATCATTAAGGATTAATCTA 1140
DB 1103 GATCTTTCAGAGGTTTATCTTACTAGCACACAGCATGATCATTAAGGATTAATCTA 1162
QY 1141 ATCAACATCATCTCACTGCTTGTGCTTCCCATATCTGAATTTATTTCCACTTTG 1200
DB 1163 ATCAACATCATCTCACTGCTTGTGCTTCCCATATCTGAATTTATTTCCACTTTG 1222
QY 1201 TTCTCAAGACCTCAAAATGTCATTCATTAATTAACAGATTAACCTTTTATTAAC 1260
DB 1223 TTCTCAAGACCTCAAAATGTCATTCATTAATTAACAGATTAACCTTTTATTAAC 1282
QY 1261 TGGAGAAATTCATGTTACATGACAGCTATGGAATTAATTAATTTGTTTCCAGT 1320
DB 1283 TGGAGAAATTCATGTTACATGACAGCTATGGAATTAATTAATTTGTTTCCAGT 1342
QY 1321 GCAAAGATGACTAAGCTTATTCCTTCCCTTGTGTTGATTTTTCAGATTAAGT 1380
DB 1343 GCAAAGATGACTAAGCTTATTCCTTCCCTTGTGTTGATTTTTCAGATTAAGT 1402
QY 1381 TAAATGCTTAAGCTTGTACTGAGGCTGTATTAAGCAGCAGCCCTCCCATCCCTCAGC 1440
DB 1403 TAAATGCTTAAGCTTGTACTGAGGCTGTATTAAGCAGCAGCCCTCCCATCCCTCAGC 1462
QY 1441 CTATATCTGATCAACATCAACCCCTCCATTTTSACTTAAACAAATCTAATCTGTAAT 1500
DB 1463 CTATATCTGATCAACATCAACCCCTCCATTTTSACTTAAACAAATCTAATCTGTAAT 1522
QY 1501 CCTTGAACATGTAGGACATATATTTCTTCTGCTGAGAAAGCTTCTCTGCTCTT 1560
DB 1523 CCTTGAACATGTAGGACATATATTTCTTCTGCTGAGAAAGCTTCTCTGCTCTT 1582
QY 1561 AATTTAGATGATGATTAAGTTTGAATTAAGTGAATTAAGTGAATTAAGTGAATTAAG 1620
DB 1583 AATTTAGATGATGATTAAGTTTGAATTAAGTGAATTAAGTGAATTAAGTGAATTAAG 1642

QY 1621 ACACATATGAGATTCATCATCATGAGACAGCAATACTAAAGTATGTAATTGATTTATA 1680
|||||
Db 1643 ACACATATGAGATTCATCATCATGAGACAGCAATACTAAAGTATGTAATTGATTTATA 1702
1681 AGAGTTTGAATATAATATGAAATGCAAGAACACAGAGGAGATTTTATGGGACAGCTT 1740
1703 AGAGTTTGAATATAATATGAAATGCAAGAACACAGAGGAGATTTTATGGGACAGCTT 1762
QY 1741 TGTAAAGCTGGGATGTGAAGAAAGGACGAGACCTCATAGTATCTTATATATATCTT 1800
1763 TGTAAAGCTGGGATGTGAAGAAAGGACGAGACCTCATAGTATCTTATATATATCTT 1822
QY 1801 CATTTCTCTATCTATCATACATATCAACAAGCTTTTACAGAGATTCATGACAGTCAAA 1860
1823 CATTTCTCTATCTATCATACATATCAACAAGCTTTTACAGAGATTCATGACAGTCAAA 1882
QY 1861 TCCCCAAGGTAAACCTTATCCATTTTCATGTGTGAGTGGCTTTAGAAATTTTGGCAATCA 1920
1883 TCCCCAAGGTAAACCTTATCCATTTTCATGTGTGAGTGGCTTTAGAAATTTTGGCAATCA 1942
QY 1921 TACTGTGCTACTTATCTCAACTTTGAGATGTGTTTCTCTGTAGTTAATGAAAGAAATA 1980
1943 TACTGTGCTACTTATCTCAACTTTGAGATGTGTTTCTCTGTAGTTAATGAAAGAAATA 2002
QY 1981 GGGCAGCTTGTGAGCCACTTTAGGGTCCAGCTCCGGAATTAAGAATTTTACAAAGA 2037
2003 GGGCAGCTTGTGAGCCACTTTAGGGTCCAGCTCCGGAATTAAGAATTTTACAAAGA 2059
Db
RESULT 9
AF103908 5435 bp DNA linear PRI 14-AUG-2000
LOCUS Homo sapiens non-coding RNA D03 gene, exons 2, 3, and 4.
ACCESSION AF103908
VERSION AF103908.1 GI:6165974
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 5435)
Bussemakers,M.J.G., Van Bokhoven,A., Verhaegh,G.W., Smit,F.P.,
Karthaus,H.F., Schalken,J.A., Debruyne,F.M., Ru,N. and Isaacs,W.B.
DD3: a new prostate-specific gene, highly overexpressed in prostate
cancer
JOURNAL Cancer Res. 59 (23), 5975-5979 (1999)
MEDLINE 20072260
PubMed 10606244
REFERENCE 2 (bases 1 to 5435)
Bussemakers,M.J.G., Van Bokhoven,A., Verhaegh,G.W., Smit,F.P.,
Karthaus,H.F.M., Schalken,J.A., Debruyne,F.M.J., Ru,N. and
Isaacs,W.B.
TITLE Direct Submission
JOURNAL Submitted (28-OCT-1998) Urology Research Laboratory, University
Hospital Nijmegen, P.O. Box 9101, Nijmegen 6500 HB, Netherlands
FEATURES
source 1. 5435
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="9"
/map="9q21-q22"
1..78
repeat_region
/rpt_family="Alu"
/rpt_type="dispersed
533..697
exon
/note="alternative exon present in 5% of cDNA clones"
/number=2
repeat_region
1035..1294
/rpt_family="Alu"
/rpt_type="dispersed
join(1571..1753,1981..5435)
/product="non-coding RNA D03"
mRNA

/note="transcript III"
join(1571..1753,1981..3579)
/product="non-coding RNA D03"
/note="transcript (major) II"
join(1571..1753,1981..2517)
/product="non-coding RNA D03"
/note="transcript I"
1571..1753
exon
/number=3
1981..5435
exon
/number=4
2495..2499
polyA_signal
/note="transcript I"
2517
polyA_site
/note="transcript I"
3553..3558
polyA_signal
/note="transcript (major) II"
3579
polyA_site
/note="transcript (major) II"
5268..5423
repeat_region
/note="LINE"
/rpt_family="Alu"
/rpt_type="dispersed
5435
polyA_site
/note="transcript III"
BASE COUNT 1546 a 1188 c 1036 g 1654 t 11 others
ORIGIN
Query Match .58.2%; Score 1185; DB 9; Length 5435;
Best Local Similarity 99.5%; Pred. No. 0;
Matches 185; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
QY 445 AGATCCCTGGGAGAAATGCCGGCCATCTGGGTATGATGACCTGCCCTGTGTC 504
Db 1979 AGATCCCTGGGAGAAATGCCGGCCATCTGGGTATGATGACCTGCCCTGTGTC 2038
QY 505 CTGGTCCCGCTTGTAGGAGGAAGACATTAGAAATGAATTTGATGTCTTAAAGGATG 564
Db 2039 CTGGTCCCGCTTGTAGGAGGAAGACATTAGAAATGAATTTGATGTCTTAAAGGATG 2098
QY 565 GGCAGAAAACAGATCTGTTGTGATATTTATTTGAACGGGATTCAGATTGAAATGA 624
Db 2099 GGCAGAAAACAGATCTGTTGTGATATTTATTTGAACGGGATTCAGATTGAAATGA 2158
QY 625 AGTCACAAAGTACGATTACCAATGAGGAAACAGACGAGAAATCTGTATGGCTTCA 684
Db 2159 AGTCACAAAGTACGATTACCAATGAGGAAACAGACGAGAAATCTGTATGGCTTCA 2218
QY 685 CAAGACATGCAACAACAAATGAAATGTAATCTGTGATGATGAGCGAGCAAGCTGGGAG 744
Db 2219 CAAGACATGCAACAACAAATGAAATGTAATCTGTGATGATGAGCGAGCAAGCTGGGAG 2278
QY 745 GAGATTAACACGAGGAGGAGGTCAGGATTTCTGCGCTGCTTAACTGTGCTTCAT 804
Db 2279 GAGATTAACACGAGGAGGAGGTCAGGATTTCTGCGCTGCTTAACTGTGCTTCAT 2338
QY 805 AACCAATCATTTCTATTTTCTAACCTTCAACCAACAAACAACTGTGTAATATCGATCTCTA 864
Db 2339 AACCAATCATTTCTATTTTCTAACCTTCAACCAACAAACAACTGTGTAATATCGATCTCTA 2398
QY 865 CGGTTCTTCTGGGGCCCAACATCTCCATATATTCAGGACACATATTTTAAATATTTAG 924
Db 2399 CGGTTCTTCTGGGGCCCAACATCTCCATATATTCAGGACACATATTTTAAATATTTAG 2458
QY 925 TTCCAGATCTGTACTGTGACCTTTCTACACTGTAGAAATTAACATTACTATTTTGTCAA 984
Db 2459 TTCCAGATCTGTACTGTGACCTTTCTACACTGTAGAAATTAACATTACTATTTTGTCAA 2518
QY 985 AGACCTTCGTGTTCTGCTCCATATATGAGCTGAGATGTTTTCCTAAAGAGTCTCTGGC 1044
Db 2519 AGACCTTCGTGTTCTGCTCCATATATGAGCTGAGATGTTTTCCTAAAGAGTCTCTGGC 2578
QY 1045 CCAGGGATCTGTGAACAGGCTGGAGACATCTCAAGATCTTTCAGAGGTTATACTTACT 1104

|||||
Db 2579 CCAAGGATCTGTAAACAGGCTGGAGACATCTAAGATCTTTCAGGGTATATCTACT 2638
QY 1105 AGCAGACAGCATGATCATTTACGAGAGTGAATATATCAACATCATCCTCAGTCTTT 1164
Db 2639 AGCAGACAGCATGATCATTTACGAGAGTGAATATATCAACATCATCCTCAGTCTTT 2638
QY 1165 GCCCATCTGAATTCATTTCCCACTTTTGTGCCATTTCTCAAGACCTCAAAATGTCAAT 1224
Db 2699 GCCCATCTGAATTCATTTCCCACTTTTGTGCCATTTCTCAAGACCTCAAAATGTCAAT 2758
QY 1225 CCATTAATATCAGAGATTAACCTTTTAACTGAGAGATTAATCAATTTTCAATGCA 1284
Db 2759 CCATTAATATCAGAGATTAACCTTTTAACTGAGAGATTAATCAATTTTCAATGCA 2818
QY 1285 GCTATGGGAATTTAATTAACATATTTTTCAGATCAAGATGACTAAGTCTTATTC 1344
Db 2819 GCTATGGGAATTTAATTAACATATTTTTCAGATCAAGATGACTAAGTCTTATTC 2878
QY 1345 CTTCCCTTTGTTGATTTTTCAGATTAATTAAGTTAAATGCTTACCTTGTAGAG 1404
Db 2879 CTTCCCTTTGTTGATTTTTCAGATTAATTAAGTTAAATGCTTACCTTGTAGAG 2938
QY 1405 GCTATATACAGACAGCTCTCCCATCCCTCCAGCTTATCTGTCATACATCAACCC 1464
Db 2939 GCTATATACAGACAGCTCTCCCATCCCTCCAGCTTATCTGTCATACATCAACCC 2998
QY 1465 CTCCTCATNTSACCTTAACAAATCTAATCTTGAATTCCTGACATGTCAGAGATACAT 1524
Db 2999 CTCCTCATNTSACCTTAACAAATCTAATCTTGAATTCCTGACATGTCAGAGATACAT 3058
QY 1525 TTTTCTCTTCTGCTGAGAAAGCTCTTCTTCTTAAATCTGATTAATGATTAAGTTT 1584
Db 3059 TTTTCTCTTCTGCTGAGAAAGCTCTTCTTCTTAAATCTGATTAATGATTAAGTTT 3118
QY 1585 GAATTAAGTTGATCTTACTTCTATGCAAGAAAGAGGACATATGAGATTCATATACACA 1644
Db 3119 GAATTAAGTTGATCTTACTTCTATGCAAGAAAGAGGACATATGAGATTCATATACACA 3178
QY 1645 TGAGACAGCAAAATCTAATAAGTGAATTTGATTAAGAGTTTGAATTAATATATGAAT 1704
Db 3179 TGAGACAGCAAAATCTAATAAGTGAATTTGATTAAGAGTTTGAATTAATATATGAAT 3238
QY 1705 GCAAGACACACAGAGGAAATGTTATGGGACAGCTTTGTAAAGCTGGAGTGAAGAAA 1764
Db 3239 GCAAGACACACAGAGGAAATGTTATGGGACAGCTTTGTAAAGCTGGAGTGAAGAAA 3298
QY 1765 GCGAGGAACTCTATAGTATCTATATATATATATATATCTATCTATCTATACATA 1824
Db 3299 GCGAGGAACTCTATAGTATCTATATATATATATATATATCTATCTATCTATACATA 3358
QY 1825 TCCAAAGCTTTTACAGAAATTCAGATGCAATGCCCAAGTAACTTATTCAT 1884
Db 3359 TCCAAAGCTTTTACAGAAATTCAGATGCAATGCCCAAGTAACTTATTCAT 3418
QY 1885 TTCTATGATGAGTGGCTTTTGAATTTTGGCAATCATCTGCTATCTCAACTTTG 1944
Db 3419 TTCTATGATGAGTGGCTTTTGAATTTTGGCAATCATCTGCTATCTCAACTTTG 3478
QY 1945 AGATGATGTTGCTCTTGTAGTAAATTAAGAAATAGGCACTTTTGAAGCCCTTAG 2004
Db 3479 AGATGATGTTGCTCTTGTAGTAAATTAAGAAATAGGCACTTTTGAAGCCCTTAG 3538
QY 2005 GGTTCACCTCTGCAATTAAGAAATTTACAAGA 2037
Db 3539 GGTTCACCTCTGCAATTAAGAAATTTACAAGA 3571

RESULT 10
AR261038/c
LOCUS AR261038 2426 bp DNA linear PAT 29-JAN-2003
DEFINITION Sequence 470 from patent US 6321716.
ACCESSION AR261038

VERSION AR261038.1 GI:28071801
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2426)
AUTHORS Mashiki,Z. and Harada,J.
TITLE Negative pressure control apparatus for engine mounted in vehicle
JOURNAL Patent: US 6321716-A 470 27-NOV-2001;
FEATURES location/Qualifiers
SOURCE 1..2426
BASE COUNT 717 a 476 c 548 g 685 t
ORIGIN
Query Match 56.7%; Score 1154; DB 6; Length 2426;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 263 GGTGAGAAATTAAGAAAGCTGCTGACTTTTACCATCTGAGGCCACACATCTGTAATGG 322
Db 1769 GGTGAGAAATTAAGAAAGCTGCTGACTTTTACCATCTGAGGCCACACATCTGTAATGG 1710
QY 323 AGATTAATTAACATCTAGTAAGAAACGCAAGATGACATATATATATATATATATATAT 382
Db 1709 AGATTAATTAACATCTAGTAAGAAACGCAAGATGACATATATATATATATATATATAT 1650
QY 383 TTTTGCACATTTCCAGCCCTTTTAAATATCCACACACAGAGAAAGCAAAAGAGACAC 442
Db 1649 TTTTGCACATTTCCAGCCCTTTTAAATATATCCACACACAGAGAAAGCAAAAGAGACAC 1590
QY 443 AGAGATCCCTGAGGAAATGCGCGCCCATCTTGGGTCATGAGTACGCTCGCCCTGT 502
Db 1589 AGAGATCCCTGAGGAAATGCGCGCCCATCTTGGGTCATGAGTACGCTCGCCCTGT 1530
QY 503 GCCGTGTCGCTGAGGAAAGACATTAAGAAATGATGATGATGATGATGATGATGATGATGAT 562
Db 1529 GCCGTGTCGCTGAGGAAAGACATTAAGAAATGATGATGATGATGATGATGATGATGATGAT 1470
QY 563 TGCGCAGGAAACAGATCTGTTGTGATATTTTGAACGGGATTAACAGATTTGAAT 622
Db 1469 TGCGCAGGAAACAGATCTGTTGTGATATTTTGAACGGGATTAACAGATTTGAAT 1410
QY 623 GAACTCAAAAGTGAGCATTAACCAATGAGAGAAACAGACGAGAAATCTTGATGGCTT 662
Db 1409 GAACTCAAAAGTGAGCATTAACCAATGAGAGAAACAGACGAGAAATCTTGATGGCTT 1350
QY 663 CACAGACATGCAACCAAAATGGAATCTGATGATGATGATGATGATGATGATGATGATGAT 742
Db 1349 CACAGACATGCAACCAAAATGGAATCTGATGATGATGATGATGATGATGATGATGATGAT 1290
QY 743 AGGAGATTAACAGGAGGACAGAGGTGAGATTTGCGCTGCTGCTAAACTGTGCGTT 802
Db 1289 AGGAGATTAACAGGAGGACAGAGGTGAGATTTGCGCTGCTGCTAAACTGTGCGTT 1230
QY 803 ATTAACCAATCATTTTCTATTTTCTAACCTTCAAAACAAAGCTGTTGAATATCTGATCT 862
Db 1229 ATTAACCAATCATTTTCTATTTTCTAACCTTCAAAACAAAGCTGTTGAATATCTGATCT 1170
QY 863 TAGGGTTCCTTGGGGCCCAAAATCTCCATATATCCAGGACACACTATTTTAATATTT 922
Db 1169 TAGGGTTCCTTGGGGCCCAAAATCTCCATATATCCAGGACACACTATTTTAATATTT 1110
QY 923 AGTTCCAGATCTGATCTGACCTTCTACACTGTGAGATTAACATTAATCTATTTGTTTC 982
Db 1109 AGTTCCAGATCTGATCTGACCTTCTACACTGTGAGATTAACATTAATCTATTTGTTTC 1050
QY 983 AAAGACCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1042
Db 1049 AAAGACCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 990
QY 1043 GCCCAGGAGATCTGTAAGAGGCTGGGACCATCTCAAGATCTTCCAGGCTTATCTTA 1102

Db 989 GCCCAGGGGANTCTGTAAGAGCGCTGGGAAGCATCTCAAGATCTTCCAGGGTTACTTAA 930

QY 1103 CTAGACACACAGCATGATATATACGGAGTGAATATCTATATCAACATCATCTCAGTGTCT 1162

Db 929 CTAGACACACAGCATGATATATACGGAGTGAATATCTATATCAACATCATCTCAGTGTCT 870

QY 1163 TTGGCCACACTGAAATTCATTTCCTCCACTTTGTGGCCATTCCTCAAGACCTCAAAATGTCA 1222

Db 869 TTGGCCACACTGAAATTCATTTCCTCCACTTTGTGGCCATTCCTCAAGACCTCAAAATGTCA 810

QY 1223 TTCCATTATATATACAGGATTAATCTTTTCTTAACTGGAAAGATTCATGTTATCATG 1282

Db 809 TTCCATTATATATACAGGATTAATCTTTTCTTAACTGGAAAGATTCATGTTATCATG 750

QY 1283 CAGCATATGGAATTAATTAATACATATTTGTTTCCAGTAAAGTGAAGTGAAGTCTTAA 1342

Db 749 CAGCATATGGAATTAATTAATACATATTTGTTTCCAGTAAAGTGAAGTGAAGTCTTAA 690

QY 1343 TCCCTCCCTTTGTTGATTTTTCAGTATAAAGTTAAATGCTTAAAGCTTGTACTG 1402

Db 689 TCCCTCCCTTTGTTGATTTTTCAGTATAAAGTGAAGTGAAGTCTTGTACTG 630

QY 1403 AGCGTATATACAGC 1416

Db 629 AGCGTATATACAGC 616

RESULT 11
AR278569/c 2426 bp DNA linear PAT 10-APR-2003

LOCUS AR278569 Sequence 470 from patent US 6512094.

DEFINITION AR278569

ACCESSION AR278569

VERSION AR278569.1 GI:29712815

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 2426)

AUTHORS Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y., Kalos,M.D., Fanger,G.R., Retter,M.W., Stolk,J.A., Day,C.H., Vedyck,T.S., Carter,D., Li,S.X., Wang,A., Skelky,I.A.W., Hepler,W.T. and Henderson,R.A.

TITLE Compositions and methods for the therapy and diagnosis of prostate cancer.

JOURNAL Patent: US 6512094-A 470 28-JAN-2003;

FEATURES

source 1..2426

BASE COUNT 717 a 476 c 548 g 685 t

ORIGIN

Query Match 56.7%; Score 1154; DB 6; Length 2426;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1529 GCCTGTCCCGCTTGAGGAGGAAGACATTAGAAATGATGTGTCCTTAAGGA 1470

QY 563 TGGGAGAGAAAAACAGATCCTGTGTGATATTTATTGAAGGGATTACAGATTTGAAT 622

Db 1469 TGGGAGAGAAAAACAGATCCTGTGTGATATTTATTGAAGGGATTACAGATTTGAAT 1410

QY 623 GAAAGTCACAAAGTGAAGATTTACCAATGAGAGAAACAGAGAAATCTTGATGGCT 682

Db 1409 GAAAGTCACAAAGTGAAGATTTACCAATGAGAGAAACAGAGAAATCTTGATGGCT 1350

QY 683 CACAAGACATGCACAAACAAATGAAATCTGTGATGACATGAGCAGCCAGCTGGGG 742

Db 1349 CACAAGACATGCACAAACAAATGAAATCTGTGATGACATGAGCAGCCAGCTGGGG 1290

QY 743 AGGATATACACAGGGGAGAGGGTACAGATTTGCGCTGTAACTGTGCGTTC 802

Db 1289 AGGATATACACAGGGGAGAGGGTACAGATTTGCGCTGTAACTGTGCGTTC 1230

QY 803 ATAAACCAATCATTTATATTTCTAACCCTCAAAACAAAGCTTTGTAATATCTGATCTC 862

Db 1229 ATAAACCAATCATTTATATTTCTAACCCTCAAAACAAAGCTTTGTAATATCTGATCTC 1170

QY 863 TAGGTTCTCTTGCGGCCCAACATTTCTCAATATATCAGCACACTCATTTTAAATTT 922

Db 1169 TAGGTTCTCTTGCGGCCCAACATTTCTCAATATATCAGCACACTCATTTTAAATTT 1110

QY 923 AGTTCCAGATCTGTACTGTGACCTTTTACACTGTAAATATACATTTACTTTTGTTC 982

Db 1109 AGTTCCAGATCTGTACTGTGACCTTTTACACTGTAAATATACATTTACTTTTGTTC 1050

QY 983 AAAGACCTTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 1042

Db 1049 AAAGACCTTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 990

QY 1043 GCCCAGGGGANTCTGTAACAGGCTGGGAAGCATCTCAAGATCTTCCAGGGTTATATCTTA 1102

Db 989 GCCCAGGGGANTCTGTAACAGGCTGGGAAGCATCTCAAGATCTTCCAGGGTTATATCTTA 930

QY 1103 CTAGACACACAGCATGATATATACGGAGTGAATATCTATATCAACATCATCTCAGTGTCT 1162

Db 929 CTAGACACACAGCATGATATATACGGAGTGAATATCTATATCAACATCATCTCAGTGTCT 870

QY 1163 TTGGCCACACTGAAATTCATTTCCTCCACTTTGTGGCCATTCCTCAAGACCTCAAAATGTCA 1222

Db 869 TTGGCCACACTGAAATTCATTTCCTCCACTTTGTGGCCATTCCTCAAGACCTCAAAATGTCA 810

QY 1223 TTCCATTATATATACAGGATTAATCTTTTCTTAACTGGAAAGATTCATGTTATCATG 1282

Db 809 TTCCATTATATATACAGGATTAATCTTTTCTTAACTGGAAAGATTCATGTTATCATG 750

QY 1283 CAGCATATGGAATTAATTAATACATATTTGTTTCCAGTAAAGTGAAGTGAAGTCTTAA 1342

Db 749 CAGCATATGGAATTAATTAATACATATTTGTTTCCAGTAAAGTGAAGTGAAGTCTTAA 690

QY 1343 TCCCTCCCTTTGTTGATTTTTCAGTATAAAGTTAAATGCTTAAAGCTTGTACTG 1402

Db 689 TCCCTCCCTTTGTTGATTTTTCAGTATAAAGTGAAGTGAAGTCTTGTACTG 630

QY 1403 AGCGTATATACAGC 1416

Db 629 AGCGTATATACAGC 616

RESULT 12
AX106206/c 2426 bp DNA linear PAT 30-APR-2001

LOCUS AX106206 Sequence 344 from Patent W0015273.

DEFINITION AX106206

ACCESSION AX106206

VERSION AX106206.1 GI:13921895

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE 1 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
AUTHORS Skeiky, Y.A., Xu, J., Cheever, M.A. and Reed, S.G.
TITLE Compositions and methods for wtl specific immunotherapy
JOURNAL Patent: WO 0125273-A 344 12-APR-2001;
CORIXA CORPORATION (US)
FEATURES Location/Qualifiers
SOURCE 1. 2426
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
BASE COUNT 717 a 476 c 548 g 685 t
ORIGIN
Query Match 56.7%; Score 1154; DB 6; Length 2426;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 263 GGTGAGAAATTAAGAAAGGCTGCTGACCTTTACATCTGAGCCACACATCTGCTGAATGG 322
DB 1769 GGTGAGAAATTAAGAAAGGCTGCTGACCTTTACATCTGAGCCACACATCTGCTGAATGG 1710
QY 323 AGATTAATTAACATCACTAGAAACAGCAAGATGACATATATATGCTAGTAGTACATGT 382
DB 1709 AGATTAATTAACATCACTAGAAACAGCAAGATGACATATATATGCTAGTAGTACATGT 1650
QY 383 TTTTGACATTTCCAGCCCTTTAAATATCCACACACAGAGCAAGCAAAAGAGACAC 442
DB 1649 TTTTGACATTTCCAGCCCTTTAAATATCCACACACAGAGCAAGCAAAAGAGACAC 1590
QY 443 AGAGATCCCTGGGAGAAATGCTCCGCGCCATCTGGGTGATGATGAGCTGCTGCTGT 502
DB 1589 AGAGATCCCTGGGAGAAATGCTCCGCGCCATCTGGGTGATGATGAGCTGCTGCTGT 1530
QY 503 GCCTGCTCCGCTTGAGGAGAAAGACATTAAGAAATGATGCTGCTTAAAGGA 562
DB 1529 GCCTGCTCCGCTTGAGGAGAAAGACATTAAGAAATGATGCTGCTTAAAGGA 1470
QY 563 TGGGCGAGAAACAGATCTGTTGTGATATTTATTTGAACGGGATTACAGATTTGAAT 622
DB 1469 TGGGCGAGAAACAGATCTGTTGTGATATTTATTTGAACGGGATTACAGATTTGAAT 1410
QY 623 GAAGTCACAAGTGAGATTAACCAATGAGAGAAACAGAGAAATCTTGATGCTT 682
DB 1409 GAAGTCACAAGTGAGATTAACCAATGAGAGAAACAGAGAAATCTTGATGCTT 1350
QY 683 CACAAGACATGCAACAAACAAATGATATCTGATGATGATGAGCAGCAAGCTGGG 742
DB 1349 CACAAGACATGCAACAAACAAATGATATCTGATGATGATGAGCAGCAAGCTGGG 1290
QY 743 AGAGATTAACCCAGGGGAGAGGTCAGATTTCTGCCCTGCTTAAACTGTGCTTC 802
DB 1289 AGAGATTAACCCAGGGGAGAGGTCAGATTTCTGCCCTGCTTAAACTGTGCTTC 1230
QY 803 ATTAACCAATCACTTCAATTTTCAACCCCAACAAACAGCTGTTGAATCTGATCTC 862
DB 1229 ATTAACCAATCACTTCAATTTTCAACCCCAACAAACAGCTGTTGAATCTGATCTC 1170
QY 863 TAGGTTCTCTTGGGCGCAACATTTCTCATATATCCAGCCACACTATTTTAAATTT 922
DB 1169 TAGGTTCTCTTGGGCGCAACATTTCTCATATATCCAGCCACACTATTTTAAATTT 1110
QY 923 AGTTCCAGATCTGTACTGTGACCTTTCTACACTGTAGATTAACATTTACTATTTGCTC 982
DB 1109 AGTTCCAGATCTGTACTGTGACCTTTCTACACTGTAGATTAACATTTACTATTTGCTC 1050
QY 983 AAAGACCTTCGTTGCTGCTTAATTAATGAGGATGCTTTTCCAAAGAGGCTCTG 1042
DB 1049 AAAGACCTTCGTTGCTGCTTAATTAATGAGGATGCTTTTCCAAAGAGGCTCTG 990
QY 1043 GCCCAGGGGATCTGTGAAAGAGGCTGGGAACATCTCAAGATCTTTCCAGGGTTATACTTA 1102
DB 989 GCCCAGGGGATCTGTGAAAGAGGCTGGGAACATCTCAAGATCTTTCCAGGGTTATACTTA 930

QY 1103 CTAGCACACACAGATGATTAACGAGAGTAATTAATCAACATCATCTCAGTGTCT 1162
DB 929 CTACACACACAGATGATTAACGAGAGTAATTAATCAACATCATCTCAGTGTCT 870
QY 1163 TTGCCCCATACGAAATTCATTTCCCACTTTTGTGCCATCTCTCAAGACCTCAAAATGTCA 1222
DB 869 TTGCCCCATACGAAATTCATTTCCCACTTTTGTGCCATCTCTCAAGACCTCAAAATGTCA 810
QY 1223 TTCCATTAATTAATCAAGATTAATCTTTTAACTTTTAACTGGAGAAATTAATGTTACATG 1282
DB 809 TTCCATTAATTAATCAAGATTAATCTTTTAACTTTTAACTGGAGAAATTAATGTTACATG 750
QY 1283 CAGCTATGGAATTAATTAATCAATTTTGTGTTCCAGTGCAAGAGATGATGATGCTTTA 1342
DB 749 CAGCTATGGAATTAATTAATCAATTTTGTGTTCCAGTGCAAGAGATGATGATGCTTTA 690
QY 1343 TCCTCCCTCTTGTGATTTTTCACAGATTAAGTTAAATGCTTACGCTTGTACTG 1402
DB 689 TCCTCCCTCTTGTGATTTTTCACAGATTAAGTTAAATGCTTACGCTTGTACTG 630
QY 1403 AGGCTGTATACAGC 1416
DB 629 AGGCTGTATACAGC 616
RESULT 13
AX106689/c 2426 bp DNA linear PAT 30-APR-2001
LOCUS Sequence 470 from Patent WO0125272.
DEFINITION AX106689
ACCESSION AX106689
VERSION AX106689.1 GI:13922354
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1
AUTHORS Xu, J., Skeiky, Y.A., Reed, S.G. and Cheever, M.A.
TITLE Compositions and methods for therapy and diagnosis of prostate cancer
JOURNAL Patent: WO 0125273-A 470 12-APR-2001;
CORIXA CORPORATION (US)
FEATURES Location/Qualifiers
SOURCE 1. 2426
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
BASE COUNT 717 a 476 c 548 g 685 t
ORIGIN
Query Match 56.7%; Score 1154; DB 6; Length 2426;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 263 GGTGAGAAATTAAGAAAGGCTGCTGACCTTTACATCTGAGCCACACATCTGCTGAATGG 322
DB 1769 GGTGAGAAATTAAGAAAGGCTGCTGACCTTTACATCTGAGCCACACATCTGCTGAATGG 1710
QY 323 AGATTAATTAACATCACTAGAAACAGCAAGATGACATATATATGCTAGTAGTACATGT 382
DB 1709 AGATTAATTAACATCACTAGAAACAGCAAGATGACATATATATGCTAGTAGTACATGT 1650
QY 383 TTTTGACATTTCCAGCCCTTTAAATATCCACACACAGAGCAAGCAAAAGAGACAC 442
DB 1649 TTTTGACATTTCCAGCCCTTTAAATATCCACACACAGAGCAAGCAAAAGAGACAC 1590
QY 443 AGAGATCCCTGGGAGAAATGCTCCGCGCCATCTGGGTGATGATGAGCTGCTGCTGT 502
DB 1589 AGAGATCCCTGGGAGAAATGCTCCGCGCCATCTGGGTGATGATGAGCTGCTGCTGT 1530
QY 503 GCCTGCTCCGCTTGAGGAGAAAGACATTAAGAAATGATGCTGCTTAAAGGA 562
DB 1529 GCCTGCTCCGCTTGAGGAGAAAGACATTAAGAAATGATGCTGCTTAAAGGA 1470

Db	1529	GCCTGTCCTCCCTGTTGAGGAGACATTTAGAAAATGATGTGCTTAAAGGA	1470
QY	563	TGGGAGGAAAAAGATCTGTGTGATTTTATTTGAAGGGATTCAGATTGAAT	622
Db	1469	TGGGAGGAAAAAGATCTGTGTGATTTTATTTGAAGGGATTCAGATTGAAT	1410
QY	623	GAAGTCAACAAATGATTTACCAATGAGAGAAAACAGAGAAAATCTTGATGCTT	682
Db	1409	GAAGTCAACAAATGATTTACCAATGAGAGAAAACAGAGAAAATCTTGATGCTT	1350
QY	683	CACAGACATCAACAAACAAATGGAATCTGTGATGACATGAGCAGCCAGCTGGGG	742
Db	1349	CACAGACATCAACAAACAAATGGAATCTGTGATGACATGAGCAGCCAGCTGGGG	1290
QY	743	AGGAGATTAACACAGGGGAGAGGGGATTCGGCCCTGCTGCTAAAGCTGCGTTC	802
Db	1289	AGGAGATTAACACAGGGGAGAGGGGATTCGGCCCTGCTGCTAAAGCTGCGTTC	1230
QY	803	ATAACCAATCATTTTCATATTTCTAACCCCTCAAAAAGCTGTGTAATCTGATCTC	862
Db	1229	ATAACCAATCATTTTCATATTTCTAACCCCTCAAAAAGCTGTGTAATCTGATCTC	1170
QY	863	TACGGTCTCTTGCGGCCCAACATTTCTCATATATCCAGCAGCACTCATTTTAAATTT	922
Db	1169	TACGGTCTCTTGCGGCCCAACATTTCTCATATATCCAGCAGCACTCATTTTAAATTT	1110
QY	923	AGTTCCAGATCTGACTGTGACCTTCTACAGCTTAATAACATTTCTCATTTTGTTC	982
Db	1109	AGTTCCAGATCTGACTGTGACCTTCTACAGCTTAATAACATTTCTCATTTTGTTC	1050
QY	983	AAAGACCTTCTGTGCTGCTTAATATGAGCTGACTGTTTCTTCAAGAGAGTGTCTG	1042
Db	1049	AAAGACCTTCTGTGCTGCTTAATATGAGCTGACTGTTTCTTCAAGAGAGTGTCTG	990
QY	1043	GCCAGAGGAGCTGTGAACAGGCTGGGAGAGATCTCAAGATCTTCCAGGGTTATATCTTA	1102
Db	989	GCCAGAGGAGCTGTGAACAGGCTGGGAGAGATCTCAAGATCTTCCAGGGTTATATCTTA	930
QY	1103	CTAGACACAGCATGATATTAAGAGATTAATCTATCAACATTCATCCATGCTCT	1162
Db	929	CTAGACACAGCATGATATTAAGAGATTAATCTATCAACATTCATCCATGCTCT	870
QY	1163	TTGGCCATATCTGAATTTCCACTTTTGCCGCAATCTCAAGACCTCAAAATGTCA	1222
Db	869	TTGGCCATATCTGAATTTCCACTTTTGCCGCAATCTCAAGACCTCAAAATGTCA	810
QY	1223	TTTCATTAATATCAAGAGATTAATTTTAACTGGAAGAATTCATGTTATCATG	1282
Db	809	TTTCATTAATATCAAGAGATTAATTTTAACTGGAAGAATTCATGTTATCATG	750
QY	1283	CAGCATATGGAATTAATTAATATTTTGTTCAGTGCAGCAAGATGACTAGTCTTTA	1342
Db	749	CAGCATATGGAATTAATTAATATTTTGTTCAGTGCAGCAAGATGACTAGTCTTTA	690
QY	1343	TCCCTCCCTTTGTTGATTTTTTTTCCAGTATAAAGTTAAATCTTACGCTTATGCT	1402
Db	689	TCCCTCCCTTTGTTGATTTTTTTTCCAGTATAAAGTTAAATCTTACGCTTATGCT	630
QY	1403	AGGCTGATATACAGC 1416	
Db	629	AGGCTGATATACAGC 616	

RESULT 14

AX140980/c 2426 bp DNA linear PAT 31-MAY-2001
LOCUS AX140980
DEFINITION Sequence 470 from Patent WO0134802.
ACCESSION AX140980
VERSION AX140980.1 GI:14281077
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE	1	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
AUTHORS	Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y., Reed,S.G., Kalos,M.D., Retter,M.W., Stolk,J.A., Day,C.H., Skelky,Y.A. and Wang,A.	
TITLE	Compositions and methods for the therapy and diagnosis of prostate cancer	
JOURNAL	Patent: WO 0134802-A 470 17-MAY-2001;	
FEATURES	CORIXA CORPORATION (US)	
source	location/Qualifiers	
	1..2426	
	/organism="Homo sapiens"	
	/mol_type="genomic DNA"	
	/db_xref="taxon:9606"	
BASE COUNT	717 a 476 c 548 g 685 t	
ORIGIN		
Query Match	56.7%; Score 1154; DB 6; Length 2426;	
Best Local Similarity	100.0%; Pred. No. 0;	
Matches 1154; Conservative	0; Mismatches 0; Indels 0; Gaps 0;	
QY	263	GGTGAAGAAATGAAGAGCTGCTGACTTTACCATCTGAGGCCACACATCTGCTGAATGG 322
Db	1769	GGTGAAGAAATGAAGAGCTGCTGACTTTACCATCTGAGGCCACACATCTGCTGAATGG 1710
QY	323	AGATTAATTAACATCTAGTGAAGAACAGCAAGATGACATTAATGCTAAGTAGTACATGT 382
Db	1709	AGATTAATTAACATCTAGTGAAGAACAGCAAGATGACATTAATGCTAAGTAGTACATGT 1650
QY	383	TTTTCACATTTCCAGCCCTTTAAATATCCACACACAGAGAACACAAAAAGAGAGAC 442
Db	1649	TTTTCACATTTCCAGCCCTTTAAATATCCACACACAGAGAACACAAAAAGAGAGAC 1590
QY	443	AGAGATCCCTGGGAGAAATCCCGCCGCAATCTTGGGTATGATGAGCCCTGCCCTGT 502
Db	1589	AGAGATCCCTGGGAGAAATCCCGCCGCAATCTTGGGTATGATGAGCCCTGCCCTGT 1530
QY	503	GCTGTCCTCCGCTTGTAGGAGAGACATTAAGAAATGATGATGCTTCTTAAAGA 562
Db	1529	GCTGTCCTCCGCTTGTAGGAGAGACATTAAGAAATGATGATGCTTCTTAAAGA 1470
QY	563	TGGGAGGAAAAAGATCTGTGTGATTTTATTTGAACGGATTCAGATTTGAAT 622
Db	1469	TGGGAGGAAAAAGATCTGTGTGATTTTATTTGAACGGATTCAGATTTGAAT 1410
QY	623	GAAGTCAACAAAGTACATTTACCAATGAGAGAAAACAGAGAAAATCTTGATGCTT 682
Db	1409	GAAGTCAACAAAGTACATTTACCAATGAGAGAAAACAGAGAAAATCTTGATGCTT 1350
QY	683	CACAGACATCAACAAACAAATGGAATTAATCTGATGACATGAGAGGCCAAGCTGGGG 742
Db	1349	CACAGACATCAACAAACAAATGGAATTAATCTGATGACATGAGAGGCCAAGCTGGGG 1290
QY	743	AGGAGATTAACACAGGGGAGAGGGTCAAGATTTGCGCTGCTTAACTGTCGTTTC 802
Db	1289	AGGAGATTAACACAGGGGAGAGGGTCAAGATTTGCGCTGCTTAACTGTCGTTTC 1230
QY	803	ATAACCAATCATTTTCATATTTCTAACCCCTCAAAAAGCTGTGTAATCTGATCTC 862
Db	1229	ATAACCAATCATTTTCATATTTCTAACCCCTCAAAAAGCTGTGTAATCTGATCTC 1170
QY	863	TACGGTCTCTTGCGGCCCAACATTTCTCATATATCCAGCAGCACTCATTTTAAATTT 922
Db	1169	TACGGTCTCTTGCGGCCCAACATTTCTCATATATCCAGCAGCACTCATTTTAAATTT 1110
QY	923	AGTTCCAGATCTGACTGTGACCTTTCTACACTGATGAATTAACATTAATCTGATCTC 982
Db	1109	AGTTCCAGATCTGACTGTGACCTTTCTACACTGATGAATTAACATTAATCTGATCTC 1050
QY	983	AAAGACCTTCTGTGCTGCTTAAATATGATGAGTACTGTTTCTTAAAGAGTGTCTG 1042
Db	1049	AAAGACCTTCTGTGCTGCTTAAATATGATGAGTACTGTTTCTTAAAGAGTGTCTG 990

QY 1043 GCCCAGGGGATCTGTGAACAGGCTGGAGACATCTCAAGATCTTTCCAGGGTTTACTTA 1102
| | | | |
Db 989 GCCCAGGGGATCTGTGAACAGGCTGGAGACATCTCAAGATCTTTCCAGGGTTTACTTA 930
| | | | |
QY 1103 CTAGCACAACAGCATGATCATTACGAGTGAATTTCTTAATCAACATATCTCTAGTCTT 1162
| | | | |
Db 929 CTAGCACAACAGCATGATCATTACGAGTGAATTTCTTAATCAACATATCTCTAGTCTT 870
| | | | |
QY 1163 TTGGCCATCTGAATTCATTTCCACTTTTGTGCCATTTCTCAAGACCTCAAAATGTCA 1222
| | | | |
Db 869 TTGGCCATCTGAATTCATTTCCACTTTTGTGCCATTTCTCAAGACCTCAAAATGTCA 810
| | | | |
QY 1223 TTGCATTAATATCAGAGATTAATCTTTTTCACCTGGAGAAATTCATTTTACATG 1282
| | | | |
Db 809 TTGCATTAATATCAGAGATTAATCTTTTTCACCTGGAGAAATTCATTTTACATG 750
| | | | |
QY 1283 CAGCTATGGAATTAATTAATTAATTTTGTTCCTCACTGCAAGATGACATGACCTTTA 1342
| | | | |
Db 749 CAGCTATGGAATTAATTAATTAATTTTGTTCCTCACTGCAAGATGACATGACCTTTA 690
| | | | |
QY 1343 TCCCTCCCTTTGTTGATTTTTCACGATTAATAAGTTAAATGCTTACCTTGTACTG 1402
| | | | |
Db 689 TCCCTCCCTTTGTTGATTTTTCACGATTAATAAGTTAAATGCTTACCTTGTACTG 630
| | | | |
QY 1403 AGGCTGTATACAGC 1416
| | | | |
Db 629 AGGCTGTATACAGC 616
| | | | |
RESULT 15
AX200840/c 2426 bp DNA linear PAT 29-AUG-2001
LOCUS AX200840
DEFINITION Sequence 470 from Patent WO0151633.
ACCESSION AX200840
VERSION AX200840.1 GI:15390743
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y.,
Reed,S.G., Kalos,M.D., Fanger,G.R., Day,C.H., Retter,M.W.,
Stolk,J.A., Skelky,Y.A., Wang,A. and Weighner,M.J.
TITLE Compositions and methods for the therapy and diagnosis of prostate
cancer
JOURNAL Patent: WO 0151633-A 470 19-JUL-2001;
CORIXA CORPORATION (US)
FEATURES
source
location/Qualifiers
1..2426
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
BASE COUNT 717 a 476 c 548 g 685 t
ORIGIN
Query Match 56.7%; Score 1154; DB 6; Length 2426;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 263 GGTGAGAAATTAAGAAAGGCTGCTGACCTTACCATCTGAGGCACACATCTGCTGAATGG 322
| | | | |
Db 1769 GGTGAGAAATTAAGAAAGGCTGCTGACCTTACCATCTGAGGCACACATCTGCTGAATGG 1710
| | | | |
QY 323 AGATTAATTAACATCACTAGAAACAGCAAGATGACAAATATATGTCTAAGTAGACATGT 382
| | | | |
Db 1709 AGATTAATTAACATCACTAGAAACAGCAAGATGACAAATATATGTCTAAGTAGACATGT 1650
| | | | |
QY 383 TTTTGCACATTTCCAGCCCTTTAAATATCAACACACAGGAAGCAAAAGGAAGCAC 442
| | | | |
Db 1649 TTTTGCACATTTCCAGCCCTTTAAATATCAACACACAGGAAGCAAAAGGAAGCAC 1590
| | | | |
QY 443 AGAGATCCTGGAGAAATGCCGCCCATCTTGGGTATCATGATGAGCCTGCGCTGT 502
| | | | |

Db 1589 AGAGATCCTGGAGAAATGCCGCCCATCTTGGGTATCATGATGAGCCTGCGCTGT 1530
| | | | |
QY 503 GCTGTGTCCTGCTGTGAGGAAGACATTAAGAAATGAATGTATGTTCTTAAAGCA 562
| | | | |
Db 1529 GCTGTGTCCTGCTGTGAGGAAGACATTAAGAAATGAATGTATGTTCTTAAAGCA 1470
| | | | |
QY 563 TGGCAGAGAAACAGATCTGTTGTGATATTTTATTTGAACGGGATTACAGATTTGAAT 622
| | | | |
Db 1469 TGGCAGAGAAACAGATCTGTTGTGATATTTTATTTGAACGGGATTACAGATTTGAAT 1410
| | | | |
QY 623 GAATTCACAAAGTGAGCATTTACCAATGAGAGAAACAGACAGAGAAATCTTGATGCTT 682
| | | | |
Db 1409 GAATTCACAAAGTGAGCATTTACCAATGAGAGAAACAGACAGAGAAATCTTGATGCTT 1350
| | | | |
QY 683 CACAGACATGCAACAAACAAATGGAATCTGTGATGATGAGGAGGCAAGCTGGG 742
| | | | |
Db 1349 CACAGACATGCAACAAACAAATGGAATCTGTGATGATGAGGAGGCAAGCTGGG 1290
| | | | |
QY 743 AGAGATTAACCAAGGCGCAGAGGCTCAGATTTCTGCGCTGCTGCTAACTGTGCTTC 802
| | | | |
Db 1289 AGAGATTAACCAAGGCGCAGAGGCTCAGATTTCTGCGCTGCTGCTAACTGTGCTTC 1230
| | | | |
QY 803 ATTAACCAATTCATTTTCAATTTTCAACCTTCAAAACAAAGCTGTGTAATATCTGATCTC 862
| | | | |
Db 1229 ATTAACCAATTCATTTTCAATTTTCAACCTTCAAAACAAAGCTGTGTAATATCTGATCTC 1170
| | | | |
QY 863 TACGTTCTCTTTCGCGCCCAACATTTCTCAATATATATATATATATATATATATATAT 922
| | | | |
Db 1169 TACGTTCTCTTTCGCGCCCAACATTTCTCAATATATATATATATATATATATATATAT 1110
| | | | |
QY 923 AGTTCCAGATCTGTACTGTGACCTTCTCACTAGTGAATTAACATTAATCTGATTTGCTC 982
| | | | |
Db 1109 AGTTCCAGATCTGTACTGTGACCTTCTCACTAGTGAATTAACATTAATCTGATTTGCTC 1050
| | | | |
QY 983 AAGAGCCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1042
| | | | |
Db 1049 AAGAGCCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 990
| | | | |
QY 1043 GCCCAGGGGATCTGTGAACAGGCTGGAGACATCTCAAGATCTTTCCAGGGTTTACTTA 1102
| | | | |
Db 989 GCCCAGGGGATCTGTGAACAGGCTGGAGACATCTCAAGATCTTTCCAGGGTTTACTTA 930
| | | | |
QY 1103 CTAGCACAACAGCATGATCATTACGAGTGAATTTCTTAATCAACATATCTCTAGTCTT 1162
| | | | |
Db 929 CTAGCACAACAGCATGATCATTACGAGTGAATTTCTTAATCAACATATCTCTAGTCTT 870
| | | | |
QY 1163 TTGGCCATCTGAATTCATTTCCACTTTTGTGCCATTTCTCAAGACCTCAAAATGTCA 1222
| | | | |
Db 869 TTGGCCATCTGAATTCATTTCCACTTTTGTGCCATTTCTCAAGACCTCAAAATGTCA 810
| | | | |
QY 1223 TTGCATTAATATCAGAGATTAATCTTTTTCACCTGGAGAAATTCATTTTACATG 1282
| | | | |
Db 809 TTGCATTAATATCAGAGATTAATCTTTTTCACCTGGAGAAATTCATTTTACATG 750
| | | | |
QY 1283 CAGCTATGGAATTAATTAATTAATTTTGTTCCTCACTGCAAGATGACATGACCTTTA 1342
| | | | |
Db 749 CAGCTATGGAATTAATTAATTAATTTTGTTCCTCACTGCAAGATGACATGACCTTTA 690
| | | | |
QY 1343 TCCCTCCCTTTGTTGATTTTTCACGATTAATAAGTTAAATGCTTACCTTGTACTG 1402
| | | | |
Db 689 TCCCTCCCTTTGTTGATTTTTCACGATTAATAAGTTAAATGCTTACCTTGTACTG 630
| | | | |
QY 1403 AGGCTGTATACAGC 1416
| | | | |
Db 629 AGGCTGTATACAGC 616
| | | | |

Search completed: September 27, 2003, 06:44:55
Job time : 7417.95 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 26, 2003, 20:07:52 ; Search time 533.821 Seconds
(without alignments)
10300.748 Million cell updates/sec

Title: US-09-402-713A-1

Perfect score: 2037
Sequence: 1 agaagctgcgcacagaaaaa.....caataagaattacaaga 2037

Scoring table:

OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 2552756 seqs, 1349719017 residues

Word size : 0

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : N.Geneseq_19Jun03.*

1: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1980.DAT:*
2: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT:*
3: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1982.DAT:*
4: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1983.DAT:*
5: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1984.DAT:*
6: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1985.DAT:*
7: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1987.DAT:*
8: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1987.DAT:*
9: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1988.DAT:*
10: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1989.DAT:*
11: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1990.DAT:*
12: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1991.DAT:*
13: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1992.DAT:*
14: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1993.DAT:*
15: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1994.DAT:*
16: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1995.DAT:*
17: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1996.DAT:*
18: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1997.DAT:*
19: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1998.DAT:*
20: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1999.DAT:*
21: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2000.DAT:*
22: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT:*
23: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT:*
24: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT:*
25: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2003.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2037	100.0	2037	19	AAV62427
2	1775	87.1	1872	19	AAV62428
3	1629	80.0	3923	22	AAV64026
4	1629	80.0	3923	22	AAH93861
5	1629	80.0	3923	24	ABK92196
6	1629	80.0	3923	24	ABL95397
7	1629	80.0	3923	25	ACA59834
8	1578	77.5	3582	19	AAV62430

C	9	1154	56.7	2426	21	AAAO6689	Human immunogenic
C	10	1154	56.7	2426	22	AAV63898	Human prostate CDN
C	11	1154	56.7	2426	22	AAH93805	Human prostate-spe
C	12	1154	56.7	2426	22	AAH85119	Human prostate-spe
C	13	1154	56.7	2426	22	AAH02870	Prostate tumour an
C	14	1154	56.7	2426	22	AAV686948	Human P710P Invent
C	15	1154	56.7	2426	24	ABL95269	Human P710P CDNA s
C	16	1154	56.7	2426	25	ACA59706	Prostate cancer th
C	17	1154	56.7	3112	21	AAAO6687	Human immunogenic
C	18	1154	56.7	3112	22	AAV63896	Human prostate CDN
C	19	1154	56.7	3112	22	AAH93803	Human prostate-spe
C	20	1154	56.7	3112	22	AAH85117	Human prostate-spe
C	21	1154	56.7	3112	22	AAH02868	Prostate tumour an
C	22	1154	56.7	3112	22	AAV686946	Human P710P Invent
C	23	1154	56.7	3112	22	ABL95267	Human P710P CDNA s
C	24	1154	56.7	3112	25	ACA58704	Prostate cancer th
C	25	1033	50.7	2229	21	AAAO6688	Human immunogenic
C	26	1033	50.7	2229	22	AAV63897	Human prostate CDN
C	27	1033	50.7	2229	22	AAH93804	Human prostate-spe
C	28	1033	50.7	2229	22	AAH85118	Human prostate-spe
C	29	1033	50.7	2229	22	AAH02869	Prostate tumour an
C	30	1033	50.7	2229	22	AAV686947	Human P710P Invent
C	31	1033	50.7	2229	24	ABL95268	Human P710P CDNA s
C	32	1033	50.7	2229	25	ACA59705	Prostate cancer th
C	33	738	36.2	876	24	AAV63815	Human PSNA CDNA, P
C	34	723	35.5	820	19	AAV62429	Prostate cancer an
C	35	720	35.3	812	21	AAAO6690	Human immunogenic
C	36	720	35.3	812	22	AAV63899	Human prostate CDN
C	37	720	35.3	812	22	AAH93806	Human prostate-spe
C	38	720	35.3	812	22	AAH85120	Human prostate-spe
C	39	720	35.3	812	22	AAH02871	Prostate tumour an
C	40	720	35.3	812	22	AAV686949	Human P710P Invent
C	41	720	35.3	812	24	ABL95270	Human P710P CDNA s
C	42	720	35.3	812	25	ACA59707	Prostate cancer th
C	43	475	23.3	671	23	ABV42450	Human prostate exp
C	44	475	23.3	671	23	ABV41330	Human prostate exp
C	45	473	23.2	597	20	AAV37486	Human secreted pro

ALIGNMENTS

RESULT 1	AAV62427	standard: CDNA; 2037 BP.
ID	AAV62427	
AC	AAV62427;	
XX		
XX	30-DEC-1998	(first entry)
DT		
XX		
XX	Prostate cancer antigen (PCA3) cDNA splice variant 1.	
XX		
KW	Prostate cancer antigen cDNA splice variant 1; PCA3; prostatic cancer;	
KW	PC; ds.	
XX		
OS	Homo sapiens.	
XX		
FH	Key	Location/Qualifiers
FT	CDS	379..534
FT		/*tag= a
FT		/product= "PCA3 protein variant 1"
FT	polyA_signal	2019..2024
FT		/*tag= b
XX		
PN	W09845420-A1.	
XX		
PD	15-OCT-1998.	
XX		
PF	09-APR-1998;	98WO-CA00346.
XX		
PR	10-APR-1997;	97US-0041836.
XX		
PA	(DIAG-) DIAGNOCURE INC.	

XX Bussemakers MJG;
PI
XX
DR WPI: 1998-568347/48.
P-PSDB; AAM79736.
XX
PT New nucleic acid encoding prostate cancer antigen 3 - for diagnosis,
PT prevention and treatment of prostatic cancer
XX
PS Claim 3; Fig 2b-2j; 111pp; English.
XX
CC The present sequence represents the prostate cancer antigen (PCA3)
CC cDNA splice variant 1 sequence comprising of exons 1, 2, 3, 4a and
CC 4b of the PCA3 gene. The PCA3 cDNA splice variant 1 sequence,
CC isolated from a human primary prostatic tumour tissue cDNA library,
CC was found in approximately 5% of the cDNA clones isolated. The
CC invention claims for PCA3 cDNA variants and the proteins they encode.
CC The invention also claims for antibodies against PCA3 protein. The
CC antibodies are claimed to be useful for detecting PCA3 protein in
CC immunoassay tests, for diagnosing, assessing and prognosing of
CC prostatic cancer (PC). Antibodies, optionally coupled to a cytotoxin
CC or radioisotope, and nucleic acids antisense to PCA3 cDNA are claimed
CC to be useful for treating PC, while determining elevated levels of
CC PCA3 (as RNA or protein) is useful for detecting a predisposition
CC to development of PC, e.g. in prenatal tests. Detecting PCA3 protein
CC allows differentiation between malignant and benign prostatic disease,
CC and the level of PCA3 expression allows correlation with the grade of
CC tumour. PCA3 protein and its fragments are also claimed to be useful
CC in vaccines for preventing PC; in drug screens for identifying
CC specific (ant)agonists (potentially useful therapeutically) and for
CC studying protein-DNA interactions.
XX
SQ Sequence 2037 BP; 622 A; 426 C; 406 G; 575 T; 8 other;

Query Match 100.0%; Score 2037; DB 19; Length 2037;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2037; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGAAGCTGGCATCAGAAAAACAGAGGGAGATTGTGTGCTCAGCCGAGGAGACAC 60
DB 1 AGAAGCTGGCATCAGAAAAACAGAGGGAGATTGTGTGCTCAGCCGAGGAGACAC 60
QY 61 GAAGATCTGCATGGTGGGAAGGACCTGATACAGAGGAATTACAAACATATCTAG 120
DB 61 GAAGATCTGCATGGTGGGAAGGACCTGATACAGAGGAATTACAAACATATCTAG 120
QY 121 TGTTCATGTAACACCAAGTAATTAAGTAAGACAGCTAGTCCCTGTGAGTCTCCAGT 180
DB 121 TGTTCATGTAACACCAAGTAATTAAGTAAGACAGCTAGTCCCTGTGAGTCTCCAGT 180
QY 181 GACACAGGGCTGGATCACCATCGAGGCACTTCTGATCTCAGTGCAGCAAGAAAGA 240
DB 181 GACACAGGGCTGGATCACCATCGAGGCACTTCTGATCTCAGTGCAGCAAGAAAGA 240
QY 241 CTACACACATCTCAATGAGGAGGAGGAGAAATGAAGAGGCTGCTGACTTACCATTG 300
DB 241 CTACACACATCTCAATGAGGAGGAGGAGAAATGAAGAGGCTGCTGACTTACCATTG 300
QY 301 GGGCACAACATCTCTGAAATGAGATTAATTAACATCACTGAAACAGCAAGATGACATA 360
DB 301 GGGCACAACATCTCTGAAATGAGATTAATTAACATCACTGAAACAGCAAGATGACATA 360
QY 361 TAATGCTAAGTAGTACATGTTTTCACATTTCCAGCCCTTTAAATATCCACACACA 420
DB 361 TAATGCTAAGTAGTACATGTTTTCACATTTCCAGCCCTTTAAATATCCACACACA 420
QY 421 CAGGAAGCACAAGAGACAGACAGATCCTTGGAATATGCCCGCCCATCTTGGG 480
DB 421 CAGGAAGCACAAGAGACAGACAGATCCTTGGAATATGCCCGCCCATCTTGGG 480
QY 481 TCATCATGAGGCTCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 540
DB 481 TCATCATGAGGCTCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 540

QY 541 AATTGATGTGCTTCTTAAAGATGGCAGAGAAAACAGATCCTGTGTGATATATTTG 600
DB 541 AATTGATGTGCTTCTTAAAGATGGCAGAGAAAACAGATCCTGTGTGATATATTTG 600
QY 601 AACGGATTACAGATTTGAAATGATGACAAAGTGACATTTCAATGAGAGAAACA 660
DB 601 AACGGATTACAGATTTGAAATGATGACAAAGTGACATTTCAATGAGAGAAACA 660
QY 661 GACGAGAAATCTTGATGGCTTCAACAAGATGACCAACAAAGGAATGATGATG 720
DB 661 GACGAGAAATCTTGATGGCTTCAACAAGATGACCAACAAAGGAATGATGATG 720
QY 721 ACATGAGGACGCAAGCTGGGAGAGATTAACACAGGGGAGAGGTCAGATTCGGCC 780
DB 721 ACATGAGGACGCAAGCTGGGAGAGATTAACACAGGGGAGAGGTCAGATTCGGCC 780
QY 781 CTGCTGCTTAACTGCTGCTTCAATACCAATATTTCAATTTCAATACCTCAAAACA 840
DB 781 CTGCTGCTTAACTGCTGCTTCAATACCAATATTTCAATTTCAATACCTCAAAACA 840
QY 841 AGCTGTTGTAATATGATCTACAGGTTCTCTGAGCCCAACATTTCTCATATATCCA 900
DB 841 AGCTGTTGTAATATGATCTACAGGTTCTCTGAGCCCAACATTTCTCATATATCCA 900
QY 901 GCCACACTATTTTAAATATTTAGTCCAGATCTGATCTGACCTTCTACACTGTAG 960
DB 901 GCCACACTATTTTAAATATTTAGTCCAGATCTGATCTGACCTTCTACACTGTAG 960
QY 961 AATTAACATTTCTATTTTGTCAAAAGACCTTGTGTGTGCTGCTTAATGATGCTACT 1020
DB 961 AATTAACATTTCTATTTTGTCAAAAGACCTTGTGTGTGCTGCTTAATGATGCTACT 1020
QY 1021 GTTTTCCCTAAGAGAGTCTTGGCCAGAGGATCTGTGAACAGCTGGAGAGATCTCAA 1080
DB 1021 GTTTTCCCTAAGAGAGTCTTGGCCAGAGGATCTGTGAACAGCTGGAGAGATCTCAA 1080
QY 1081 GATCTTCCAGGGTTATATCTTACTAGACACAGCATGATCATTAAGGATGAATATCTA 1140
DB 1081 GATCTTCCAGGGTTATATCTTACTAGACACAGCATGATCATTAAGGATGAATATCTA 1140
QY 1141 ATCAACATCTCTCCAGTGTCTTGGCCATACAGAAATTCATTTCCACTTTGTCCCA 1200
DB 1141 ATCAACATCTCTCCAGTGTCTTGGCCATACAGAAATTCATTTCCACTTTGTCCCA 1200
QY 1201 TTCTCAAGACCTCAAAATGTCATTCATTAATATCAAGAGATTAACCTTTTAAAC 1260
DB 1201 TTCTCAAGACCTCAAAATGTCATTCATTAATATCAAGAGATTAACCTTTTAAAC 1260
QY 1261 TGGAGAAATCAATGTTACATGACGATGAGGAAATTAATACATATTTGTTCCAGT 1320
DB 1261 TGGAGAAATCAATGTTACATGACGATGAGGAAATTAATACATATTTGTTCCAGT 1320
QY 1321 GCAAAAGTACATGATGCTTATCCCTCCCTTGTGATTTTTCAGATATTAAGT 1380
DB 1321 GCAAAAGTACATGATGCTTATCCCTCCCTTGTGATTTTTCAGATATTAAGT 1380
QY 1381 TAAATGCTTAGGCTGTACTGAGGCTGTATACAGACACACCTCCCACTCCCTCAG 1440
DB 1381 TAAATGCTTAGGCTGTACTGAGGCTGTATACAGACACACCTCCCACTCCCTCAG 1440
QY 1441 CTTATCTGTCATCAGCATCAACCCCTCCATNYSACCTAAACAAATCTAATCTGTAAT 1500
DB 1441 CTTATCTGTCATCAGCATCAACCCCTCCATNYSACCTAAACAAATCTAATCTGTAAT 1500
QY 1501 CCTTGAACATGTAGAGCATATATTTCTCTGCTGAGAGCTCTTCTGCTCTT 1560
DB 1501 CCTTGAACATGTAGAGCATATATTTCTCTGCTGAGAGCTCTTCTGCTCTT 1560
QY 1561 AANTTAGAATGATGTAAGTTTGAATAGTGAATAGTGAATAGTGAATAGTGAATAG 1620
DB 1561 AANTTAGAATGATGTAAGTTTGAATAGTGAATAGTGAATAGTGAATAGTGAATAG 1620

|||||
Db 263 CTAGAGACATCTCAATGCGAGGGGTGAGAAATAGAAAGGCTGCTGATCTTACCATCTGA 322
Qy 301 GGGCCACACATCTGCTGAAATGAGATATTAACATCACTAGAAACAGCAATGACATA 360
Db 323 GGGCCACACATCTGCTGAAATGAGATATTAACATCACTAGAAACAGCAATGACATA 382
Qy 361 TAATGTCTAAGTAGTGCATGTTTTCGACATTTTCAGCCCTTAAATATCCACACA 420
Db 383 TAAATGTCTAAGTAGTGCATGTTTTCGACATTTTCAGCCCTTAAATATCCACACA 442
Qy 421 CAGAGACACAAAAGGAAGACACAGATCCCTGGAGAAATGCCGGCTGATCTTGGG 480
Db 443 CAGAGACACAAAAGGAAGACACAGATCCCTGGAGAAATGCCGGCTGATCTTGGG 502
Qy 481 TCATGATGAGCCCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 540
Db 503 TCATGATGAGCCCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 562
Qy 541 AATGATGCTGTTCTTAAAGATGGCGAGAAACAGATCCCTGCTGCTGCTGCTGCTGCTG 600
Db 563 AATGATGCTGTTCTTAAAGATGGCGAGAAACAGATCCCTGCTGCTGCTGCTGCTGCTG 622
Qy 601 AACGGATTACAGATTTGAAATGAGTCACAAAGTGAGCATTTACCAATGAGAGAAAACA 660
Db 623 AACGGATTACAGATTTGAAATGAGTCACAAAGTGAGCATTTACCAATGAGAGAAAACA 682
Qy 661 GAGAGAAAATCTGATGGCTTCACAGACATGCAACAAACAAATGGAATACGTGATG 720
Db 683 GAGAGAAAATCTGATGGCTTCACAGACATGCAACAAACAAATGGAATACGTGATG 742
Qy 721 ACATGAGGACGCCAAGCTGGGGAGAGATTAACACAGGGGCGAGAGATTCAGATTCGCC 780
Db 743 ACATGAGGACGCCAAGCTGGGGAGAGATTAACACAGGGGCGAGAGATTCAGATTCGCC 802
Qy 781 CTGCTGCTTAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 840
Db 803 CTGCTGCTTAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 862
Qy 841 AGCTGTGTAATATCTGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 900
Db 863 AGCTGTGTAATATCTGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 922
Qy 901 GCCACACTATTTTAAATATTTAGTCCAGATCTGTACTGTGACTCTTACACTGTAG 960
Db 923 GCCACACTATTTTAAATATTTAGTCCAGATCTGTACTGTGACTCTTACACTGTAG 982
Qy 961 AATTAACATTTACTATTTTGTCAAAAGACCTTCTGCTGCTGCTGCTGCTGCTGCTGCTG 1020
Db 983 AATTAACATTTACTATTTTGTCAAAAGACCTTCTGCTGCTGCTGCTGCTGCTGCTGCTG 1042
Qy 1021 GTTTTTCCTAAGGAGTGTGCGCCAGGGGATCTGTCAAAAGGCTGGGAAGCATCTCAA 1080
Db 1043 GTTTTTCCTAAGGAGTGTGCGCCAGGGGATCTGTCAAAAGGCTGGGAAGCATCTCAA 1102
Qy 1081 GATCTTTCAGAGGTTTAACTACTAGACACAGCATGATCTTACAGAGTGAATATATCTA 1140
Db 1103 GATCTTTCAGAGGTTTAACTACTAGACACAGCATGATCTTACAGAGTGAATATATCTA 1162
Qy 1141 ATCAACATCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1200
Db 1163 ATCAACATCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1222
Qy 1201 TTTCAGAGACCTCAAAATGTCATTCATTAATATCAAGAGTTAACTTTTAAATACC 1260
Db 1223 TTTCAGAGACCTCAAAATGTCATTCATTAATATCAAGAGTTAACTTTTAAATACC 1282
Qy 1261 TGAAGAATTCATTAATGATGACAGTATGGGAATTTAAATACATTTTGTTCAGCT 1320
Db 1283 TGAAGAATTCATTAATGATGACAGTATGGGAATTTAAATACATTTTGTTCAGCT 1342
Qy 1321 GCAAAAGATGACTAAGTCCCTTATCCCTCCCTTGTGATTTTTCACAGTAAAGT 1380
|||||

Db 1343 GCAAAAGATGACTAAGTCCCTTATCCCTCCCTTGTGATTTTTCAGATATAAGT 1402
Qy 1381 TAAATGCTTACGCTTGTACAGAGCTGTATACAGCAGCTCCCATCCCTCCAGC 1440
Db 1403 TAAATGCTTACGCTTGTACAGAGCTGTATACAGCAGCTCCCATCCCTCCAGC 1462
Qy 1441 CTATCTGCTCATCAACATCAACCCCTCCCATNYSNACCTAAACAAATCTACTGTAAT 1500
Db 1463 CTATCTGCTCATCAACATCAACCCCTCCCATNYSNACCTAAACAAATCTACTGTAAT 1522
Qy 1501 CCTTGACATGCTCAGAGCATCATCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1560
Db 1523 CCTTGACATGCTCAGAGCATCATCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1582
Qy 1561 AANCTAGATGATGATAAGTTTGAATAGTGAATGCTGCTGCTGCTGCTGCTGCTGCTGCT 1620
Db 1583 AANCTAGATGATGATAAGTTTGAATAGTGAATGCTGCTGCTGCTGCTGCTGCTGCTGCT 1642
Qy 1621 ACACATATGAGATTCATCATCATGAGACAGCAAAATCTAAAGTGAATTTGATTTATA 1680
Db 1643 ACACATATGAGATTCATCATCATGAGACAGCAAAATCTAAAGTGAATTTGATTTATA 1702
Qy 1681 AGAGTTTGAATTAATATATGTAATGCAAGACACAGAGGATTTTATGGGACGCTT 1740
Db 1703 AGAGTTTGAATTAATATATGTAATGCAAGACACAGAGGATTTTATGGGACGCTT 1762
Qy 1741 TGTAAAGCTGGGATGTAAGAAAGGCGAGGGAACCTCATAGATCTTATTAATTAATCTT 1800
Db 1763 TGTAAAGCTGGGATGTAAGAAAGGCGAGGGAACCTCATAGATCTTATTAATTAATCTT 1822
Qy 1801 CATTTCTCTATCTCATCAATATCAACAAAGCTTTTACAGAAATTCATGCGAGTCAAA 1860
Db 1823 CATTTCTCTATCTCATCAATATCAACAAAGCTTTTACAGAAATTCATGCGAGTCAAA 1882
Qy 1861 TCCCAAAAGGTAACTTTATTCATTTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1920
Db 1883 TCCCAAAAGGTAACTTTATTCATTTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1942
Qy 1921 TACTGTGCTTATCTCAACTTTTGAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1980
Db 1943 TACTGTGCTTATCTCAACTTTTGAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2002
Qy 1981 GGGCAGCTTGTGAGCCACTTTAGGGTTCACCTCGCAATTAAGAAATTTACAAGA 2037
Db 2003 GGGCAGCTTGTGAGCCACTTTAGGGTTCACCTCGCAATTAAGAAATTTACAAGA 2059

RESULT 4
AAH93861
ID AAH93861 standard; cDNA; 3923 BP.
XX
AC AAH93861;
XX
DT 04-OCT-2001 (first entry)
XX
DE Gene DD3 cDNA sequence.
XX
KW Human; prostate cancer; prostate-specific; diagnosis; vaccine;
KW cytosolic; gene therapy; metastasis; ss.
XX
OS Homo sapiens.
XX
PN WO200151633-A2.
XX
PD 19-JUL-2001.
XX
PF 16-JAN-2001; 2001WO-US01574.
XX
PR 14-JAN-2000; 2000US-0483672.
XX
PA (CORI-) CORIYA CORP.
XX
PI Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Reed SG;

PI Kalos MD, Fanger GR, Day CH, Retter MW, Stolk JA, Skeiky YAW;
PI Wang A, Meagher MD;
XX WPL; 2001-425873/45.
XX
PT New polynucleotide encoding a prostate-specific protein, for
PT diagnosing, monitoring and treating prostate cancer in a patient and
PT for use in vaccines -
XX
PS Claim 1; Page 452-453; 543pp; English.
XX
CC The present invention describes polynucleotide sequences (I) which encode
CC prostate-specific proteins (II). (I) and (II) have cytostatic activity,
CC and can be used in vaccine production and gene therapy. (I), (II),
CC antibodies to (II), fusion proteins comprising (II), and isolated
CC T cells prepared using (I) or (II) are used treat cancer in a patient.
CC (I) and the antibodies are also used in the detection of cancer in a
CC patient. The cancer that is diagnosed or treated is particularly
CC prostate cancer. (I) and (II) can be used in vaccines. The antibodies or
CC (I) can be used for monitoring the progression of cancer in a patient.
CC (I) and (II) can also be used to improve diagnostic and therapeutic
CC methods for prostate cancer. They can indicate the level of metastasis
CC as well as the prostate volume. A493357 to A493944 and A490115 to
CC A490138 represent polynucleotide and amino acid sequences used in the
CC exemplification of the present invention.
CC
XX
SQ Sequence 3923 BP; 1157 A; 840 C; 740 G; 1186 T; 0 other;

Query Match 80.0%; Score 1629; DB 22; Length 3923;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 2029; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 AGAAGCTGGCAGAAAAACAGAGGGAGATTGTGTGCTGACGCGGAGAGACAG 60
DB 23 AGAAGCTGGCAGAAAAACAGAGGGAGATTGTGTGCTGACGCGGAGAGACAG 82
QY 61 GAAGATCTGATGGTGGGAGGACCTGATATACAGAGGAATTACACATATCTTAG 120
DB 83 GAAGATCTGATGGTGGGAGGACCTGATATACAGAGGAATTACACATATCTTAG 142
QY 121 TGTTCATGACACCAAGATTAATAGTGAAGAGTATGCGCTGAGTCTCTCAGT 180
DB 143 TGTTCATGACACCAAGATTAATAGTGAAGAGTATGCGCTGAGTCTCTCAGT 202
QY 181 GACACAGGGCTGATACCATGACGCGACTTTCTGAGTACTGATGACCAAGAAAGA 240
DB 203 GACACAGGGCTGATACCATGACGCGACTTTCTGAGTACTGATGACCAAGAAAGA 262
QY 241 CTACACACATCTCAATGCGGCGGTGAGAAATGAAGAGGCTGCTACTTACCATCTGA 300
DB 263 CTACACACATCTCAATGCGGCGGTGAGAAATGAAGAGGCTGCTACTTACCATCTGA 322
QY 301 GGCCACACATCTGCTGAATGAGATTAATTAACATCACTGAGAAACAGACATGACAATA 360
DB 323 GGCCACACATCTGCTGAATGAGATTAATTAACATCACTGAGAAACAGACATGACAATA 382
QY 361 TAATGCTAATGATGATGATTTTTCACATTTCCAGCCCTTAAATATCCACACACA 420
DB 383 TAATGCTAATGATGATGATTTTTCACATTTCCAGCCCTTAAATATCCACACACA 442
QY 421 CAGGAGCAAAAGAGAGACAGAGATCCCTGGGAGAAATGCCGCGCCCACTCTTGGG 480
DB 443 CAGGAGCAAAAGAGAGACAGAGATCCCTGGGAGAAATGCCGCGCCCACTCTTGGG 502
QY 481 TCATCGATGAGCTCGCCCTGTGCTGCTCCCTGTGAGGAGAGACATTTGAAGATG 540
DB 503 TCATCGATGAGCTCGCCCTGTGCTGCTCCCTGTGAGGAGAGACATTTGAAGATG 562
QY 541 AATTGATGTTCTTAAAGAGTGGCAGAGAAACAGATCTGTGATATTTATTTG 600
DB 563 AATTGATGTTCTTAAAGAGTGGCAGAGAAACAGATCTGTGATATTTATTTG 622
QY 601 AACGGATTACAGATTGAAGTAAGTCAACAAAGTAGATTACCAATGAGAGAAACA 660

DB 623 AACGGATTACAGATTGAAGTAAGTCAACAAAGTAGATTACCAATGAGAGAAACA 682
QY 661 GAGAGAAATCTTGATGCGCTTACAGACATGCAACAAACAAATGATATCTGATG 720
DB 683 GAGAGAAATCTTGATGCGCTTACAGACATGCAACAAACAAATGATATCTGATG 742
QY 721 ACATGAGGACGCCAAGCTGGGAGAGATTAACACGCGGAGAGAGGATTTGGCC 780
DB 743 ACATGAGGACGCCAAGCTGGGAGAGATTAACACGCGGAGAGAGGATTTGGCC 802
QY 781 CTGCTGCTTAACCTGCTGCTTATACCAATATATTTCTAATCCCTCAAAACA 840
DB 803 CTGCTGCTTAACCTGCTGCTTATACCAATATATTTCTAATCCCTCAAAACA 862
QY 841 AGCTGTTGATATTCGATGCTGATACGCTGCTGCTGCTGCTGCTGCTGCTGCTG 900
DB 863 AGCTGTTGATATTCGATGCTGATACGCTGCTGCTGCTGCTGCTGCTGCTGCTG 922
QY 901 GCCACACTATTTTATATTTAGTCCAGATCTGATGCTGATGCTGCTGCTGCTGCTG 960
DB 923 GCCACACTATTTTATATTTAGTCCAGATCTGATGCTGATGCTGCTGCTGCTGCTG 982
QY 961 AATTAATTAATCTATTTTGTCAAGACCTTGTGCTGCTGCTGCTGCTGCTGCTGCT 1020
DB 983 AATTAATTAATCTATTTTGTCAAGACCTTGTGCTGCTGCTGCTGCTGCTGCTGCT 1042
QY 1021 GTTTTCCCTAAGAGTGTCTGCGCCAGGAGATCTGTGAACAGCGGGAGACATGCA 1080
DB 1043 GTTTTCCCTAAGAGTGTCTGCGCCAGGAGATCTGTGAACAGCGGGAGACATGCA 1102
QY 1081 GATCTTCCAGGGTTATCTTACTTACTAGCACACACATGATCATATGAGAGTATCTA 1140
DB 1103 GATCTTCCAGGGTTATCTTACTTACTAGCACACACATGATCATATGAGAGTATCTA 1162
QY 1141 ATCAACATCTCTCTGAGTGTCTTGGCCATACAGAAATTCATTTCCACTTTGTGCCA 1200
DB 1163 ATCAACATCTCTCTGAGTGTCTTGGCCATACAGAAATTCATTTCCACTTTGTGCCA 1222
QY 1201 TTCTCAAGACCTCAAAATGTCATTCATTAATATCACAGATTAATCTTTTATTAAC 1260
DB 1223 TTCTCAAGACCTCAAAATGTCATTCATTAATATCACAGATTAATCTTTTATTAAC 1282
QY 1261 TGGAGAAATTAATGTTACATGCGAGCTATGGAATTAATTAATATTTGTTCCAGT 1320
DB 1283 TGGAGAAATTAATGTTACATGCGAGCTATGGAATTAATTAATATTTGTTCCAGT 1342
QY 1321 GCAAGATGACTAAGTCCCTTATCCCTCCCTGTTGATTTTTCAGATTAAGT 1380
DB 1343 GCAAGATGACTAAGTCCCTTATCCCTCCCTGTTGATTTTTCAGATTAAGT 1402
QY 1381 TAAATGCTTAACTGTACTGAGGCTGTATACAGACAGGCTCTCCCATCCCTCAGC 1440
DB 1403 TAAATGCTTAACTGTACTGAGGCTGTATACAGACAGGCTCTCCCATCCCTCAGC 1462
QY 1441 CTTATCTGTACATCACTCAACCCCTCCCATATNSACCTTAACAAATCTAATCTGAAT 1500
DB 1463 CTTATCTGTACATCACTCAACCCCTCCCATATNSACCTTAACAAATCTAATCTGAAT 1522
QY 1501 CCTTGAACATGTCAGACATCACTTCTCTCTGCTGAGAGGCTCTCTCTCTCTCT 1560
DB 1523 CCTTGAACATGTCAGACATCACTTCTCTCTGCTGAGAGGCTCTCTCTCTCTCT 1582
QY 1561 AANTCTAGATGATGTAAGTTTGAATGTAAGTTGACTATCTTCAATGCAAGAGG 1620
DB 1583 AANTCTAGATGATGTAAGTTTGAATGTAAGTTGACTATCTTCAATGCAAGAGG 1642
QY 1621 ACACATATGAGATTCATCATCATGACAGACAAATTAATAAGTATATTTGATTA 1680
DB 1643 ACACATATGAGATTCATCATCATGACAGACAAATTAATAAGTATATTTGATTA 1702
QY 1681 AGAGTTAGTAAATATGAAATGCAAGKCCAGAGAGGATGTTTAAAGGGGCGGTT 1740

Db	1703	AGAGTTAGATTAATATATATGAATATGCAAGACCACAGAGGAATGTTATATGGGCACCTT	1762
OY	1741	TGTAAAGCCCTGGAGATGTGAGAAAGGACGGAACCTCATAGATATCTTATATATATACTT	1800
Db	1763	TGTAAAGCCCTGGAGATGTGAGAAAGGACGGAACCTCATAGATATATATATATACTT	1822
OY	1801	CATTTCCTATCTCTATACACAATATCCACAAGCTTTTCACAGAAATTCATGCATGTGAAA	1860
Db	1823	CATTTCCTATCTCTATACACAATATCCACAAGCTTTTCACAGAAATTCATGCATGTGAAA	1882
OY	1861	TCCCCAAAGGTAAACCTTTATTCACATTTCAAGTGAGTGCGCTTTAGAAATTTTGGCAAAATCA	1920
Db	1883	TCCCCAAAGGTAAACCTTTATTCACATTTATGAGTGAGTGCGCTTTAGAAATTTTGGCAAAATCA	1942
OY	1921	TACTGGACATTAATCTCAACTTATGAGATGTGTGTCTGTAGTAAATGTAAGAAAGAATA	1980
Db	1943	TACTGGACATTAATCTCAACTTATGAGATGTGTGTCTGTAGTAAATGTAAGAAAGAATA	2002
OY	1981	GGGCACTCTGTGTGAGCACTTTTAGGGTTCACCTCTGSCAATAAAGAAATTTACAAGA	2037
Db	2003	GGGCACTCTGTGTGAGCACTTTTAGGGTTCACCTCTGSCAATAAAGAAATTTACAAGA	2059

RESULT 5
ABK92196
ID ABK92196 standard: DNA: 3923 BP.

AC ABK92196;

DT 15-AUG-2002 (first entry)

DE Prostate cancer-associated DNA sequence #82.

KM Prostate cancer; prostate tumour tissue; human; mammal; cytostatic;
KM gene therapy; gene; ds.

Mammalia.

PN W0200230268-A2.

PD 18-APR-2002.

PF 12-OCT-2001; 2001WO-US32045.

PR 13-OCT-2000; 2000US-0687576.

PR 08-DEC-2000; 2000US-0733742.

PR 16-MAR-2001; 2001US-276791P.

PR 06-APR-2001; 2001US-281922P.

PR 30-APR-2001; 2001US-0847046.

XX

XX

XX

XX

PT patient, useful for diagnosis

PT are expressed in a prostate

PS Claim 22; Page 365-366; 436p

CC The present invention relates

CC comprises contacting a bio

CC selectively hybridise to a s

Query Match	Best local similarity	80.0% ; Score 1629 ; DB 24 ; Length 3923 ;	Matches 2029 ;	Conservative	0 ; Mismatches	8 ; Indels	0 ; Gaps	0
CC	to them. The prostate cancer-associated polynucleotide sequences							
CC	are differentially expressed in prostate tumour tissue or in							
CC	prostate cancer and are derived from the tissues of various							
CC	organisms such as humans or other mammals (e.g. mice, sheep and dogs).							
CC	The methods of the invention are useful for diagnosing and treating							
CC	prostate cancer in mammals. The prostate cancer-associated genes are							
CC	useful for diagnosing or treating prostate cancer, as well as for							
CC	identifying modulators of prostate cancer or agents that inhibit							
CC	prostate cancer. The nucleic acid sequences are particularly useful							
CC	in gene therapy, as a vaccine or in antisense applications.							
CC	ABK92115-ABK92263 represent prostate cancer-associated polynucleotide							
CC	sequences.							
XX								
SO	Sequence 3923 BP; 1157 A; 840 C; 740 G; 1186 T; 0 other;							
Query Match	Best local similarity	80.0% ; Score 1629 ; DB 24 ; Length 3923 ;						
Matches 2029 ;	Conservative	0 ; Mismatches	8 ; Indels	0 ; Gaps	0			
OY	1	AGAACCTGGCATCAGAAAAACAGAGGGAGATTGTGTGGCTGACCGGAGGAGACCG	60					
DB	23	AGAGCTGGCATCAGAAAAACAGAGGGAGATTGTGTGGCTGACCGGAGGAGACCG	82					
OY	61	GAAATCTGCATGGTGGGAGGACCTGATGATACGAGAGATTACACACATATCTTGG	120					
DB	83	GAAATCTGCATGGTGGGAGGACCTGATGATACGAGAGAAATACACACATATCTTGG	142					
OY	121	TGTTTCATGTAACACCAAGATTAATTAAGGAAGACTCTGTCGCTGTGATCTCCACT	180					
DB	143	TGTTTCATGTAACACCAAGATTAATTAAGGAAGACTCTGTCGCTGTGATCTCCACT	202					
OY	181	GACACAGGGCTGGATCACCATTGACGGGACTTCTGAATCTCATCTGACGACGAAAGAA	240					
DB	203	GACACAGGGCTGGATCACCATTGACGGGACTTCTGAATCTCATCTGACGACGAAAGAA	262					
OY	241	CTACAGACATCTCAATGGCAGGGGTGAGAAATAGAAAAGCTGCTGACTTTACCATCTGA	300					
DB	263	CTACAGACATCTCAATGGCAGGGGTGAGAAATAGAAAAGCTGCTGACTTTACCATCTGA	322					
OY	301	GGCCGACATCTGCGTGAATGGAGATTAATTAACATCCTAGAAAACGACAGATGACATA	360					
DB	323	GGCCGACATCTGCGTGAATGGAGATTAATTAACATCCTAGAAAACGACAGATGACATA	382					
OY	361	TAATGCTTAAGTAGACATGTTTGTGCACATTTCCACCCCTTTAAATATCCACACAA	420					
DB	383	TAATGCTTAAGTAGACATGTTTGTGCACATTTCCACCCCTTTAAATATCCACACAA	442					
OY	421	CAGGAAGCAGAAAAGAGACACAGAGATCCCTGGAGAAATCCCGCCGCATCTTGGG	480					
DB	443	CAGGAAGCAGAAAAGAGACACAGAGATCCCTGGAGAAATCCCGCCGCATCTTGGG	502					
OY	481	TCATCGATGAGCGTCGCCCTGTGCTGCCCTGTGAGGGAAGGACATTAGAAAATG	540					
DB	503	TCATCGATGAGCGTCGCCCTGTGCTGCCCTGTGAGGGAAGGACATTAGAAAATG	562					
OY	541	AATTGATGTGTTCCCTTAAGAGATGGGACAGAAAACAGATCCGTTGTGGATTTATTTG	600					
DB	563	AATTGATGTGTTCCCTTAAGAGATGGGACAGAAAACAGATCCGTTGTGGATTTATTTG	622					
OY	601	AACGGGATTACAGATTTGAATGAAGTCACAAAGTAGAGCATTTACCAATGACGAGAAACA	660					
DB	623	AACGGGATTACAGATTTGAATGAAGTCACAAAGTAGAGCATTTACCAATGACGAGAAACA	682					
OY	661	GACGAGAAATCTTGATGGCTTCCACAAGACATGCAAAACAAATGAAATGCAATCTGTGATG	720					
DB	683	GACGAGAAATCTTGATGGCTTCCACAAGACATGCAAAACAAATGAAATGCAATCTGTGATG	742					
OY	721	ACATGAGGACAGCAAGCTGTGGGAGAGATTAACACAGGGGACAGAGCTCAGATTTCTGGCC	780					
DB	743	ACATGAGGACAGCAAGCTGTGGGAGAGATTAACACAGGGGACAGAGCTCAGATTTCTGGCC	802					
OY	781	CTGCTGCCCTAAACTGTGCTTCAATACCAAAATCATTTATTTTAAACCTCAAAACAA	840					

Db 803 CTGCTGCTTAAGTGTGCTTCATACCAAAATCATTTCTAATACCTCAAAACAA 862
QY 841 AGGTGTGTAATATCTGATCTCTACGGTCTCTTGAGGCCCAACATCTCCATATATCA 900
Db 863 AGCGTGTAAATATCTATCTCTACGGTCTCTTGAGGCCCAACATCTCCATATATCA 922
QY 901 GCCACACTATTTTTAAATTAATTAAGTCCAGATCTGATGACCTTTCTACACTAG 960
Db 923 GCCACACTATTTTTAAATTAATTAAGTCCAGATCTGATGACCTTTCTACACTAG 982
QY 961 AATAACTTACTATTTGTTCAAAGACCCCTGCTGTGCTGCTAATATGATGATGAT 1020
Db 983 AATTAATCTTACTATTTGTTCAAAGACCCCTGCTGTGCTGCTAATATGATGATGAT 1042
QY 1021 GTTTTCTTAAGAGAGTCTTGAGGCCAGGGGATCTGTAACAGGCTGGGAAGCTCA 1080
Db 1043 GTTTTCTTAAGAGAGTCTTGAGGCCAGGGGATCTGTAACAGGCTGGGAAGCTCA 1102
QY 1081 GATCTTCCAGGGTATATCTTACTAGACACAGCATATCATTAAGGAGTGAATATCTA 1140
Db 1103 GATCTTCCAGGGTATATCTTACTAGACACAGCATATCATTAAGGAGTGAATATCTA 1162
QY 1141 ATCAACATCATCTCAGTGTCTTGCCCATCTGAATATGATTTCCACCTTTGTGCCA 1200
Db 1163 ATCAACATCATCTCAGTGTCTTGCCCATCTGAATATGATTTCCACCTTTGTGCCA 1222
QY 1201 TTCTCAAGACCTCAAAATGTATTCATTAATATACAGAGATTAATCTTTTATTAAC 1260
Db 1223 TTCTCAAGACCTCAAAATGTATTCATTAATATACAGAGATTAATCTTTTATTAAC 1282
QY 1261 TGGAGAAATTCATATGATGAGAGATGAGAAATTAATATGATTTGTTCAGT 1320
Db 1283 TGGAGAAATTCATATGATGAGAGATGAGAAATTAATATGATTTGTTCAGT 1342
QY 1321 GCAAGATGACTAAGTCTTATCCCTCCCTTTGTTGATTTTTCAGATTAAGT 1380
Db 1343 GCAAGATGACTAAGTCTTATCCCTCCCTTTGTTGATTTTTCAGATTAAGT 1402
QY 1381 TAAATGCTTACCTGTCTGATGAGGCTGATACGACACCTCTCCCTCCCTCAGC 1440
Db 1403 TAAATGCTTACCTGTCTGATGAGGCTGATACGACACCTCTCCCTCCCTCAGC 1462
QY 1441 CTATATGCTATACCATCAACCCCTCCCATNTSACCTAACAATACTAATCTGATAT 1500
Db 1463 CTATATGCTATACCATCAACCCCTCCCATNTSACCTAACAATACTAATCTGATAT 1522
QY 1501 CCTTGAACATGTAGGNCATATATTTCTCTGCTGAGAAAGCTTCTCTGTCTT 1560
Db 1523 CCTTGAACATGTAGGNCATATATTTCTCTGCTGAGAAAGCTTCTCTGTCTT 1582
QY 1561 AATTCATGATGATGATTAAGTGTGAATTAAGTACTATCTTATCTGCAAGAAGAGG 1620
Db 1583 AATTCATGATGATGATTAAGTGTGAATTAAGTACTATCTTATCTGCAAGAAGAGG 1642
QY 1621 ACACATATGATGATTCATCATCATGAGACGAATAATCAAAAGTATTTGATATATA 1680
Db 1643 ACACATATGATGATTCATCATCATGAGACGAATAATCAAAAGTATTTGATATATA 1702
QY 1681 AGAGTTAGATTAATATATGAAATGCAAGACCCAGAGGGAATGTTATGGGGACGT 1740
Db 1703 AGAGTTAGATTAATATATGAAATGCAAGACCCAGAGGGAATGTTATGGGGACGT 1762
QY 1741 TGTAACTCTGGGATGTGAAGMAAAGGAGGAACTTCATAGATCTTATTAATATATCT 1800
Db 1763 TGTAACTCTGGGATGTGAAGMAAAGGAGGAACTTCATAGATCTTATTAATATATCT 1822
QY 1801 CATTTCTATCTCTATCAACATATATCAAAAGCTTTTCAAGAAATTCATGCAAGTGA 1860
Db 1823 CATTTCTATCTCTATCAACATATATCAAAAGCTTTTCAAGAAATTCATGCAAGTGA 1882
QY 1861 TCCCAAAAGGTAACCTTTATCATTTGATGAGTGGCTTTAGAAATTTGGCAATCA 1920
Db 1883 TCCCAAAAGGTAACCTTTATCATTTGATGAGTGGCTTTAGAAATTTGGCAATCA 1942

QY 1921 TACTGTCACCTTATCTCAACTTTGAGATGATGTTGCTCTGTAGTATTAATGAAGAATA 1980
Db 1943 TACTGTCACCTTATCTCAACTTTGAGATGATGTTGCTCTGTAGTATTAATGAAGAATA 2002
QY 1981 GGGCACTCTCTGAGCCACCTTTAGGTTCACTCTGCAATAAAGAAATTAACAAGA 2037
Db 2003 GGGCACTCTCTGAGCCACCTTTAGGTTCACTCTGCAATAAAGAAATTAACAAGA 2059
RESULT 6
ABL95397
ID ABL95397 standard; cDNA: 3923 BP.
XX ABL95397;
AC 19-JUL-2002 (first entry)
DT 19-JUL-2002 (first entry)
DE Human DD3 cDNA sequence SEQ ID NO 690.
XX Human DD3 cDNA sequence SEQ ID NO 690.
KW Human; cancer; prostate cancer; vaccine; cytostatic; immunostimulant;
KM gene therapy; gene; ss.
XX Homo sapiens.
XX US2002022248-A1.
PD 21-FEB-2002.
XX 12-JAN-2001; 2001US-0759143.
PF 25-FEB-1997; 97US-0806099.
PR 01-AUG-1997; 97US-0904804.
PR 09-FEB-1998; 98US-0020956.
PR 25-FEB-1998; 98US-0030607.
PR 14-JUL-1998; 98US-0115453.
PR 23-SEP-1998; 98US-0159812.
PR 15-JAN-1999; 99US-0232149.
PR 09-APR-1999; 99US-0288946.
PR 13-JUL-1999; 99US-0352616.
PR 12-NOV-1999; 99US-0439313.
PR 18-NOV-1999; 99US-0443686.
PR 14-JAN-2000; 2000US-0483672.
PR 27-MAR-2000; 2000US-0536857.
PR 09-MAY-2000; 2000US-0568100.
PR 12-MAY-2000; 2000US-0570737.
PR 13-JUN-2000; 2000US-0593793.
PR 27-JUN-2000; 2000US-0605783.
PR 10-AUG-2000; 2000US-0636215.
PR 29-AUG-2000; 2000US-0651236.
PR 06-SEP-2000; 2000US-0657279.
PR 02-OCT-2000; 2000US-0679426.
PR 10-OCT-2000; 2000US-0685166.
XX
PA (XUJ/) XU J.
PA (DILL) DILLON D C.
PA (MITC) MITCHAM J L.
PA (HARL) HARLOCKER S L.
PA (JIANG) JIANG Y.
PA (KALOS) KALOS M D.
PA (FRANG) FRANGER G R.
PA (REIT) REITER M W.
PA (STOL) STOLK J A.
PA (DAYC) DAY C H.
PA (VEDV) VEDVICK T S.
PA (CART) CARTER D.
PA (LISX) LI S X.
PA (WANG) WANG A.
PA (SKEI) SKEIKY Y A W.
PA (HEPL) HEPLER W T.
PA (HEND) HENDERSON R A.
PI Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Kalos MD;

PI Fanger GR, Retter MW, Stolk JA, Day CH, Vedvick TS, Carter D;
PI Li SX, Wang A, Skeiky YAW, Hepler WT, Henderson RA;
XX
XX
DR WPI: 2002-255649/30.
PT New prostate-specific polynucleotides for diagnosing and treating
PT diseases, in particular prostate cancer, and as markers for the
PT progression of cancer
XX
XX
PS Claim 1: SEQ ID NO 690; 87pp; English.
CC The present invention provides prostate-specific coding sequences and
CC their encoded proteins. These can be used in the diagnosis and treatment
CC of cancers, particularly prostate cancer. The present sequence is a cDNA
CC described in the invention.
XX
SQ Sequence 3923 BP; 1157 A; 840 C; 740 G; 1186 T; 0 other;
Query Match 80.0%; Score 1629; DB 24; Length 3923;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 2029; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
QY 1 AGAAGCTGGCATCAGAAAAACAGAGGAGAGATTGTGTGCTGCAGCCGAGGAGACCCAG 60
DB 23 AGAAGCTGGCATCAGAAAAACAGAGGAGAGATTGTGTGCTGCAGCCGAGGAGACCCAG 82
QY 61 GAAGATCTGCATGCTGGGAGAGACCTGATGATACAGAGAAATTAAACACATATCTTAG 120
DB 83 GAAGATCTGCATGCTGGGAGAGACCTGATGATACAGAGAAATTAAACACATATCTTAG 142
QY 121 TGTTCATATGAACACCAAGATAAATAGTGAAGACTAGTCCGTGTGAGTCTCCTCAGT 180
DB 143 TGTTCATATGAACACCAAGATAAATAGTGAAGACTAGTCCGTGTGAGTCTCCTCAGT 202
QY 181 GACACAGGCTGGATGACCATGACGCGCATCTTGTGACTACTAGTGCAGCAAGAAAGA 240
DB 203 GACACAGGCTGGATGACCATGACGCGCATCTTGTGACTACTAGTGCAGCAAGAAAGA 262
QY 241 CTACGACATCTCATATGCGAGGGGTGAGAAATTAAGAGGCTGCTTAACTTAACTTGA 300
DB 263 CTACGACATCTCATATGCGAGGGGTGAGAAATTAAGAGGCTGCTTAACTTAACTTGA 322
QY 301 GGGCCACATCTGCTGAAGATGAGATTAATTAACATCAGTAGAAGACGAGATGACATA 360
DB 323 GGGCCACATCTGCTGAAGATGAGATTAATTAACATCAGTAGAAGACGAGATGACATA 382
QY 361 TAATGCTTAAGTATGACATGTTTTGACATTTCCAGCCCTTTAAATATCCACACACA 420
DB 383 TAATGCTTAAGTATGACATGTTTTGACATTTCCAGCCCTTTAAATATCCACACACA 442
QY 421 CAGGAAGCAGAAAAGAGACAGAGATCCCTGGGAGAAATGCCGGCCGCGCATCTTGGG 480
DB 443 CAGGAAGCAGAAAAGAGACAGAGATCCCTGGGAGAAATGCCGGCCGCGCATCTTGGG 502
QY 481 TCATGATGAGCCTGCGCTGTGCTGCTCCGCTTTGAGAGGAGAGACATTTAGAAAATG 540
DB 503 TCATGATGAGCCTGCGCTGTGCTGCTCCGCTTTGAGAGGAGAGACATTTAGAAAATG 562
QY 541 AATGATGCTGTTCTTAAGAGATGGGAGAAAACAGATCCTGTTGTGATTTTAAATTTG 600
DB 563 AATGATGCTGTTCTTAAGAGATGGGAGAAAACAGATCCTGTTGTGATTTTAAATTTG 622
QY 601 AACGGATTACAGATTGAATGAATGACAAAGTACATTTACCAATGAGAGGAGAAACA 660
DB 623 AACGGATTACAGATTGAATGAATGACAAAGTACATTTACCAATGAGAGGAGAAACA 682
QY 661 GACGAGAAATCTTGATGCTTACAGACATGCAACAACAAAATGGAATCTGTATG 720
DB 683 GACGAGAAATCTTGATGCTTACAGACATGCAACAACAAAATGGAATCTGTATG 742
QY 721 ACATGAGGAGCAAGCTGGGAGAGATTAACACAGGGGAGAGGTTACAGATTGTGGCC 780
DB 743 ACATGAGGAGCAAGCTGGGAGAGATTAACACAGGGGAGAGGTTACAGATTGTGTGGCC 802

QY 761 CTGCTGCTAAACCTGGGCTTCATTAACCAAAATCATTTTCATATTTCTAACCCGCAAAACA 840
DB 803 CTGCTGCTAAACCTGGGCTTCATTAACCAAAATCATTTTCATATTTCTAACCCGCAAAACA 862
QY 841 AGCTGTGTAATATCTGATCTCTAGGCTTCTTCCGAGCCCAACATTCCTCATATATATCA 900
DB 863 AGCTGTGTAATATCTGATCTCTAGGCTTCTTCCGAGCCCAACATTCCTCATATATCA 922
QY 901 GCCACAGCATTTTAAATATTTAGTTCACAGATCTGTACTGTGACCTTTCTACACTTAG 960
DB 923 GCCACAGCATTTTAAATATTTAGTTCACAGATCTGTACTGTGACCTTTCTACACTTAG 982
QY 961 AATACATTTACTCATTTTGTTCAAAGACCTTCGCTGCTGCTCCCAATATGAGTGA 1020
DB 983 AATACATTTACTCATTTTGTTCAAAGACCTTCGCTGCTGCTCCCAATATGAGTGA 1042
QY 1021 GTTTTCCCTAAGAGATGTTCTGGCCAGGGATCTGTAAACAGGCTGGGAGACATCTCA 1080
DB 1043 GTTTTCCCTAAGAGATGTTCTGGCCAGGGATCTGTAAACAGGCTGGGAGACATCTCA 1102
QY 1081 GATCTTCCAGGCTTATCTTACTAGACACAGCATGATCATTTACGAGTGAATATCTA 1140
DB 1103 GATCTTCCAGGCTTATCTTACTAGACACAGCATGATCATTTACGAGTGAATATCTA 1162
QY 1141 ATCAACATATCCAGTGTCTTGGCCCATCTGAATTCATTTCCCATTTTGTGCCCA 1200
DB 1163 ATCAACATATCCAGTGTCTTGGCCCATCTGAATTCATTTCCCATTTTGTGCCCA 1222
QY 1201 TTCTCAAGACCTCAAAATATGCTATTCATTAATATACAGAGATTAACTTTTAACTTAA 1260
DB 1223 TTCTCAAGACCTCAAAATATGCTATTCATTAATATACAGAGATTAACTTTTAACTTAA 1282
QY 1261 TGGAAATTTCAATGTTCATGACGACCTATGGGAATTAATTAATATTTTGTTCAGT 1320
DB 1283 TGGAAATTTCAATGTTCATGACGACCTATGGGAATTAATTAATATTTTGTTCAGT 1342
QY 1321 GCAAGATGACATGCTTATCCCTTATCCCTCCCTTGTGATTTTTCAGATTAAGT 1380
DB 1343 GCAAGATGACATGCTTATCCCTTATCCCTCCCTTGTGATTTTTCAGATTAAGT 1402
QY 1381 TAAATGCTTACCTTGTACTGAGGCTGTATACAGACAGCCCTCCCATCCCTCAGC 1440
DB 1403 TAAATGCTTACCTTGTACTGAGGCTGTATACAGACAGCCCTCCCATCCCTCAGC 1462
QY 1441 CTTATCTGTATCATCATCAACCCCTCCCATATVSCCTTAACAAATTAATCTTGAAT 1500
DB 1463 CTTATCTGTATCATCATCAACCCCTCCCATACACACTAAACAAATCTAATCTTGAAT 1522
QY 1501 CCTTGAACATGTCAGGACATACATTTTCCTTCTGAGAGAGCTTCTGCTCTT 1560
DB 1523 CCTTGAACATGTCAGGACATACATTTTCCTTCTGAGAGAGCTTCTGCTCTT 1582
QY 1561 AANTCTAGATGATTAAGTTTGAATTAAGTATGCTATCTTCAATGCAAGAGGG 1620
DB 1583 AANTCTAGATGATTAAGTTTGAATTAAGTATGCTATCTTCAATGCAAGAGGG 1642
QY 1621 ACACATATGAGATTTATCATCATGAGACAGCAAAATCTAAACTGTAAATTTGATTA 1680
DB 1643 ACACATATGAGATTTATCATCATGAGACAGCAAAATCTAAACTGTAAATTTGATTA 1702
QY 1681 AGAGTTTATGATTAATATGAAATGCAAGACACAGAGGAAATTTATGGGACGCT 1740
DB 1703 AGAGTTTATGATTAATATGAAATGCAAGACACAGAGGAAATTTATGGGACGCT 1762
QY 1741 TGTAACTGAGATGAGAAAGAGGAGAACTCATATCTTATTAATATTAATCTT 1800
DB 1763 TGTAACTGAGATGAGAAAGAGGAGAACTCATATCTTATTAATATTAATCTT 1822
QY 1801 CATTTCTATCTATCATCAATATCCAAAGCTTTTACAGAGATTTATGACAGTGCA 1860
DB 1823 CATTTCTATCTATCATCAATATCCAAAGCTTTTACAGAGATTTATGACAGTGCA 1882

OY	1861	TCGCCAAGGTAACCTTATTCATTCATGAGTGCAGCTTTCGCAATTC	1920
DB	1863	TCGCCAAGGTAACCTTATTCATTCATGAGTGCAGCTTTCGCAATTC	1942
OY	1921	TACTGTCACCTATCTCAACTTTGAGATGTTGTTCCTTGACTTAATGAAGAATA	1980
DB	1943	TACTGTCACCTATCTCAACTTTGAGATGTTGTTCCTTGACTTAATGAAGAATA	2002
OY	1991	GGGCACTCTTGTGAGCCACTTTAGGGTTCTCTGGCATAAAGAAATTTACAAGA	2037
DB	2003	GGGCACTCTTGTGAGCCACTTTAGGGTTCTCTGGCATAAAGAAATTTACAAGA	2059
RESULT 7			
ID	ACA59834	standard; cDNA: 3923 BP.	
XX	ACA59834;		
XX	10-JUN-2003	(first entry)	
DE	Prostate cancer therapy associated cDNA #545.		
XX	Prostate cancer; vaccine; gene therapy; cytostatic; fusion protein;		
KW	immunogen; cancer; prostate specific antigen; PSA;		
KW	prostatic acid phosphatase; PAP; prostate specific membrane antigen;		
KW	PSMA; gene; ss.		
XX	Homo sapiens.		
PN	US2002192763-A1.		
PD	19-DEC-2002.		
PE	29-JUN-2001; 2001US-0895793.		
PR	17-APR-2000; 2000US-157455P.		
PR	04-OCT-2000; 2000US-0679272.		
XX	28-MAR-2001; 2001US-0822827.		
PA	(XUJ/) XU J.		
PA	(DILL/) DILLON D C.		
PA	(MITC/) MITCHAM J L.		
PA	(HARL/) HARLOCKER S L.		
PA	(JIAN/) JIANG Y.		
PA	(KALO/) KALOS M D.		
PA	(FANG/) FANGER G R.		
PA	(RETT/) RETTER M W.		
PA	(STOL/) STOLK J A.		
PA	(DAYC/) DAY C H.		
PA	(VEDV/) VEDVICK T S.		
PA	(CART/) CARTER D.		
PA	(LISX/) LI S X.		
PA	(WANG/) WANG A.		
PA	(SKEI/) SKEIKY Y A W.		
PA	(HEPL/) HEPLER Y T.		
PA	(HEND/) HENDERSON R A.		
PA	(HURA/) HURAL J.		
PA	(MCNE/) MCNETIL P D.		
PA	(HOUG/) HOUGHTON R L.		
PA	(DBAS/) Y DE BASSOLS C V.		
PA	(FOYT/) FOY T M.		
XX	Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Kalos MD;		
PI	Fanger GR, Retter MW, Stoik JA, Day CH, Vedvick TS, Carter D;		
PI	Li SX, Wang A, Skeiky YAW, Hepler WT, Henderson RA, Hural J;		
PI	Mcneill PD, Houghton RL, Y De Bassols CV, Foy TM;		
XX	WPI: 2003-352711/33.		
XX	New fusion protein comprising prostate-specific polypeptides, or its		
PT	immunogenic portions, useful for diagnosing, preventing and/or treating		
PT	cancer, particularly prostate cancer -		

XX	PS	XX	Example 16; SEQ ID NO 690; 85pp; English.
XX	CC	XX	The invention describes a fusion protein comprising at least one amino
CC	acid	sequence of immunogenic portions of any of the 3 sequences not	
CC	defined	in the specification, or sequences having at least 70 or 90 %	
CC	sequence	identity to any one of the 35 sequences defined in the USPTO	
CC	web	site, which is encoded by any of the 4 nucleotide sequences not	
CC	defined	in the specification. The fusion protein, composition and	
CC	methods	are useful for diagnosing, preventing and/or treating cancer,	
CC	particularly	prostate cancer. The proteins are useful as markers to	
CC	indicate	the presence or absence of cancer. This sequence	
CC	represents	a prostate cancer therapy associated cDNA.	
CC	Note:	The sequence data for this patent did not form part of the	
CC	printed	specification, but was obtained in electronic format directly	
CC	from	the US patent office at	
CC	seqdata.uspto.gov/sequence.html?docID=US20020192763.		
XX	Seq	Sequence 3923 BP; 1157 A; 840 C; 740 G; 1186 T; 0 other;	
XX	Query Match	80.0%; Score 1529; DB 25; Length 3923;	
XX	Best Local Similarity	99.6%; Pred. No. 0;	
XX	Matches 2029; Conservative	0; Mismatches 8; Indels 0; Gaps 0;	
QY	1	AGAACTGCATCAGAAAAACAGAGGGAGATTTGTGTGGCTGCAGCCGAGGAGACAG 60	
DB	23	AGAACTGCATCAGAAAAACAGAGGGAGATTTGTGTGGCTGCAGCCGAGGAGACAG 82	
QY	61	GAAATCTGCATGTGTGGAGAGACCTGATGATCAGAGAAATTACACACATATCTTAG 120	
DB	83	GAAATCTGCATGTGTGGAGAGACCTGATGATCAGAGAAATTACACACATATCTTAG 142	
QY	121	TGTTTCATGTAACCCAGATTAATTAATGAAAGCTGTCCGCTGAGTCTCTCAGT 180	
DB	143	TGTTTCATGTAACCCAGATTAATTAATGAAAGCTGTCCGCTGAGTCTCTCAGT 202	
QY	181	GACACAGGGCTGAGTACCATCGAGCGCACTTTCAGACTACTCACTGACGAGAAAGAA 240	
DB	203	GACACAGGGCTGAGTACCATCGAGCGCACTTTCAGACTACTCACTGACGAGAAAGAA 262	
QY	241	CTACAGACATCTCAATGGCAGGGGTGAGAAATAGAAAGGCTGCTGACTTTACCATCTGA 300	
DB	263	CTACAGACATCTCAATGGCAGGGGTGAGAAATAGAAAGGCTGCTGACTTTACCATCTGA 322	
QY	301	GGCCACACATCTGCGGAATGAGATTAATTAACATCACTATACAAACAGACAGATGACATA 360	
DB	323	GGCCACACATCTGCGGAATGAGATTAATTAACATCACTATACAAACAGACAGATGACATA 382	
QY	361	TAATGCTAAGTAGTACATGTTTTTGGACATTTCCAGCCCTTTAAATATCCACACACA 420	
DB	383	TAATGCTAAGTAGTACATGTTTTTGGACATTTCCAGCCCTTTAAATATCCACACACA 442	
QY	421	CAGGAGACAAAAAGGAAGCAACAGATCCCTGGGAGAAATGCCCGCGGCATCTTGGG 480	
DB	443	CAGGAGACAAAAAGGAAGCAACAGATCCCTGGGAGAAATGCCCGCGGCATCTTGGG 502	
QY	481	TCATCGATGACCTTCGCCCTGTGCTGCTGCCGCTGTGAGGGAAGACATTAGAAATG 540	
DB	503	TCATCGATGACCTTCGCCCTGTGCTGCTGCCGCTGTGAGGGAAGACATTAGAAATG 562	
QY	541	AATGATGATGTTCTTAAAGATGGGCAAGAAACAGATCCTGTTGTGGAATATTTATTTG 600	
DB	563	AATGATGATGTTCTTAAAGATGGGCAAGAAACAGATCCTGTTGTGGAATATTTATTTG 622	
QY	601	AACGGGATTCAGATTTTGAATGAAAGTACACAAAGTACATTTACCAATGAGAGAAAACA 660	
DB	623	AACGGGATTCAGATTTTGAATGAAAGTACACAAAGTACATTTACCAATGAGAGAAAACA 682	
QY	661	GACGAGAAATCTTGATGCTTCACAGACATGCACAAACAAATGGAATACTGTGTAGT 720	
DB	683	GACGAGAAATCTTGATGCTTCACAGACATGCACAAACAAATGGAATACTGTGTAGT 742	
QY	721	ACATGAGGACATCCAAAGCTGGGGGAGAGATTAACACAGGGGCTGAGAGGATCTGTGGCC 780	

```

Db      743 ACATAGGAGGAGCAAGCTGGGGAGAGATTAACACAGGGGAGAGGCTGAGGTTGTGGCC 802
Qy      741 CTGTCGCTAAACCTGCGCTTCATTAACCAATCATTTTCTTAACCTCAAAACA 840
Db      803 CTGCGCTTAAACCTGCGCTTCATTAACCAATCATTTTCTTAACCTCAAAACA 862
Qy      841 AGCGTGTGAATATCTAGGTTCCCTTCGGGGCCCAACCTTCCTCCATATATCA 900
Db      863 AGCGTGTGAATATCTAGGTTCCCTTCGGGGCCCAACCTTCCTCCATATATCA 922
Qy      901 GCCACACTATTTTAAATATTTAGTCCAGATCTGTACTGTGACCTTTCACACTAG 960
Db      923 GCCACACTATTTTAAATATTTAGTCCAGATCTGTACTGTGACCTTTCACACTAG 982
Qy      961 AATAACATTTACTATTTTGTTCAAAGACCTTGTGTGCTGCTTAATATGTAGTACT 1020
Db      983 AATAACATTTACTATTTTGTTCAAAGACCTTGTGTGCTGCTTAATATGTAGTACT 1042
Qy      1021 GTTTTTCCTAAGGAGTCTTCGGCCGAGGGATCTGTAAACGCTGGGAACATCTCA 1080
Db      1043 GTTTTTCCTAAGGAGTCTTCGGCCGAGGGATCTGTAAACGCTGGGAACATCTCA 1102
Qy      1081 GATCTTTCAGGGTATCTTACTAGCACACAGATGATCATTTAGGAGTGAATATCTA 1140
Db      1103 GATCTTTCAGGGTATCTTACTAGCACACAGATGATCATTTAGGAGTGAATATCTA 1162
Qy      1141 ATCAACATCATCTCAGTGTCTTGGCCATACTGAATTCATTTCCACTTTTGTGCCA 1200
Db      1163 ATCAACATCATCTCAGTGTCTTGGCCATACTGAATTCATTTCCACTTTTGTGCCA 1222
Qy      1201 TTTCGAAGACCTCAAAATGTCAATTCATTAATATACAGGATTAATTTTAAACC 1260
Db      1223 TTTCGAAGACCTCAAAATGTCAATTCATTAATATACAGGATTAATTTTAAACC 1282
Qy      1261 TGGGAATTCATTAATGTACATGACAGCTATGGGAATTTAATTCATTTTGTTCACAGT 1320
Db      1283 TGGGAATTCATTAATGTACATGACAGCTATGGGAATTTAATTCATTTTGTTCACAGT 1342
Qy      1321 GCAAAAGATGACTAGTCTTATCCCTCCCTCTTGTGTGATTTTTCACATTAAGT 1380
Db      1343 GCAAAAGATGACTAGTCTTATCCCTCCCTCTTGTGTGATTTTTCACATTAAGT 1402
Qy      1381 TAAATGTGTTAGCCTGTACAGAGGCTGTATACACACAGCCTCCCATCCCTCCAGC 1440
Db      1403 TAAATGTGTTAGCCTGTACAGAGGCTGTATACACACAGCCTCCCATCCCTCCAGC 1462
Qy      1441 CTTATCTGTCATCACCATCAACCCCTCCCATNYSACTAAACAATCTAATCTGTAAT 1500
Db      1463 CTTATCTGTCATCACCATCAACCCCTCCCATNYSACTAAACAATCTAATCTGTAAT 1522
Qy      1501 CCTTGACATGTGAGGNCATATCTTTCCTTCCTGAGAGAGCTCTTCTGTCTCT 1560
Db      1523 CCTTGACATGTGAGGNCATATCTTTCCTTCCTGAGAGAGCTCTTCTGTCTCT 1582
Qy      1561 AANTCTAGAATGATTAAGTTTGAATTAAGTGAATCTTACTTCATGCAAAAGAGG 1620
Db      1583 AANTCTAGAATGATTAAGTTTGAATTAAGTGAATCTTACTTCATGCAAAAGAGG 1642
Qy      1621 ACACATATGATGATTCATCATGAGACAGCAACATTAATAAGTGAATTTGATTA 1680
Db      1643 ACACATATGATGATTCATCATGAGACAGCAACATTAATAAGTGAATTTGATTA 1702
Qy      1681 AGAGTTTGAATTAATTAATGAATGAAGCAAGCAAGAGGAGTCTTAATGGGACGTT 1740
Db      1703 AGAGTTTGAATTAATTAATGAATGAAGCAAGCAAGAGGAGTCTTAATGGGACGTT 1762
Qy      1741 TGTAGCCGTGGATGTGAAGMAAGGAGGAGGAACTCTAGATCTTATATATATACT 1800
Db      1763 TGTAGCCGTGGATGTGAAGMAAGGAGGAGGAACTCTAGATCTTATATATATACT 1822
Qy      1801 CATTTCTATCTATCATCATATATCAACAAAGCTTTTACAGATTCATGAGAGCAAA 1860

```

```

Db      1823 CATTTCTATCTATCATCATATATCAACAAAGCTTTTCAAGATTCATGAGTCAAA 1882
Qy      1861 TCCCAAGAGTATACCTTATTCATTTATGAGATGGGCTTATACAATTTTGGCAATCA 1920
Db      1883 TCCCAAGAGTATACCTTATTCATTTATGAGATGGGCTTATACAATTTTGGCAATCA 1942
Qy      1921 TACTGTGACTATATCTCAACTTTGAGATGTGTTGCTTCCTGTAGTTAATTTGAAGAAATA 1980
Db      1943 TACTGTGACTATATCTCAACTTTGAGATGTGTTGCTTCCTGTAGTTAATTTGAAGAAATA 2002
Qy      1981 GGGCACTCTTGTGAGCCACTTTAGGTTCTACTCTGCGAATTAAGAAATTTACAAAGA 2037
Db      2003 GGGCACTCTTGTGAGCCACTTTAGGTTCTACTCTGCGAATTAAGAAATTTACAAAGA 2059

RESULT 8
AAV62430
ID AAV62430 standard; cDNA; 3582 BP.
XX
AC AAV62430;
XX
DT 30-DEC-1998 (first entry)
XX
DE Prostate cancer antigen (PCA3) wild-type cDNA.
XX
KW Prostate cancer antigen cDNA; PCA3; prostatic cancer;
KW PC; ds.
XX
OS Homo sapiens.
XX
FH Key
FH CDS 401..556
FT /*tag= a
FT /*product= "PCA3 protein"
FT polyA_signal 983..987
FT /*tag= b
FT polyA_signal 2041..2046
FT /*tag= c
FT polyA_signal 2597..2602
FT /*tag= d
FT polyA_signal 3494..3496
FT /*tag= e
XX
PN W09845420-A1.
XX
PD 15-OCT-1998.
XX
PF 09-APR-1998; 98WO-CA00346.
XX
PR 10-APR-1997; 97US-0041836.
XX
(DIAG-) DIAGNOCURE INC.
XX
Bussemakers MJG;
XX
WPI: 1998-568347/48.
XX
P-PSDB: AAM79738.
XX
New nucleic acid encoding prostate cancer antigen 3 - for diagnosis,
PT prevention and treatment of prostatic cancer
XX
Claim 3; Fig 5B-5F; 11pp; English.
XX
The present sequence represents the prostate cancer antigen (PCA3)
CC wild-type cDNA sequence comprising of exons 1, 2, 3, 4a-4d of the
CC PCA3 gene. The invention claims for PCA3 cDNA variants and the
CC proteins they encode. The invention also claims for antibodies
CC against PCA3 protein. The antibodies are claimed to be useful for
CC detecting PCA3 protein in immunoassay tests, for diagnosing, assessing
CC and prognosing of prostatic cancer (PC). Antibodies, optionally
CC coupled to a cytotoxin or radioisotope, and nucleic acids antisense
CC to PCA3 cDNA are claimed to be useful for treating PC, while determining
CC elevated levels of PCA3 (as RNA or protein) is useful for detecting a

```

CC predisposition to development of PC, e.g. in prenatal tests. Detecting
CC PCA3 protein allows differentiation between malignant and benign
CC prostatic disease, and the level of PCA3 expression allows correlation
CC with the grade of tumour. PCA3 protein and its fragments are also
CC claimed to be useful in vaccines for preventing PC; in drug screens
CC for identifying specific (ant)agonists (potentially useful
CC therapeutically) and for studying protein-DNA interactions.

XX Sequence 3582 BP; 1052 A; 788 C; 679 G; 1063 T; 0 other;

Query Match 77.5%; Score 1578; DB 19; Length 3582;

Best Local Similarity 99.6%; Pred. No. 0;

Matches 2028; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1 AGAAGCTGCAATCAGAAAAACAGAGGGAGATTGTTGCTGCTGCAGCCGAGGAGACAG 60
DB 23 AGAAGCTGCGATCAGAAAAACAGAGGGAGATTGTTGCTGCTGCAGCCGAGGAGACAG 82
QY 61 GAAGATCTGATGCTGGGAAGACCTGATATACAGAGGAATTACAAACATATCTTAG 120
DB 83 GAAGATCTGATGCTGGGAAGACCTGATATACAGAGGAATTACAAACATATCTTAG 142
QY 121 TGTTCATTAACACCAAGATTAATTAAGTAGAAGCTAGTCCGCTGATCTCCAGT 180
DB 143 TGTTCATTAACACCAAGATTAATTAAGTAGAAGCTAGTCCGCTGATCTCCAGT 202
QY 181 GACACAGGCTGATCACCATCGACGCACTTCTGTAGTACTAGTGCAGCAAAAGAGA 240
DB 203 GACACAGGCTGATCACCATCGACGCACTTCTGTAGTACTAGTGCAGCAAAAGAGA 262
QY 241 CTACAGACATCTCAAGGCGAGGGGTGAGAAATTAAGAAAGCTGTGACTTTACATCTGA 300
DB 263 CTACAGACATCTCAAGGCGAGGGGTGAGAAATTAAGAAAGCTGTGACTTTACATCTGA 322
QY 301 GGGCACACATCTCTGTAATGAGATTAATTAACATCTAGAAAACAGACAGATGACATA 360
DB 323 GGGCACACATCTCTGTAATGAGATTAATTAACATCTAGAAAACAGACAGATGACATA 382
QY 361 TAATGTCTAAGTAGTGAATGATTTTTCACATTTCCAGCCCTTTAAATATCCACACACA 420
DB 383 TAATGTCTAAGTAGTGAATGATTTTTCACATTTCCAGCCCTTTAAATATCCACACACA 442
QY 421 CAGGAAGCACAAAAGGAGACAGAGATCCCTGGGAGAAATGCCCGGCGCCCAATCTGGG 480
DB 443 CAGGAAGCACAAAAGGAGACAGAGATCCCTGGGAGAAATGCCCGGCGCCCAATCTGGG 502
QY 481 TCATCGATGAGCCTCGCCCTGTGCTGTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 540
DB 503 TCATCGATGAGCCTCGCCCTGTGCTGTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 562
QY 541 AATTGATGTGCTCTTAAGAGATGGCAGAGAAAACAGATCTGTGTGTGATATTTATTTG 600
DB 563 AATTGATGTGCTCTTAAGAGATGGCAGAGAAAACAGATCTGTGTGTGATATTTATTTG 622
QY 601 AATGGGATTACAGATTGAATGAATGATCAACAAAGTAGCAATTCATGAGAGAAACA 660
DB 623 AATGGGATTACAGATTGAATGAATGATCAACAAAGTAGCAATTCATGAGAGAAACA 682
QY 661 GAGGAGAAAATCTTGATGCTTCAACAAGATGCAACAACAAATGGAATGATGATGATG 720
DB 683 GAGGAGAAAATCTTGATGCTTCAACAAGATGCAACAACAAATGGAATGATGATGATG 742
QY 721 ACATGAGGAGCCAGAGCTGGGAGAGATTAACAGAGGGGAGAGAGGTCAGAGATCTGGCC 780
DB 743 ACATGAGGAGCCAGAGCTGGGAGAGATTAACAGAGGGGAGAGAGGTCAGAGATCTGGCC 802
QY 781 CTGCTGCTTAATGCTGCTTCAATACCAATGATTTTCAATTTCTTAACCTCAAAAACA 840
DB 803 CTGCTGCTTAATGCTGCTTCAATACCAATGATTTTCAATTTCTTAACCTCAAAAACA 862
QY 841 AGCTGTTGTAATATCTGATCTACAGTTCCTTCTGGGCCCAACATTTCTCATATATCCA 900
DB 863 AGCTGTTGTAATATCTGATCTACAGTTCCTTCTGGGCCCAACATTTCTCATATATCCA 922

QY 901 GCCACACTCATTTTAAATATTAATAGTCCAGATCTGACTGACCTTTCTACACTGTAG 960
DB 923 GCCACACTCATTTTAAATATTAATAGTCCAGATCTGACTGACCTTTCTACACTGTAG 982
QY 961 AATTAACATTAATCTATTTTGTTCAAAGACCTTGCTGCTGCTTATATGATGCTGACT 1020
DB 983 AATTAACATTAATCTATTTTGTTCAAAGACCTTGCTGCTGCTTATATGATGCTGACT 1042
QY 1021 GTTTTTCCTAAGAGATGTTTCTGGCCGAGGAGATCTGTGAACAGAGCTGGAGATCTCAA 1080
DB 1043 GTTTTTCCTAAGAGATGTTTCTGGCCGAGGAGATCTGTGAACAGAGCTGGAGATCTCAA 1102
QY 1081 GATCTTTCAGAGGTTATCTTACTAGCACACAGATGATCATTAACGAGTGAATATCTA 1140
DB 1103 GATCTTTCAGAGGTTATCTTACTAGCACACAGATGATCATTAACGAGTGAATATCTA 1162
QY 1141 ATCAACATCATCTCTGACTGTCTTGGCCATACAGAAATTTATTTCCACTTTGTGCCCA 1200
DB 1163 ATCAACATCATCTCTGACTGTCTTGGCCATACAGAAATTTATTTCCACTTTGTGCCCA 1222
QY 1201 TTCTCAAGACCTCAAAATGATCATTCATTAATATACAGAGATTAACCTTTTATTAAC 1260
DB 1223 TTCTCAAGACCTCAAAATGATCATTCATTAATATACAGAGATTAACCTTTTATTAAC 1282
QY 1261 TGGAGAATTCAAATGTTTACATGACAGCTATGGAATTTAAATTAATTTTGTTCAGT 1320
DB 1283 TGGAGAATTCAAATGTTTACATGACAGCTATGGAATTTAAATTAATTTTGTTCAGT 1342
QY 1321 GCAAAAGTACTAAGTCTTATTCCTCCCTTTGTTGATTTTTCAGATATAAGT 1380
DB 1343 GCAAAAGTACTAAGTCTTATTCCTCCCTTTGTTGATTTTTCAGATATAAGT 1402
QY 1381 TAAATGCTTAGCCTTGTACTGAGGCTGTATACAGACACACCTTCGCCCTCCAGC 1440
DB 1403 TAAATGCTTAGCCTTGTACTGAGGCTGTATACAGACACACCTTCGCCCTCCAGC 1462
QY 1441 CTATCTGTCTACATCAATCAACCCCTCCATPNTSACCTAAACAATACTAATCTGTAAT 1500
DB 1463 CTATCTGTCTACATCAATCAACCCCTCCATPNTSACCTAAACAATACTAATCTGTAAT 1522
QY 1501 CCTTGAACATGTCAGGACATACATTTTCTGCTGCTGAGAGCTCTTCCCTGCTCTT 1560
DB 1523 CCTTGAACATGTCAGGACATACATTTTCTGCTGCTGAGAGCTCTTCCCTGCTCTT 1582
QY 1561 AANTCTAGATGATGTAAGTTTGAATAGTTGACTATCTTACTCATGCAAGAAGGG 1620
DB 1583 AANTCTAGATGATGTAAGTTTGAATAGTTGACTATCTTACTCATGCAAGAAGGG 1642
QY 1621 ACACATATGAGATTCATCATGAGAGACGCAAAATCTAAGAGTAAATTTGATTTA 1680
DB 1643 ACACATATGAGATTCATCATGAGAGACGCAAAATCTAAGAGTAAATTTGATTTA 1702
QY 1681 AGAGTTAGTAATTAATTAATGAATGCAAGAKCCACAGAGGATGTTTGGGGCCAGTT 1740
DB 1703 AGAGTTAGTAATTAATTAATGAATGCAAGAKCCACAGAGGATGTTTGGGGCCAGTT 1762
QY 1741 TGTAAAGCTGGAGTGTGAAGMAAGGACAGGAACCTCATAGTATCTTATATATATACTT 1800
DB 1763 TGTAAAGCTGGAGTGTGAAGMAAGGACAGGAACCTCATAGTATCTTATATATATACTT 1822
QY 1801 CATTTCTATCTCTATCATCAATATCCAAACAGCTTTTACAGAAATTCATGCAAGTCAAA 1860
DB 1823 CATTTCTATCTCTATCATCAATATCCAAACAGCTTTTACAGAAATTCATGCAAGTCAAA 1882
QY 1861 TCCCAAGGTAACCTTTATCCATTCATGAGTGAAGGCTTGAAGATTTTGGCAATCA 1920
DB 1883 TCCCAAGGTAACCTTTATCCATTCATGAGTGAAGGCTTGAAGATTTTGGCAATCA 1942
QY 1921 TACTGTCTCAATTAATCAACTTTGAGATGTGTTGCTGTGATTAATTTGAAGAATAA 1980
DB 1943 TACTGTCTCAATTAATTAATCAACTTTGAGATGTGTTGCTGTGATTAATTTGAAGAATAA 2002

Qy 1981 GGGACATCTGTGACCCACTTATGGCTTCTGCAATTAAGATTACAAAGA 2037
|||||
Db 2003 GGGACATCTGTGACCCACTTATGGCTTCTGCAATTAAGATTACAAAGA 2059

RESULT 9
AAA06689/c
ID AAA06689 standard; cDNA; 2426 BP.

XX AAA06689;

DT 13-JUN-2000 (first entry)

DE Human immunogenic prostate tumour protein cDNA sequence SEQ ID NO:470.

KM Human; prostate cancer; diagnosis; tumour; gene therapy; detection;

XX Immunogenic; cytosolic; vaccine; ss.

OS Homo sapiens.

PN MO200004149-A2.

PD 27-JAN-2000.

PF 14-JUL-1999; 99WO-US15838.

PR 14-JUL-1998; 98US-0115453.

PR 14-JUL-1998; 98US-0116134.

PR 23-SEP-1998; 98US-0159812.

PR 15-JAN-1999; 99US-0232149.

PR 15-JAN-1999; 99US-0232880.

PR 09-APR-1999; 99US-0288946.

PA (CORI-) CORIXA CORP.

PI Dillon DC, Harlocker SL, Yugu J, Xu J, Mitcham JL;

XX WPI: 2000-171268/15.

XX New polypeptide useful for treating and diagnosing prostate cancer

PT comprises an immunogenic portion of prostate tumor protein -

PS Claim 1: Page 261-262; 263pp; English.

CC The present invention describes isolated polypeptides, comprising an
CC immunogenic portion of a prostate tumor protein (PTP). The polypeptides
CC and polynucleotides encoding them have cytostatic activity and can be
CC used in vaccines and in gene therapy. The polypeptides and
CC polynucleotides encoding them, antigen presenting cells which express
CC the polypeptides, antibodies against the polypeptides and vaccines
CC comprising them can be used for inhibiting the development of prostate
CC cancer in a patient. The polypeptides can be used to generate antibodies
CC or anti-idiotypic antibodies for passive immuno therapy. A portion of
CC the polynucleotides encoding the polypeptides can be used as a probe or
CC to modulate the expression of the polypeptides. AAA06689 to AAA06691 and
CC AA182000 to AA182020 represent sequences used in the exemplification of
CC the present invention.

XX Sequence 2426 BP: 717 A; 476 C; 548 G; 685 T; 0 other;

Qy Query Match 56.7%; Score 1154; DB 21; Length 2426;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 263 GGTGAATAAAGAGGCTGCTTACCATCTGAGCCACACATCTGCTGAATGG 322

1769 GGTGAATAAAGAGGCTGCTTACCATCTGAGCCACACATCTGCTGAATGG 1710

Qy 323 AGATTAATTACATCTAGAAAACAGCAAGATGACATAATATGTCTAGTAGTGCATGT 382

1709 AGATTAATTACATCTAGAAAACAGCAAGATGACATAATATGTCTAGTAGTGCATGT 1650

Qy 383 TTTTCACATTTTCAGCCCTTTAAATATCCACACACAGGAGACACAAAAGAGAC 442

1649 TTTTCACATTTTCAGCCCTTTAAATATCCACACACAGGAGACACAAAAGAGAC 1590

Qy 443 AGAGATCCCTGGGAGAAATGCCCGCCGCATCTTGGGTATCATGATGAGCCCTGCT 502

1589 AGAGATCCCTGGGAGAAATGCCCGCCGCATCTTGGGTATCATGATGAGCCCTGCT 1530

Qy 503 GCCTGTCCTCCGCTTGTGAGGAGAGACATTAAGAAATGAATGATGTCTTAAAGA 562

1529 GCCTGTCCTCCGCTTGTGAGGAGAGACATTAAGAAATGAATGATGTCTTAAAGA 1470

Qy 563 TGGCAGGAAAAACAGATCCTGTGTGATATTTATTTAGCGGATTCAGATTGAAT 622

1469 TGGCAGGAAAAACAGATCCTGTGTGATATTTATTTAGCGGATTCAGATTGAAT 1410

Qy 623 GAAGTCACAAAGTGAATTTACCAATGAGAGAAAACAGACAGAAAATCTTGATGCTT 682

1409 GAAGTCACAAAGTGAATTTACCAATGAGAGAAAACAGACAGAAAATCTTGATGCTT 1350

Qy 683 CACAAGACATGCAACAAAACAAATGGAATGATGATGATGATGATGATGATGATG 742

1349 CACAAGACATGCAACAAAACAAATGGAATGATGATGATGATGATGATGATGATG 1290

Qy 743 AGGAGATACCAAGGAGGAGAGGATTCAGGATTCAGGATTCAGGATTCAGGATTC 802

1289 AGGAGATACCAAGGAGGAGAGGATTCAGGATTCAGGATTCAGGATTCAGGATTC 1230

Qy 803 ATAAACCAATGATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTT 862

1229 ATAAACCAATGATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTT 1170

Qy 863 TACGTTCTCTTGGGCCCCAACATTTCTCATATATCCAGCCACTCTTTTATATTT 922

1169 TACGTTCTCTTGGGCCCCAACATTTCTCATATATCCAGCCACTCTTTTATATTT 1110

Qy 923 AGTCCAGATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 982

1109 AGTCCAGATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1050

Qy 983 AAAGACCTTCTGTTGCTGCTTATATATATATATATATATATATATATATATATAT 1042

1049 AAAGACCTTCTGTTGCTGCTTATATATATATATATATATATATATATATATATAT 990

Qy 1043 GCCCAGGGGATCTGGAACAGGCTGGGAAGCATCTCAAGATCTTCCAGGGTTATCTTA 1102

989 GCCCAGGGGATCTGGAACAGGCTGGGAAGCATCTCAAGATCTTCCAGGGTTATCTTA 930

Qy 1103 CTAGCAGACAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1162

929 CTAGCAGACAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 870

Qy 1163 TTGCCATACGAAATTAATTTCCATTTTCCATTTTCCATTTTCCATTTTCCATTTT 1222

869 TTGCCATACGAAATTAATTTCCATTTTCCATTTTCCATTTTCCATTTTCCATTTT 810

Qy 1223 TTCCATTAATATACAGATTAATTTTATTTTATTTTATTTTATTTTATTTTATTTT 1282

809 TTCCATTAATATACAGATTAATTTTATTTTATTTTATTTTATTTTATTTTATTTT 750

Qy 1283 CAGCTATGGAATTAATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTAT 1342

749 CAGCTATGGAATTAATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTAT 690

Qy 1343 TCCCTCCCTTTGTTGATTTTTCAGATTAATTTTATTTTATTTTATTTTATTTTAT 1402

669 TCCCTCCCTTTGTTGATTTTTCAGATTAATTTTATTTTATTTTATTTTATTTTAT 630

Qy 1403 AGGCTGTATACAGC 1416

629 AGGCTGTATACAGC 616

RESULT 10
AAS63898/c
ID AAS63898 standard: cDNA; 2426 BP.
XX
XX AAS63898:
XX
XX 29-JAN-2002 (first entry)
XX
XX Human prostate cDNA sequence #432.
XX
XX Human; prostate cancer; ss; cytostatic; immunostimulant; tumour.
XX
XX Homo sapiens.
XX
XX WO200173032-A2.
XX
XX 04-OCT-2001.
XX
XX 27-MAR-2001; 2001MO-US09919.
XX
XX 27-MAR-2000; 2000US-0536857.
XX
XX 09-MAY-2000; 2000US-0568100.
XX
XX 12-MAY-2000; 2000US-0570737.
XX
XX 13-JUN-2000; 2000US-0593793.
XX
XX 27-JUN-2000; 2000US-0605783.
XX
XX 10-AUG-2000; 2000US-0636215.
XX
XX 29-AUG-2000; 2000US-0651236.
XX
XX 06-SEP-2000; 2000US-0657279.
XX
XX 02-OCT-2000; 2000US-0679426.
XX
XX 10-OCT-2000; 2000US-0685166.
XX
XX (CORI-) CORIXA CORP.
XX
XX Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Kalos MD,
PI Fanger GR, Retter MW, Stolk JA, Day CH, Vedvick TS, Carter D;
PI Li SX, Wang A, Skelky YAM, Hepler WT, Henderson RA;
XX
XX WPI; 2001-639232/73.
XX
XX New human prostate-specific polypeptides and polynucleotides useful for
PT the diagnosis and treatment of cancer, especially prostate cancer -
XX
XX Claim 1; Page 386; 579pp; English.
XX
XX The invention relates to isolated prostate-specific
CC polynucleotides, polypeptides, fusion proteins of the polypeptides,
CC antibodies raised against the polypeptides (or antigenic epitopes
CC derived from them) and antigen-presenting cells expressing the
CC polypeptides. The antibodies are useful for detecting the presence of
CC cancer, especially prostate cancer. The polypeptides, polynucleotides and
CC the antigen-presenting cells are useful for stimulating and/or expanding
CC T cells specific for a tumour protein, and for inhibiting the development
CC of cancer especially prostate cancer. Compositions comprising the
CC polynucleotide and/or polypeptide are useful for stimulating an immune
CC response, and for treating cancer. The oligonucleotide is useful for
CC detecting cancer. The present sequence is a prostate specific
CC polynucleotide of the invention.
XX
XX Sequence 2426 BP; 717 A; 476 C; 548 G; 685 T; 0 other;
SQ
Query Match 56.7%; Score 1154; DB 22; Length 2426;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1649 TTTTGACATTTCCAGCCCTTTAAATATCCACACACAGGAAGCAAAAGGAAGCAC 1590
Qy 443 AGAGATCCCTGGGAGAAATGCCGGCGGCATCTTGGGTCATGATGAGCCTGCCCTG 502
Db 1589 AGAGATCCCTGGGAGAAATGCCGGCGGCATCTTGGGTCATGATGAGCCTGCCCTG 1530
Qy 503 GCCTGTCCCGCTTGAGGAGAGACATTAGAAAATGAATGTATGTCTCTTAAAGGA 562
Db 1529 GCCTGTCCCGCTTGAGGAGAGACATTAGAAAATGAATGTATGTCTCTTAAAGGA 1470
Qy 563 TGGGACAGAAAACAGATCCCTGTGTGATTTATTTGAACGGGATTTACAGATTTGAAT 622
Db 1469 TGGGACAGAAAACAGATCCCTGTGTGATTTATTTGAACGGGATTTACAGATTTGAAT 1410
Qy 623 GAAGTCAAAAAGTACATTTACCAATGAGAGAAAACAGACGAGAAAATCTTGATGCTT 682
Db 1409 GAAGTCAAAAAGTACATTTACCAATGAGAGAAAACAGACGAGAAAATCTTGATGCTT 1350
Qy 683 CACAAGACATGCAACAAACAAATGGAATATCTGTATGACATGAGCAGCCAAAGCTGGG 742
Db 1349 CACAAGACATGCAACAAACAAATGGAATATCTGTATGACATGAGCAGCCAAAGCTGGG 1290
Qy 743 AGAGATTAACCAAGGGGACAGAGGTGAGATTTCTGGCCCTGCTTAAACCTGGGCTC 802
Db 1289 AGAGATTAACCAAGGGGACAGAGGTGAGATTTCTGGCCCTGCTTAAACCTGGGCTC 1230
Qy 803 ATAAACCAATCATTTATATTTCTTAACCCCAAAACAAAGCTTGTATATCTGATCTC 862
Db 1229 ATAAACCAATCATTTATATTTCTTAACCCCAAAACAAAGCTTGTATATCTGATCTC 1170
Qy 863 TACGGTTCCTTCTGGGCCCCAACAATTCCTCAATATCCAGCACATCATTTTAAATTT 922
Db 1169 TACGGTTCCTTCTGGGCCCCAACAATTCCTCAATATCCAGCACATCATTTTAAATTT 1110
Qy 923 AGTTCCAGATCTGTCTGTGACCTTCTCACTGATAGAAATACATTTACTGATTTGTC 982
Db 1109 AGTTCCAGATCTGTCTGTGACCTTCTCACTGATAGAAATACATTTACTGATTTGTC 1050
Qy 983 AAAGACCCTTCTGTGTGCTGCTCAATATATGATGACTGTTTCTTAAGAGATGTCG 1042
Db 1049 AAAGACCCTTCTGTGTGCTGCTCAATATATGATGACTGTTTCTTAAGAGATGTCG 990
Qy 1043 GCCCAGGGATCTGTGAACAGGCTGGGAAGCATCTCAAGTCTTCCAGGTTATACTTA 1102
Db 989 GCCCAGGGATCTGTGAACAGGCTGGGAAGCATCTCAAGTCTTCCAGGTTATACTTA 930
Qy 1103 CTAGCACACAGATGATCATTTACGAGTGAATATCTTAATCAACATCATCTCAGTGTG 1162
Db 929 CTAGCACACAGATGATCATTTACGAGTGAATATCTTAATCAACATCATCTCAGTGTG 870
Qy 1163 TTGCCCATCTGAAATTCATTTCCCACTTTGTGCCCATCTCAAGACCTCAAAATGTCA 1222
Db 869 TTGCCCATCTGAAATTCATTTCCCACTTTGTGCCCATCTCAAGACCTCAAAATGTCA 810
Qy 1223 TTCCATTAATATACAGGATTAATTTTCTTAACTCGGAAGTAATCAAGTTGCATG 1282
Db 809 TTCCATTAATATACAGGATTAATTTTCTTAACTCGGAAGTAATCAAGTTGCATG 750
Qy 1283 CAGCTATGGAATTAATTAATATATTTGTTTCCAGTGAAGATGACTAATCTCTTA 1342
Db 749 CAGCTATGGAATTAATTAATATATTTGTTTCCAGTGAAGATGACTAATCTCTTA 690
Qy 1343 TCCCTCCCTCTTGTGTGATTTTCTTCCAGTGAAGATGACTAATCTCTTACTG 1402
Db 689 TCCCTCCCTCTTGTGTGATTTTCTTCCAGTGAAGATGACTAATCTCTTACTG 630
Qy 1403 AGGCTGATATCAGC 1416
Db 629 AGGCTGATATCAGC 616

RESULT 11

AAH93805/c
ID AAH93805 standard; cDNA; 2426 BP.
XX
AC AAH93805;
XX
DT 04-OCT-2001 (first entry)
XX
DE Human prostate-specific cDNA sequence p710P #3.
XX
XX Human; prostate cancer; prostate-specific; diagnosis; vaccine;
KM cytosolic; gene therapy; metastasis; ss.
XX
OS Homo sapiens.
XX
PM WO200151633-A2.
XX
PD 19-JUL-2001.
XX
PF 16-JAN-2001; 2001MO-US01574.
XX
PR 14-JAN-2000; 2000US-0483672.
XX
PA (CORI-) CORIXA CORP.
XX
PI Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Reed SG;
PI Kalos MD, Fanger GR, Day CH, Retter MW, Stolk JA, Skelley YAM;
PI Wang A, Meagher MJ;
XX
DR WPI; 2001-425873/45.
XX
XX
PT New polynucleotide encoding a prostate-specific protein, for
PT diagnosing, monitoring and treating prostate cancer in a patient and
PT for use in vaccines -
XX
PS Claim 1: Page 384-385; 543pp; English.
XX
CC The present invention describes polynucleotide sequences (I) which encode
CC prostate-specific proteins (II). (I) and (II) have cytosolic activity,
CC and can be used in vaccine production and gene therapy. (I), (II),
CC antibodies to (II), fusion proteins comprising (II), and isolated
CC T cells prepared using (I) or (II) are used treat cancer in a patient.
CC (I) and the antibodies are also used in the detection of cancer in a
CC patient. The cancer that is diagnosed or treated is particularly
CC prostate cancer. (I) and (II) can be used in vaccines. The antibodies or
CC (I) can be used for monitoring the progression of cancer in a patient.
CC (I) and (II) can also be used to improve diagnostic and therapeutic
CC methods for prostate cancer. They can indicate the level of metastasis
CC as well as the prostate volume. AAH93357 to AAH93944 and AAH01115 to
CC AAH01318 represent polynucleotide and amino acid sequences used in the
CC exemplification of the present invention.
XX
SQ Sequence 2426 BP; 717 A; 476 C; 548 G; 685 T; 0 other;
XX
Query Match 56.7%; Score 1154; DB 22; Length 2426;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 263 GGTGAGAAATAGAAAGGCTGCTGACTTTACCATCTGAGGCCACACATCTGCTGAATGG 322
DB 1769 GGTGAGAAATAGAAAGGCTGCTGACTTTACCATCTGAGGCCACACATCTGCTGAATGG 1710
OY 323 AGATTATTAACATCTGTAAGAAAGCAAGATGACAAATTAATGCTAGTGTGACATGT 382
DB 1709 AGATTATTAACATCTGTAAGAAAGCAAGATGACAAATTAATGCTAGTGTGACATGT 1650
OY 383 TTTTGCACATTTCCAGCCCTTTTAAATATCCACACACAGGAAGCAGAAAAGAGAC 442
DB 1649 TTTTGCACATTTCCAGCCCTTTTAAATATCCACACACAGGAAGCAGAAAAGAGAC 1590
OY 443 AGAGATCCCTGGGAGAAATGCGCGCCGCAATCTTGGTCAATGATGAGCCTGCGCTGT 502
DB 1589 AGAGATCCCTGGGAGAAATGCGCGCCGCAATCTTGGTCAATGATGAGCCTGCGCTGT 1530

OY 503 GCCTGTCCCGCTTGTGAGGAGAGACATTAAGAAATGATGTGCTCTTAAGCA 562
DB 1529 GCCTGTCCCGCTTGTGAGGAGAGACATTAAGAAATGATGTGCTCTTAAGCA 1470
OY 563 TGGGAGAGAAACAGATCCTGTGTGATATTTATTTAGGAGATTAACATTTGAAT 622
DB 1469 TGGGAGAGAAACAGATCCTGTGTGATATTTATTTAGGAGATTAACATTTGAAT 1410
OY 623 GAATGCACAAAGTGAACATTTACCAATGAGAGAAACAGACAGAAATCTTGATGCTT 682
DB 1409 GAATGCACAAAGTGAACATTTACCAATGAGAGAAACAGACAGAAATCTTGATGCTT 1350
OY 683 CACAAGACATGCAACAAACAAATGAGTACGTGATGATGACATGAGGAGCCAGCTGGGG 742
DB 1349 CACAAGACATGCAACAAACAAATGAGTACGTGATGATGACATGAGGAGCCAGCTGGGG 1290
OY 743 AGAGATTAACACAGGGGAGAGGGTCAAGATTTCTGGCCCTGCTTAACCTGCTTC 802
DB 1289 AGAGATTAACACAGGGGAGAGGGTCAAGATTTCTGGCCCTGCTTAACCTGCTTC 1230
OY 803 ATACCAAAATCATTTCAATTTCTAACCCTCAAAACAAAGCTGTGTAAATCTGATCTC 862
DB 1229 ATACCAAAATCATTTCAATTTCTAACCCTCAAAACAAAGCTGTGTAAATCTGATCTC 1170
OY 863 TACGTTCTCTTGGGGCCCAACATCTGCTATATCCAGCCACACTCAATTTTATATT 922
DB 1169 TACGTTCTCTTGGGGCCCAACATCTGCTATATCCAGCCACACTCAATTTTATATT 1110
OY 923 AGTTCCAGATCTGACTGTGACCTTTCTACACTTAATTAATCAATTTCTGATCTC 982
DB 1109 AGTTCCAGATCTGACTGTGACCTTTCTACACTTAATTAATCAATTTCTGATCTC 1050
OY 983 AAAGACCTTGCTGTGCTGCTTAATTAATTAATTAATTAATTAATTAATTAATTA 1042
DB 1049 AAAGACCTTGCTGTGCTGCTTAATTAATTAATTAATTAATTAATTAATTAATTA 990
OY 1043 GCCCGGGGATCTGGAACAGGCTGGAAGCATCAAGATCTTCCAGGGTAACTTA 1102
DB 989 GCCCGGGGATCTGGAACAGGCTGGAAGCATCAAGATCTTCCAGGGTAACTTA 930
OY 1103 CTAGCAGACAGATGATCATTAAGGAGTAATTAATTAATTAATTAATTAATTAATTA 1162
DB 929 CTAGCAGACAGATGATCATTAAGGAGTAATTAATTAATTAATTAATTAATTAATTA 870
OY 1163 TTGCCCACTGAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1222
DB 869 TTGCCCACTGAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 810
OY 1223 TTCCATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1282
DB 809 TTCCATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 750
OY 1283 CAGCTATGGAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1342
DB 749 CAGCTATGGAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 690
OY 1343 TCCCTCCCTTTGTTGATTTTTCAGATTAAGTTAAATGCTTAAGCTTACTG 1402
DB 689 TCCCTCCCTTTGTTGATTTTTCAGATTAAGTTAAATGCTTAAGCTTACTG 630
OY 1403 AGGCTGTATACAGC 1416
DB 629 AGGCTGTATACAGC 616
RESULT 12
AAH85119/c
ID AAH85119 standard; cDNA; 2426 BP.
XX
AC AAH85119;
XX
DT 25-SEP-2001 (first entry)
XX

DE Human prostate-specific cDNA sequence P710P #3.
XX
KM Human; prostate cancer; therapy; diagnosis; cat eye syndrome;
KM chromosome 22q11.2; prostate-specific protein; chromosome 1;
KM prostate specific antigen; PSA; ss.
XX
OS Homo sapiens.
XX
PN W0200134802-A2.
PD 17-MAY-2001.
XX
PE 09-NOV-2000; 2000MO-US30904.
XX
PR 12-NOV-1999; 99US-0439313.
PR 18-NOV-1999; 99US-0443686.
XX
PA (CORI-) CORIXA CORP.
XX
PI Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Reed SG;
PI Kalos MD, Reltter MW, Stolk JA, Day CH, Skeiky YAM, Wang A;
DR WPI; 2001-308785/32.
XX
PT Isolated polypeptide comprising at least an immunogenic portion of a
PT prostate-specific protein, useful in the diagnosis and therapy of
PT prostate cancer -
XX
PS Claim 5; Page 284; 325pp; English.
XX
CC The present invention describes an isolated polypeptide (P1) comprising
CC at least an immunogenic portion of a prostate-specific protein, or its
CC variant. Also described are polynucleotides (N1) encoding (P1). (P1) and
CC (N1) have cytostatic activity and can be used in vaccine production.
CC The polypeptides, nucleic acids and antibodies from the present
CC invention are useful in the diagnosis and therapy of prostate cancer.
CC Prostate specific genes P704P, P712P, P774P, P775P and B305D are located
CC in a genomic region on chromosome 22q11.2 known as the Cat Eye Syndrome
CC region. Prostate specific antigen (PSA) P501S was located on
CC chromosome 1. AAH84671 to AAH85143 and AAG99000 to AAG99077 represent
CC chromonucleotide and polypeptide sequences used in the exemplification
CC of the present invention.
XX
SQ Sequence 2426 BP; 717 A; 476 C; 548 G; 685 T; 0 other;

Query Match 56.7%; Score 1154; DB 22; Length 2426;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 263 GGTGAGAAATTAAGAAGCGTCTGACTTTACCATCTGAGGCCACACATCTGCTGAATGG 322
DB 1769 GGTGAGAAATTAAGAAGCGTCTGACTTTACCATCTGAGGCCACACATCTGCTGAATGG 1710
QY 323 AGATTAATTAACATCACTAGAAACAGCAAGATGACATTAATGCTTAAGTAGACATGT 382
DB 1709 AGATTAATTAACATCACTAGAAACAGCAAGATGACATTAATGCTTAAGTAGACATGT 1650
QY 383 TTTTGACATTTCCAGCCCTTTAAATATCCACACACACAGAGACAAAGAAAGCAC 442
DB 1649 TTTTGACATTTCCAGCCCTTTAAATATCCACACACAGAGACAAAGAAAGCAC 1590
QY 443 AGGATTCCTGGGAGAAATGCCGGCCGACATTTGGGTATGATGAGCCTTGGCCTGT 502
DB 1589 AGGATTCCTGGGAGAAATGCCGGCCGACATTTGGGTATGATGAGCCTTGGCCTGT 1530
QY 503 GCTGTGCTCCGCTTTGAGAGGAGGACATTAGAAAATGAATGATGTTCTTAAAGGA 562
DB 1529 GCTGTGCTCCGCTTTGAGAGGAGGACATTAGAAAATGAATGATGTTCTTAAAGGA 1470
QY 563 TGGGCGAGAAACAGATCTCTGTGTGATATTTATTTGAACGGGATTACAGATTGAAT 622
DB 1469 TGGGCGAGAAACAGATCTCTGTGTGATATTTATTTGAACGGGATTACAGATTGAAT 1410

QY 623 GAAGTCACAAAGTGACATTACCAATGAGAGAGAAACAGACGAGAAAATCTTGATGGCTT 682
DB 1409 GAAGTCACAAAGTGAGGACATTACCAATGAGAGAGAAACAGACGAGAAAATCTTGATGGCTT 1350
QY 683 CACAAGCATGCAACAAACAAATGGAATCTGTGATGACATAGGACGAGCAAGCTGGGG 742
DB 1349 CACAAGCATGCAACAAACAAATGGAATCTGTGATGACATAGGACGAGCAAGCTGGGG 1290
QY 743 AGGAGATTAACGAGGGGACAGAGGTCAGATTTGGCCCTGCTCTAAACTGTGGCTTC 802
DB 1289 AGGAGATTAACGAGGGGACAGAGGTCAGATTTGGCCCTGCTCTAAACTGTGGCTTC 1230
QY 803 ATAACCAATCAATTCATATTTCTAAACCTCAAAACAAAGCTGTGTAATATCTGATCTC 862
DB 1229 ATAACCAATCAATTCATATTTCTAAACCTCAAAACAAAGCTGTGTAATATCTGATCTC 1170
QY 863 TAGGGTTCCTTCGGGCGCCCAACATCTCCATATATCCAGCCACATCTTTTAAATATT 922
DB 1169 TAGGGTTCCTTCGGGCGCCCAACATCTCCATATATCCAGCCACATCTTTTAAATATT 1110
QY 923 AGTTCCAGATCTGTACTGTGACCTTCTTACACTGTAGATTAACATTAATCTATTTGTTTC 982
DB 1109 AGTTCCAGATCTGTACTGTGACCTTCTTACACTGTAGATTAACATTAATCTATTTGTTTC 1050
QY 983 AAAGACCTTCCTGCTGCTGCTGCTCAATATGATGACTGCTTTTCTTAAGAGTGTCTG 1042
DB 1049 AAAGACCTTCCTGCTGCTGCTGCTCAATATGATGACTGCTTTTCTTAAGAGTGTCTG 990
QY 1043 GCCAGGGGATCTGTATACAGGCTGGGAGGATCTCAAGATCTTTCAGGGTATACCTTA 1102
DB 989 GCCAGGGGATCTGTATACAGGCTGGGAGGATCTCAAGATCTTTCAGGGTATACCTTA 930
QY 1103 CTAGCACACAGCATGATCATTTAGGAGTGAATTAATCAACATCATCTCAGTGTCT 1162
DB 929 CTAGCACACAGCATGATCATTTAGGAGTGAATTAATCAACATCATCTCAGTGTCT 870
QY 1163 TTCCCATCATCTGAATTTCAATTTCCCATTTTGGCCCATTTCTCAACACCTCAAAAGTCA 1222
DB 869 TTCCCATCATCTGAATTTCAATTTCCCATTTTGGCCCATTTCTCAACACCTCAAAAGTCA 810
QY 1223 TTCCATTAATATCACAGATTAATTTTCTTTTAACTGTGAAGAAATTAAGTTCATG 1282
DB 809 TTCCATTAATATCACAGATTAATTTTCTTTTAACTGTGAAGAAATTAAGTTCATG 750
QY 1283 CAGCTATGGGAATTAATTAATATTTTGTTCAGTGCAGCAAGATAGTACGCTTTTA 1342
DB 749 CAGCTATGGGAATTAATTAATATTTTGTTCAGTGCAGCAAGATAGTACGCTTTTA 690
QY 1343 TCCCTCCCTTTGTTGATTTTTCACAGTATAAAGTTAAAGTTCAGCTTGTACTG 1402
DB 689 TCCCTCCCTTTGTTGATTTTTCACAGTATAAAGTTAAAGTTCAGCTTGTACTG 630
QY 1403 AGGCTGTATACAGC 1416
DB 629 AGGCTGTATACAGC 616

RESULT 13
AAH02870/c
ID AAH02870 standard; cDNA; 2426 BP.
XX
AC AAH02870;
XX
DT 14-JUN-2001 (first entry)
XX
DE Prostate tumour antigen cDNA sequence for P710P #3.
XX
KM Human; prostate tumour antigen; prostate tumour; therapy; diagnosis;
KM prostate cancer; immunogenic; cytostatic; vaccine; ss.
XX
OS Homo sapiens.
XX
PN W0200125272-A2.

DR WPI: 2001-328324/34.
XX Polypeptide comprising part of the Wilm's Tumour gene product sequence is
PT used in the diagnosis and treatment of malignant diseases e.g. leukemia
PT and cancer associated with WT1
XX
PS Disclosure: Page 219-220; 228pp; English.
XX
CC The present invention describes compositions comprising peptides derived
CC from the Wilm's tumour protein WT1 and methods for their use in treating
CC malignant diseases. Peptides derived from both the murine and human WT1
CC proteins are provided. The human WT1 gene is found on chromosome 11p13,
CC and the protein was shown to be a zinc finger transcription factor. The
CC immunogenic peptides of the invention are particularly useful in the
CC diagnosis and treatment of cancer and leukemia. The present sequence is
CC a coding sequence used in the exemplification of the invention.
XX
SQ Sequence 2426 BP; 717 A; 476 C; 548 G; 685 T; 0 other;
Query Match 56.7%; Score 1154; DB 22; Length 2426;
Best Local Similarly 100.0%; Pred. No. 0;
Matches 1154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 263 GGTGAGAAATAGAAAGGCTGTGACTTACATCTGAGGCCACACATCTGCTGAATGG 322
DB 1769 GGTGAGAAATAGAAAGGCTGTGACTTACATCTGAGGCCACACATCTGCTGAATGG 1710
QY 323 AGATTAATTAACATCAGTGAAGACGAGATGACATTAATGTCATAGTAGTACATGT 382
DB 1709 AGATTAATTAACATCAGTGAAGACGAGATGACATTAATGTCATAGTAGTACATGT 1650
QY 383 TTTTGCACATTTCCAGCCCTTTAAATATCCACACACAGCAAGCAAAAGAGAC 442
DB 1649 TTTTGCACATTTCCAGCCCTTTAAATATCCACACACAGCAAGCAAAAGAGAC 1590
QY 443 AGAGATCCCTGGGAGAAATGCCGCCCATCTGGGTATGATGAGCTGCCCTGT 502
DB 1589 AGAGATCCCTGGGAGAAATGCCGCCCATCTGGGTATGATGAGCTGCCCTGT 1530
QY 503 GCCTGTCCCGCTTGTGAGGAGAGACATTAAGAAATGAATGATGTTCTTAAAGA 562
DB 1529 GCCTGTCCCGCTTGTGAGGAGAGACATTAAGAAATGAATGATGTTCTTAAAGA 1470
QY 563 TGGGCAAGAAAGACATCTGTTGTGATATTTATTTGAACGGGATTTACGATTTGAAT 622
DB 1469 TGGGCAAGAAAGACATCTGTTGTGATATTTATTTGAACGGGATTTACGATTTGAAT 1410
QY 623 GAAGTACAAAGTGAGCATTAACATGAGAGAAACAGACGAGAAATCTTGATGGCTT 682
DB 1409 GAAGTACAAAGTGAGCATTAACATGAGAGAAACAGACGAGAAATCTTGATGGCTT 1350
QY 683 CACAGACATGCAACAAACAAATGAAATAGTGTGATGACATGAGCAGCAAGCTGGG 742
DB 1349 CACAGACATGCAACAAACAAATGAAATAGTGTGATGACATGAGCAGCAAGCTGGG 1290
QY 743 AGAGATTAACAGAGGGGAGAGGTCAGATTTCTGGCCCTGCTCTAACTGCGTTG 802
DB 1289 AGAGATTAACAGAGGGGAGAGGTCAGATTTCTGGCCCTGCTCTAACTGCGTTG 1230
QY 803 ATTAACCAATCATTTTATATTTCTTAACCCCAAAACAAAGCTTGTGAATATGATCTC 862
DB 1229 ATTAACCAATCATTTTATATTTCTTAACCCCAAAACAAAGCTTGTGAATATGATCTC 1170
QY 863 TAGGTTCTTCTGGGCCCAACATTCATATATATCCAGCAGCAGCATTTTAAATATT 922
DB 1169 TAGGTTCTTCTGGGCCCAACATTCATATATATCCAGCAGCAGCATTTTAAATATT 1110
QY 923 AGTTCACATCTGTACTGTGACCTTTTACATGTAGATTAACATTTACTATTTGTTG 982
DB 1109 AGTTCACATCTGTACTGTGACCTTTTACATGTAGATTAACATTTACTATTTGTTG 1050
QY 983 AAAGACCTTGTGTTGTGCTGCTAATATGATGATGCTGTTTCTAAGGATGTTCTG 1042

DB 1049 AAAGACCTTGTGTTGTGCTGCTAATATGATGATGCTGTTTCTAAGGATGTTCTG 990
QY 1043 GCCCAGGGATCTGTGAACAGGCTGGAGACATCTCAAGATCTTCCAGGTTATACTTA 1102
DB 989 GCCCAGGGATCTGTGAACAGGCTGGAGACATCTCAAGATCTTCCAGGTTATACTTA 930
QY 1103 CTAGCACACAGCATGATCATTTACGAGTGAATATCTAATCAACATCATCTGAGTCT 1162
DB 929 CTAGCACACAGCATGATCATTTACGAGTGAATATCTAATCAACATCATCTGAGTCT 870
QY 1163 TTGCCCCATCTGAATTCATTTCCACTTTTGGCCCATCTGCAAGACCTCAAAATGTCA 1222
DB 869 TTGCCCCATCTGAATTCATTTCCACTTTTGGCCCATCTGCAAGACCTCAAAATGTCA 810
QY 1223 TTCCATTAATATACAGATTAACCTTTTAAACCTGGAAGAAATCAATGTACATG 1282
DB 809 TTCCATTAATATACAGATTAACCTTTTAAACCTGGAAGAAATCAATGTACATG 750
QY 1283 CAGCTATGGAAATTTAATCATATTTTGTTCACAGTGCAGAAAGATGACTAAGTCTT 1342
DB 749 CAGCTATGGAAATTTAATCATATTTTGTTCACAGTGCAGAAAGATGACTAAGTCTT 690
QY 1343 TCCCTCCCTTTGTTGATTTTTCACAGTATTAAGTTAAATGCTTACCTTGTACTG 1402
DB 689 TCCCTCCCTTTGTTGATTTTTCACAGTATTAAGTTAAATGCTTGTACTG 630
QY 1403 AGGCTGTATACAGC 1416
DB 629 AGGCTGTATACAGC 616
RESULT 15
ABL95269/c
ID ABL95269 standard; cDNA; 2426 BP.
AC ABL95269;
XX
XX 19-JUL-2002 (first entry)
XX
DE Human P710P cDNA sequence SEQ ID NO 470.
XX
KW Human: cancer; prostate cancer; vaccine; cytostatic; immunostimulant;
KW gene therapy; gene; ss.
XX
XX Homo sapiens.
PN US2002022248-A1.
XX
PD 21-FEB-2002.
XX
FE 12-JAN-2001; 200105-0759143.
XX
XX 25-FEB-1997; 97US-0806099.
PR 01-AUG-1997; 97US-0904804.
PR 09-FEB-1998; 98US-0020956.
PR 25-FEB-1998; 98US-0030607.
PR 14-JUL-1998; 98US-0115453.
PR 23-SEP-1998; 98US-0159812.
PR 15-JAN-1999; 99US-0232149.
PR 09-APR-1999; 99US-0289846.
PR 13-JUL-1999; 99US-0352616.
PR 13-JUL-1999; 99US-0439213.
PR 18-NOV-1999; 99US-0443686.
PR 14-JAN-2000; 2000US-0483672.
PR 27-MAR-2000; 2000US-0536857.
PR 09-MAY-2000; 2000US-0568100.
PR 12-MAY-2000; 2000US-0570737.
PR 13-JUN-2000; 2000US-0593793.
PR 27-JUN-2000; 2000US-0605783.
PR 10-AUG-2000; 2000US-0636215.
PR 29-SEP-2000; 2000US-0651236.
PR 06-SEP-2000; 2000US-0657279.
PR 02-OCT-2000; 2000US-0679426.

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 26, 2003, 21:44:18 : Search time 472.057 Seconds
(without alignments)
10742.554 Million cell updates/sec

Title: US-09-402-713a-1

Perfect score: 2037
Sequence: 1 agaagctgcgcatacgaataa.....caataagaattacaaaga 2037

Scoring table:

OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 1678620 seqs, 1244745471 residues

Word size : 0

Total number of hits satisfying chosen parameters: 3357240

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : Published_Applications_NA:*

1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
9: /cgn2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
10: /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
13: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
14: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
15: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
16: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
17: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1629	80.0	3923	9	US-09-759-143-690 Sequence 690, App
2	1629	80.0	3923	9	US-09-780-669-690 Sequence 690, App
3	1629	80.0	3923	9	US-09-822-827-690 Sequence 690, App
4	1629	80.0	3923	10	US-09-895-793-690 Sequence 690, App
5	1629	80.0	3923	10	US-09-895-814-690 Sequence 690, App
6	1629	80.0	3923	12	US-10-144-678A-690 Sequence 690, App
7	1629	80.0	3923	13	US-10-012-896-690 Sequence 690, App
8	1629	80.0	3923	14	US-10-205-823-316 Sequence 316, App
9	1629	80.0	3923	9	US-09-759-143-470 Sequence 470, App
10	1154	56.7	2426	9	US-09-780-669-470 Sequence 470, App
11	1154	56.7	2426	9	US-09-822-827-470 Sequence 470, App
12	1154	56.7	2426	10	US-09-895-793-470 Sequence 470, App
13	1154	56.7	2426	10	US-09-895-814-470 Sequence 470, App
14	1154	56.7	2426	12	US-10-144-678A-470 Sequence 470, App
15	1154	56.7	2426	13	US-10-012-896-470 Sequence 470, App
16	1154	56.7	2426	14	US-10-010-940-470 Sequence 470, App

c	17	1154	56.7	2426	14	US-10-205-823-448	Sequence 448, App
	18	1154	56.7	3112	9	US-09-759-143-468	Sequence 468, App
	19	1154	56.7	3112	9	US-09-780-669-468	Sequence 468, App
	20	1154	56.7	3112	9	US-09-822-827-468	Sequence 468, App
	21	1154	56.7	3112	10	US-09-895-793-468	Sequence 468, App
	22	1154	56.7	3112	10	US-09-895-814-468	Sequence 468, App
	23	1154	56.7	3112	12	US-10-144-678A-468	Sequence 468, App
	24	1154	56.7	3112	13	US-10-012-896-468	Sequence 468, App
	25	1154	56.7	3112	14	US-10-010-940-468	Sequence 468, App
	26	1033	50.7	2229	9	US-09-759-143-469	Sequence 469, App
	27	1033	50.7	2229	9	US-09-780-669-469	Sequence 469, App
	28	1033	50.7	2229	9	US-09-822-827-469	Sequence 469, App
	29	1033	50.7	2229	10	US-09-895-793-469	Sequence 469, App
	30	1033	50.7	2229	10	US-09-895-814-469	Sequence 469, App
	31	1033	50.7	2229	12	US-10-144-678A-469	Sequence 469, App
	32	1033	50.7	2229	13	US-10-012-896-469	Sequence 469, App
	33	1033	50.7	2229	14	US-10-010-940-469	Sequence 469, App
	34	738	36.2	876	11	US-09-957-708-3	Sequence 3, Appl1
	35	720	35.3	812	9	US-09-759-143-471	Sequence 471, App
	36	720	35.3	812	9	US-09-780-669-471	Sequence 471, App
	37	720	35.3	812	9	US-09-822-827-471	Sequence 471, App
	38	720	35.3	812	10	US-09-895-793-471	Sequence 471, App
	39	720	35.3	812	10	US-09-895-814-471	Sequence 471, App
	40	720	35.3	812	12	US-10-144-678A-471	Sequence 471, App
	41	720	35.3	812	13	US-10-012-896-471	Sequence 471, App
	42	720	35.3	812	14	US-10-010-940-471	Sequence 471, App
	43	473	23.2	597	12	US-10-185-730-46	Sequence 46, Appl1
	44	467	22.9	1102	14	US-10-198-846-11000	Sequence 11000, A
	45	465	22.8	1036	14	US-10-198-846-13213	Sequence 13213, A

ALIGNMENTS

RESULT 1
US-09-759-143-690
Sequence 690, Application US/09759143
Patent No. US200202248A1
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, David C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Jiang, Yuqi
APPLICANT: Henderson, Robert A.
APPLICANT: Kallou, Michael D.
APPLICANT: Fanger, Gary R.
APPLICANT: Retter, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Day, Craig H.
APPLICANT: Vedyck, Thomas S.
APPLICANT: Carter, Derrick
APPLICANT: Li, Samuel
APPLICANT: Wang, Ajun
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Hepler, William
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
FILE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427C23
CURRENT APPLICATION NUMBER: US/09/759,143
CURRENT FILING DATE: 2001-01-12
NUMBER OF SEQ ID NOS: 934
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 690
LENGTH: 3923
TYPE: DNA
ORGANISM: Homo sapien
US-09-759-143-690
Query Match 80.0%; Score 1629; DB 9; Length 3923;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 2029; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 AGAAGCTGCATCAGAAAAACAGAGGGAGATTGTGTGCTGCAGCCGAGGAGACAC 60
 Db 23 AGAAGCTGCATCAGAAAAACAGAGGGAGATTGTGTGCTGCAGCCGAGGAGACAC 82
 QY 61 GAAGATCGCATGTGGAGAGACCTGATGATACAGAGGAATACAAACATATCTAG 120
 Db 83 GAAGATCGCATGTGGAGAGACCTGATGATACAGAGGAATACAAACATATCTAG 142
 QY 121 TGTTCATGACACCAAGATTAATAGTGAAGAGCTAGTCCGCTGTGATCTCAGT 180
 Db 143 TGTTCATGACACCAAGATTAATAGTGAAGAGCTAGTCCGCTGTGATCTCAGT 202
 QY 181 GACACAGGCTGATCACCATCCAGCGGCACTTTCTGATCTAGTCCAGCAAGAA 240
 Db 203 GACACAGGCTGATCACCATCCAGCGGCACTTTCTGATCTAGTCCAGCAAGAA 262
 QY 241 CTACAGACATCTCAATGCGAGGGGTGGAATTAAGAAAGCTGTGCTTACCATCTGA 300
 Db 263 CTACAGACATCTCAATGCGAGGGGTGGAATTAAGAAAGCTGTGCTTACCATCTGA 322
 QY 301 GGCCACACATCTGCTGAATGGAATTAATACATCACTAGAAACAGCAAGATGACATA 360
 Db 323 GGCCACACATCTGCTGAATGGAATTAATACATCACTAGAAACAGCAAGATGACATA 382
 QY 361 TAATGCTAGTATGATGATCTTTTGGACATTTCCAGCCCTTTAATATCCACACACA 420
 Db 383 TAATGCTAGTATGATGATCTTTTGGACATTTCCAGCCCTTTAATATCCACACACA 442
 QY 421 CAGGAAGCACAAAGAGAGACAGAGATCCCTGGAGAAATGCGCGGCGCCATCTTGGG 480
 Db 443 CAGGAAGCACAAAGAGAGACAGAGATCCCTGGAGAAATGCGCGGCGCCATCTTGGG 502
 QY 481 TCATCATGAGCTCGCCCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540
 Db 503 TCATCATGAGCTCGCCCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 562
 QY 541 AATGATGCTGCTTAAAGATGGGAGAGAAACAGATCTGTGCTGATTTATTTTGG 600
 Db 563 AATGATGCTGCTTAAAGATGGGAGAGAAACAGATCTGTGCTGATTTATTTTGG 622
 QY 601 AACGGGATTAACAGATTTGAATGAATGATCAACAAAGTACATTTACATGAGAGAAACA 660
 Db 623 AACGGGATTAACAGATTTGAATGAATGATCAACAAAGTACATTTACATGAGAGAAACA 682
 QY 661 GACGAGAAAATCTTGAATGCTTCAACAGATGCAACAAACAAATGGAATCTGTGATG 720
 Db 683 GACGAGAAAATCTTGAATGCTTCAACAGATGCAACAAACAAATGGAATCTGTGATG 742
 QY 721 ACATGAGGACGCAAGCTGGGAGAGATTAACACGGGGGAGAGGATTCGAGCC 780
 Db 743 ACATGAGGACGCAAGCTGGGAGAGATTAACACGGGGGAGAGGATTCGAGCC 802
 QY 781 CTGCTGCTTAACATGCTGCTTCAATACCAATCATTTCAATTTCTTAACCTTCAAAACA 840
 Db 803 CTGCTGCTTAACATGCTGCTTCAATACCAATCATTTCAATTTCTTAACCTTCAAAACA 862
 QY 841 AGCTGTTGAATATCTGATCTAGGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 900
 Db 863 AGCTGTTGAATATCTGATCTAGGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 922
 QY 901 GCGACACATTTTAAATATTTAGTCCAGATCTGTACCTTTCTACACTGTAG 960
 Db 923 GCGACACATTTTAAATATTTAGTCCAGATCTGTACCTTTCTACACTGTAG 982
 QY 961 AATAACATTAATCTTTTGTTCAAAGACCTTGTGTGCTGCTAATATGTAGTGA 1020
 Db 983 AATAACATTAATCTTTTGTTCAAAGACCTTGTGTGCTGCTAATATGTAGTGA 1042
 QY 1021 GTTTTTCCTAAGAGAGTGTCTGGCCAGGGGATCTGTGAACAGCTGTGGAGCATCTCAA 1080
 Db 1043 GTTTTTCCTAAGAGAGTGTCTGGCCAGGGGATCTGTGAACAGCTGTGGAGCATCTCAA 1102
 QY 1081 GATCTTTCAGGGGTATCTTACTACACACAGCATGATCATTTAGCGAGTGAATTTATCTA 1140

Db 1103 GATCTTTCAGGGGTATCTTACTACACACAGCATGATCATTCAGGAGTGAATTTATCTA 1162
 QY 1141 ATCAACATCTCCCTGCTGCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1200
 Db 1163 ATCAACATCTCCCTGCTGCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1222
 QY 1201 TTCTCAAGACCTCAAAATGCTATTCATTAATATTCACAGAGATTAATCTTTTCTTAAAC 1260
 Db 1223 TTCTCAAGACCTCAAAATGCTATTCATTAATATTCACAGAGATTAATCTTTTCTTAAAC 1282
 QY 1261 TGAAGAAATTCATTTTACATGAGCTATGAGGAAATTAATTTACATATTTTGTTCAGT 1320
 Db 1283 TGAAGAAATTCATTTTACATGAGCTATGAGGAAATTAATTTACATATTTTGTTCAGT 1342
 QY 1321 GCAAGATGACTAAGTCTTATCCCTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1380
 Db 1343 GCAAGATGACTAAGTCTTATCCCTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1402
 QY 1381 TAAATGCTTAAAGCTTGTATGAGGCTGTATACAGACAGCCCTCCCATCCCTCCAGC 1440
 Db 1403 TAAATGCTTAAAGCTTGTATGAGGCTGTATACAGACAGCCCTCCCATCCCTCCAGC 1462
 QY 1441 CTATATCTGATCATCATCAACCCCTCCCATTTTSACTTAACAAATTTTACTTGTAAAT 1500
 Db 1463 CTATATCTGATCATCATCAACCCCTCCCATTTTSACTTAACAAATTTTACTTGTAAAT 1522
 QY 1501 CCTTGAACATGTAGAGCATCATTTTCTGCTGCTGAGAGCTGCTGCTGCTGCTGCTGCTGCT 1560
 Db 1523 CCTTGAACATGTAGAGCATCATTTTCTGCTGCTGAGAGCTGCTGCTGCTGCTGCTGCTGCT 1582
 QY 1561 AANTCTAGAAATGATTAAGTTTGAATTAAGTTGACTATCTTACTTATGCAAGAGAG 1620
 Db 1583 AANTCTAGAAATGATTAAGTTTGAATTAAGTTGACTATCTTACTTATGCAAGAGAG 1642
 QY 1621 ACACATATGATGATTCATCATCATGATGAGAGCAAGAAATTTACTAAGTATTTGATTA 1680
 Db 1643 ACACATATGATGATTCATCATCATGATGAGAGCAAGAAATTTACTAAGTATTTGATTA 1702
 QY 1681 AGAGTTTGAATTAATTAATGAATTAATGAACAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1740
 Db 1703 AGAGTTTGAATTAATTAATGAATTAATGAACAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1762
 QY 1741 TGTAAAGCTGGAGTGTGAAGMAAGGACAGGAGAGCTCATATGATCTTAATTAATATATCT 1800
 Db 1763 TGTAAAGCTGGAGTGTGAAGMAAGGACAGGAGAGCTCATATGATCTTAATTAATATATCT 1822
 QY 1801 CATTTCTATCTCTATCAACAAATATTCACAAAGCTTTTCAAGAAATTCATGAGAGTCA 1860
 Db 1823 CATTTCTATCTCTATCAACAAATATTCACAAAGCTTTTCAAGAAATTCATGAGAGTCA 1882
 QY 1861 TCCCAAGAGTAACCTTTATTCATTTTCAATGATGAGTGGCTTTAGAAATTTGGCAATCA 1920
 Db 1883 TCCCAAGAGTAACCTTTATTCATTTTCAATGATGAGTGGCTTTAGAAATTTGGCAATCA 1942
 QY 1921 TACTGCTCATATTCATCAACTTTGAGATGATGTTTGTCTTGTAGTTAATTTGAAGAAATA 1980
 Db 1943 TACTGCTCATATTCATCAACTTTGAGATGATGTTTGTCTTGTAGTTAATTTGAAGAAATA 2002
 QY 1981 GGGCAGCTCTTGTGAGGCACTTTAGGTTTACATCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2037
 Db 2003 GGGCAGCTCTTGTGAGGCACTTTAGGTTTACATCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2059

RESULT 2

US-09-780-669-690
 ; Sequence 690, Application US/09780669
 ; Patent No. US2002051977A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Xu, Jiangchun
 ; APPLICANT: Dillon, Davin C.
 ; APPLICANT: Mitcham, Jennifer L.
 ; APPLICANT: Harlocker, Susan L.

APPLICANT: Jiang, Yuyui
APPLICANT: Henderson, Robert A.
APPLICANT: Kalos, Michael D.
APPLICANT: Fanger, Gary R.
APPLICANT: Retter, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Day, Craig H.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Darick
APPLICANT: Li, Samuel
APPLICANT: Wang, Aijun
APPLICANT: Skelky, Yasir A.W.
APPLICANT: Hepler, William
APPLICANT: Hural, John
APPLICANT: McNeill, Patricia D.
APPLICANT: Houghton, Raymond L.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427C24
CURRENT APPLICATION NUMBER: US/09/780,669
CURRENT FILING DATE: 2001-02-09
NUMBER OF SEQ ID NOS: 943
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO: 690
LENGTH: 3923
TYPE: DNA
ORGANISM: Homo sapien
US-09-780-669-690

Query Match 80.0%; Score 1629; DB 9; Length 3923;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 2029; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 AGAAGCTGGCATCAGAAAAACAGAGGGAGATTGTGTGCTGCAGCCGAGGAGACGAG 60
DB 23 AGAAGCTGGCATCAGAAAAACAGAGGGAGATTGTGTGCTGCAGCCGAGGAGACGAG 82
QY 61 GAAGATCTGCATGTGGGAGGACCTGATGATACAGAGGAATTAACACATATCTTGG 120
DB 83 GAAGATCTGCATGTGGGAGGACCTGATGATACAGAGGAATTAACACATATCTTGG 142
QY 121 TGTTCATGAGACACCAAGATTAATAGTGAAGAGCTAGTCCGCTGTGAGTCTCCACT 180
DB 143 TGTTCATGAGACACCAAGATTAATAGTGAAGAGCTAGTCCGCTGTGAGTCTCCACT 202
QY 181 GACACAGGGCTGTGATCACCATCGACGGCAGCTTGTGAGTACTCAGTGCAGCAAGAGAGA 240
DB 203 GACACAGGGCTGTGATCACCATCGACGGCAGCTTGTGAGTACTCAGTGCAGCAAGAGAGA 262
QY 241 CTACAGACATCTCAATGGGAGGGGTGAGAAATGAAGAGGCTGTGACTTTTACCATCTGA 300
DB 263 CTACAGACATCTCAATGGGAGGGGTGAGAAATGAAGAGGCTGTGACTTTTACCATCTGA 322
QY 301 GGCACACATCTGTGAAATGAGATTAATTAACATCCTAGAAACAGCAAGATGACAAATA 360
DB 323 GGCACACATCTGTGAAATGAGATTAATTAACATCCTAGAAACAGCAAGATGACAAATA 382
QY 361 TTAATCTTAAGTAGAGCATGTTTTTGCACATTTCCAGCCCTTTAAATATCCACACACA 420
DB 383 TTAATCTTAAGTAGAGCATGTTTTTGCACATTTCCAGCCCTTTAAATATCCACACACA 442
QY 421 CAGGAAGCAGAAAAGAGCAGAGATCCCTGGGAGAAATGCCGGCCGCCATCTTGGG 480
DB 443 CAGGAAGCAGAAAAGAGCAGAGATCCCTGGGAGAAATGCCGGCCGCCATCTTGGG 502
QY 481 TCATGATGAGCCTGCGCTGTGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 540
DB 503 TCATGATGAGCCTGCGCTGTGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 562
QY 541 AATGATGCTGCTTAAAGATGGGAGGAGAAACAGATCCCTGCTGTGATATTTATTTG 600
DB 563 AATGATGCTGCTTAAAGATGGGAGGAGAAACAGATCCCTGCTGTGATATTTATTTG 622

QY 601 AACGGATTACAGATTTGAATGAATGAGTACCAAGTGAAGCATTAACCAATGAGAGAAACA 660
DB 623 AACGGATTACAGATTTGAATGAATGAGTACCAAGTGAAGCATTAACCAATGAGAGAAACA 682
QY 661 GACGAGAAATCTGTATGGCTTACAGACATGCAACAAACAAATGAAATCTGTATG 720
DB 683 GACGAGAAATCTGTATGGCTTACAGACATGCAACAAACAAATGAAATCTGTATG 742
QY 721 ACATGAGCAGCCAAAGCTGGGAGAGATTAACACAGGGGCAAGAGGTCAAGATTTGGGC 780
DB 743 ACATGAGCAGCCAAAGCTGGGAGAGATTAACACAGGGGCAAGAGGTCAAGATTTGGGC 802
QY 781 CTGCTGCCAAACCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 840
DB 803 CTGCTGCCAAACCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 862
QY 841 ACCTGTTGTAATCTGATCTGTACGGTCTGCTGCGGCAACATCTGCAATATATCA 900
DB 863 ACCTGTTGTAATCTGATCTGTACGGTCTGCTGCGGCAACATCTGCAATATATCA 922
QY 901 GCCACATCATTTTAAATATTTAGTTCCTGAGATCTGTGAGTCTGTACCTGTAG 960
DB 923 GCCACATCATTTTAAATATTTAGTTCCTGAGATCTGTGAGTCTGTACCTGTAG 982
QY 961 AATTAACATTAATCTGATTTGTGCAAGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1020
DB 983 AATTAACATTAATCTGATTTGTGCAAGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1042
QY 1021 GTTTTCTTAAGAGAGTGTCTGCGCCAGGGGATCTGTGAACAGGCTGGGAGACATCTCA 1080
DB 1043 GTTTTCTTAAGAGAGTGTCTGCGCCAGGGGATCTGTGAACAGGCTGGGAGACATCTCA 1102
QY 1081 GATCTTTCAGGGTATTAATTAATTTAGTTCCTGAGATCTGTGAGTCTGTACCTGTAG 1140
DB 1103 GATCTTTCAGGGTATTAATTAATTTAGTTCCTGAGATCTGTGAGTCTGTACCTGTAG 1162
QY 1141 ATCAACATCATCTGATTTGTGCAAGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1200
DB 1163 ATCAACATCATCTGATTTGTGCAAGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1222
QY 1201 TTCTGAAGACCTCAAAATGCTATTCATTAATATACAGAGATTAACCTTTTTTTTAAAC 1260
DB 1223 TTCTGAAGACCTCAAAATGCTATTCATTAATATACAGAGATTAACCTTTTTTTTAAAC 1282
QY 1261 TGGAGAAATCAATGTTAATGACATGAGGAAATTAATTAATTAATTTGTTTCCACT 1320
DB 1283 TGGAGAAATCAATGTTAATGACATGAGGAAATTAATTAATTAATTTGTTTCCACT 1342
QY 1321 GCAAGATGACTAAGTCTTATCCCTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1380
DB 1343 GCAAGATGACTAAGTCTTATCCCTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1402
QY 1381 TAAATGCTTAAGCTTGTACTGAGGCTGTATACAGACAGCCCTGCCATCCCTCCAGC 1440
DB 1403 TAAATGCTTAAGCTTGTACTGAGGCTGTATACAGACAGCCCTGCCATCCCTCCAGC 1462
QY 1441 CTATCTGATCAGACATCAACCCCTCCATTTTAAATTAATTAATTTGTTTCCACT 1500
DB 1463 CTATCTGATCAGACATCAACCCCTCCATTTTAAATTAATTAATTTGTTTCCACT 1522
QY 1501 CCTGAACATGTCAGAGCAGTATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1560
DB 1523 CCTGAACATGTCAGAGCAGTATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1582
QY 1561 AANTCTAGATGATTAAGGTTTGAATTAAGTGAATCTTATCTTATGCAAGAGGG 1620
DB 1583 AANTCTAGATGATTAAGGTTTGAATTAAGTGAATCTTATCTTATGCAAGAGGG 1642
QY 1621 ACACATATGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1680
DB 1643 ACACATATGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1702
QY 1681 AGAGTTAGATTAATATATGAAATGCAAGAKCACAGAGGAGATGTTTATGGGACGTT 1740

Db	1703	AGAGTTTAGATAAATATATATGAATTAAGCAAGACCACAGAGGGAAAGTTTATGTGGGCACGTT	1762
QY	1741	TGTAAAGCCTGGGATGTGAAGMAAAGGACGAGAACCTCATAGTATCTTATATATATACTT	1800
Db	1763	TGTAAAGCCTGGGATGTGAAGCAAAAGGACGGAACTCATAGTATCTTATATATATACTT	1822
QY	1801	CATTTCCTATCTCTATACACAAATATCCAAACAGCTTTTCACGAATTCATCGACTGCAAA	1860
Db	1823	CATTTCCTATCTCTATACACAAATATCCAAACAGCTTTTCACGAATTCATCGACTGCAAA	1882
QY	1861	TCCCAAAGGTAACCTTTATTCACATTTTCATGTGTGAGTGGCGCTTTGAAATTTTGGCAATNCA	1920
Db	1883	TCCCAAAGGTAACCTTTATTCACATTTTCATGTGTGAGTGGCGCTTTGAAATTTTGGCAATNCA	1942
QY	1921	TACTGGTCACCTTATCTCAACTTGTGAGATGTGTGTTCCTGTAGTATTAATTGAAGAATA	1980
Db	1943	TACTGGTCACCTTATCTCAACTTGTGAGATGTGTGTTCCTGTAGTATTAATTGAAGAATA	2002
QY	1981	GGGCACTCTTGTGAGCCACTTTAGGGTTCACCTCGGCAATAAAGAAATTTTCAAGA	2037
Db	2003	GGGCACTCTTGTGAGCCACTTTAGGGTTCACCTCGGCAATAAAGAAATTTTCAAGA	2059

Db	383	TAATGCTAACTAGTACATGTTTTTTCACATTTCCAGCCCCCTTTAAATATCCACACACA	442
Qy	421	CAGGAAGCACAAAAGGAAGCACAGAGATCCCTGGGAGAAATGCCCGCCGCATCTTGGG	480
Db	443	CAGGAAGCACAAAAGGAAGCACAGAGATCCCTGGGAGAAATGCCCGCCGCATCTTGGG	502
Qy	481	TCATTCGATGACCTTCGCCCTGCTGCTGCTGCCCTTGTGAGGGAAAGGACATTAGAAATG	540
Db	503	TCATTCGATGACCTTCGCCCTGCTGCTGCCCTTGTGAGGGAAAGGACATTAGAAATG	562
Qy	541	AATGATGCTGTCTCTTAAGAGTGGGCGAGAAAACAGATCCGTGTGATATTATTAATTG	600
Db	563	AATGATGCTGTCTCTTAAGAGTGGGCGAGAAAACAGATCCGTGTGTGATATTATTAATTG	622
Qy	601	AACGGGATTTACAGATTTGAAATGAAAGTCACAAAGTGACATTTACCAATGAGAGGAAAAACA	660
Db	623	AACGGGATTTACAGATTTGAAATGAAAGTCACAAAGTGACATTTACCAATGAGAGGAAAAACA	682
Qy	661	GACGAGAAAATCTTGATGGCTTCACACAGACATGCACAACAAAATGGAATATCTGTATG	720
Db	683	GACGAGAAAATCTTGATGGCTTCACACAGACATGCACAACAAAATGGAATATCTGTATG	742

```

RESULT 3
US-09-822-827-690
; Sequence 690, Application US/09822827
; Patent No. US20020081680A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.534C1
; CURRENT APPLICATION NUMBER: US/09/822,827
; CURRENT FILING DATE: 2001-03-28
; NUMBER OF SEQ ID NOS: 982
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 690
; LENGTH: 3923
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-822-827-690

Query Match      80.0%; Score 1629; DB 9; Length 3923;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 2029; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY      1  AGAAGCTGGCATCGATCGAAAAACACAGAGGGGAGATTTGTGTGCTGCAGCCCGAGGAGACCAG 60
      |||
DB      23  AGAAGCTGGCATCGAAAAACAGAGGGGAGATTTGTGTGCTGCAGCCCGAGGAGACCAG 82
      |||

QY      61  GAAGATCTGCATGGTGGGAAGGACCTGATGATTCAGAGGAATTCACACATATACTTAG 120
      |||
DB      83  GAAGATCTGCATGGTGGGAAGGACCTGATGATTCAGAGGAATTCACACATATACTTAG 142
      |||

QY      121  TGTTCATGAAACCAACCAAGATAAATAAGTGAAGAGCTAGTCCGCTGTGAGTCTCTCAGT 180
      |||
DB      143  TGTTCATGAAACCAACCAAGATAAATAAGTGAAGAGCTAGTCCGCTGTGAGTCTCTCAGT 202
      |||

QY      181  GACACAGGGCTGCATCAACCATCGACGGCACTTTCTGAGTACTAGTCAGTCAGCAAGAANAAGA 240
      |||
DB      203  GACACAGGGCTGCATCAACCATCGACGGCACTTTCTGAGTACTAGTCAGTCAGCAAGAANAAGA 262
      |||

QY      241  CTACAGACATCTCAATGSGCAGGGGTGAGAAATAGAAAGGCTGCTGACTTTACCATCTGA 300
      |||
DB      263  CTACAGACATCTCAATGSGCAGGGGTGAGAAATAGAAAGGCTGCTGACTTTACCATCTGA 322
      |||

QY      301  GGCCACACATCTGCTGAAATGAGATTAATTAACTACTAGAAACAGCAAGATGACATA 360
      |||
DB      323  GGCCACACATCTGCTGAAATGAGATTAATTAACTACTAGAAACAGCAAGATGACATA 382
      |||

QY      361  TAATGTCTAAGTAGACATGTTTTTGACATTTCCAGCCCTTTAAATATCCACACACA 420
      |||

```

Db	743	ACATGAGGACACCAGCTGGGGAGAGATACACACGGGGCAGAGGGTATGAGATTCTGGCC	802
Qy	781	CTGCTGCCATAACCTGCGGTGCATPACCAAAATCATTTATATTTCTAACCCCTCAAAACGA	840
Db	803	CTGCTGCCATAACCTGCGGTGCATPACCAAAATCATTTATATTTCTAACCCCTCAAAACGA	862
Qy	841	AGCTGTTGTAATATCTGATCTCTACGGTTCTCTTCTGGGCCAACATTTCTCATATATCCA	900
Db	863	AGCTGTTGTAATATCTGATCTCTACGGTTCTCTTCTGGGCCAACATTTCTCATATATCCA	922
Qy	901	GCCACACTCATTTTAAATTAATTTACTTCCCAATCTGTACTGTGACGCTTGTACACTGTAG	960
Db	923	GCCACACTCATTTTAAATTAATTTACTTCCCAATCTGTACTGTGACGCTTGTACACTGTAG	982
Qy	961	AATAACATTAATCTATTTTGTTCAAAGACCTTCGTGTGTGCGCCATAATATAGCTGACT	1020
Db	983	AATAACATTAATCTATTTTGTTCAAAGACCTTCGTGTGTGCGCCATAATATAGCTGACT	1042
Qy	1021	GTTTTTCCTPAAAGAGTGTCTTGCGCCACAGGGGATCTGTGACAGCGCTGGGAAGCATCTCA	1080
Db	1043	GTTTTTCCTPAAAGAGTGTCTTGCGCCACAGGGGATCTGTGACAGCGCTGGGAAGCATCTCA	1102
Qy	1081	GATCTTTCACAGGGTTATTAATTAAGACACACAGCATATCAATTACAGAGTAATATATCTA	1140
Db	1103	GATCTTTCACAGGGTTATTAATTAAGACACACAGCATATCAATTACAGAGTAATATATCTA	1162
Qy	1141	ATCAACATCATCTCCAGTGTCTTTGGCCATCTGGAATTCATTTTCCCACTTTTGAGCCA	1200
Db	1163	ATCAACATCATCTCCAGTGTCTTTGGCCATCTGGAATTCATTTTCCCACTTTTGAGCCA	1222
Qy	1201	TTCTCAAGACCTCAAAATGTCATTCOCATTAATATACACAGATTAACTTTCTTTTAAAC	1260
Db	1223	TTCTCAAGACCTCAAAATGTCATTCOCATTAATATACACAGATTAACTTTCTTTTAAAC	1282
Qy	1261	TGGAAGAATTAATATTAATACATGACAGCTATGGGAATTAATTAATACATATTTGTTTCCAGT	1320
Db	1283	TGGAAGAATTAATATTAATACATGACAGCTATGGGAATTAATTAATACATATTTGTTTCCAGT	1342
Qy	1321	GCAAAAGATGACATAGTCTCTTATACCCGCCCTTTGTGTTGATTTTTTTCAGTATPAAAGT	1380
Db	1343	GCAAAAGATGACATAGTCTCTTATACCCGCCCTTTGTGTTGATTTTTTTCAGTATPAAAGT	1402
Qy	1381	TAAATATCTTAAGCCTTGACTGAGAGCTGTATACAGACAGCGCTCTCCCATCCCTCCAGC	1440
Db	1403	TAAATATCTTAAGCCTTGACTGAGAGCTGTATACAGACAGCGCTCTCCCATCCCTCCAGC	1462
Qy	1441	CTTATCTGTCAATCAACATCAACCCCTCCCATNTYBACCTAATACAAATCTTAACCTGTAAAT	1500
Db	1463	CTTATCTGTCAATCAACATCAACCCCTCCCATNTYBACCTAATACAAATCTTAACCTGTAAAT	1522

OY	1501	CCTTGACATCTCAGCNATCATCATTTTCCTTCCTTGCCCTGAGAAAGCTCTTCTTGCTCTT	1560
Db	1523	CTTTGAACATCTCAGGACATCATTAATTCCTTCCTGCGGAGAAAGCTCTTCTTGCTCTT	1582
OY	1561	AANCTGAAATGATGATTAAGTTTGAATTAAGTTGACTTCTTACTTCAATGCAAGAAAGG	1620
Db	1583	AAATCTAGAAATGATGATTAAGTTTGAATTAAGTTGACTTCTTACTTCAATGCAAGAAAGG	1642
OY	1621	ACACATATGACATTCATCATCATCATGAGACAGCAAAATCTAAAAGTGAATTTGATTATA	1680
Db	1643	ACACATATGACATTCATCATCATCATGAGACAGCAAAATCTAAAAGTGAATTTGATTATA	1702
OY	1661	AGACTTTAGATTAATTAATTAATTAATGCAAGAACACACAGAGGGAATGTTATGCGCACCTT	1740
Db	1703	AGACTTTAGATTAATTAATTAATTAATGCAAGAACACACAGAGGGAATGTTATGCGCACCTT	1762
OY	1741	TGTAAAGCCTGGAGATGTGAGAAAGGACGAGAACCTCATATATCTTATTAATATACTT	1800
Db	1763	TGTAAAGCCTGGAGATGTGAGAAAGGACGAGAACCTCATATATCTTATTAATATACTT	1822
OY	1801	CATTTCCTATCTCTATTCACAAATATCCAAACAGCTTTTCACAGAAATTCAGTGCAGAA	1860
Db	1823	CATTTCCTATCTCTATTCACAAATATCCAAACAGCTTTTCACAGAAATTCAGTGCAGAA	1882
OY	1861	TCCGCAAAAGGTAACCTTTATTCATTCATGATGCTGAGTGGCTTTGAAATTTGGCAAAATCA	1920
Db	1883	TCCGCAAAAGGTAACCTTTATTCATTCATGATGCTGAGTGGCTTTGAAATTTGGCAAAATCA	1942
OY	1921	TACTGTCACCTTATCTCAACTTGTGAGATGCTTGTGCTCTTGACTTAATTAATGAAGAATA	1980
Db	1943	TACTGTCACCTTATCTCAACTTGTGAGATGCTTGTGCTCTTGACTTAATTAATGAAGAATA	2002
OY	1981	GGGCACTCTTGTGAGCCACTTTAGGGTTCACCTCTGGCAATTAAGAATTTACAAGA	2037
Db	2003	GGGCACTCTTGTGAGCCACTTTAGGGTTCACCTCTGGCAATTAAGAATTTACAAGA	2059
RESULT 4			
US-09-895-793-690			
Sequence 690, Application US/09895793			
Publication No. US20020192763A1			
GENERAL INFORMATION:			
APPLICANT: Xu, Jiangchun			
APPLICANT: Dillon, Davin C.			
APPLICANT: Mitcham, Jennifer L.			
APPLICANT: Harlocker, Susan L.			
APPLICANT: Jiang, Yungiu			
APPLICANT: Kalos, Michael D.			
APPLICANT: Retter, Marc W.			
APPLICANT: Stolk, John A.			
APPLICANT: Day, Craig H.			
APPLICANT: Vedvick, Thomas S.			
APPLICANT: Carter, Darlick			
APPLICANT: Li, Samuel X.			
APPLICANT: Wang, Aijun			
APPLICANT: Skelky, Yasir A.W.			
APPLICANT: Hepler, William T.			
APPLICANT: Henderson, Robert A.			
APPLICANT: Hural, John			
APPLICANT: McNeill, Patricia D.			
APPLICANT: Houghton, Raymond L.			
APPLICANT: Vinals de Bassols, Carlota			
APPLICANT: Foy, Teresa			
APPLICANT: Fanger, Gary R.			
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND			
FILE REFERENCE: 210121.534C2			
CURRENT APPLICATION NUMBER: US/09/895,793			
CURRENT FILING DATE: 2001-06-29			
NUMBER OF SEQ ID NOS: 982			
SOFTWARE: FastSeq for Windows Version 3.0			
SEQ ID NO 690			

[illegible]

QY 961 AATACATCTACTATTTTGTTCAAAGACCTTGTGTTGCTGCTCAATATGTAAGTACTGACT 1020
DB 983 AATACATCTACTATTTTGTTCAAAGACCTTGTGTTGCTGCTCAATATGTAAGTACTGACT 1042
QY 1021 GTTTTCTTAAGAGGTCTTGGCCAGGGGATCTGTGAAACAGGCTGGGAAGATCTCAA 1080
DB 1043 GTTTTCTTAAGAGGTCTTGGCCAGGGGATCTGTGAAACAGGCTGGGAAGATCTCAA 1102
QY 1081 GATCTTCCAGGGTAACTTACTAGACACAGCATATCATTTACGAGTCAATATCTA 1140
DB 1103 GATCTTCCAGGGTAACTTACTAGACACAGCATATCATTTACGAGTCAATATCTA 1162
QY 1141 ATCAACATCACTCTCACTGTCTTGGCCATCTGAAATTCATTTCCACTTTTGTGCCA 1200
DB 1163 ATCAACATCACTCTCACTGTCTTGGCCATCTGAAATTCATTTCCACTTTTGTGCCA 1222
QY 1201 TTCTCAGACCTCAAAATGTCAATTCATTCATATACAGATTAATCTTTTAAACC 1260
DB 1223 TTCTCAGACCTCAAAATGTCAATTCATTCATATACAGATTAATCTTTTAAACC 1282
QY 1261 TGGAGAAATCAATGTATCATATGACAGTATGGGAATTAATTAATTTTGTTCAGT 1320
DB 1283 TGGAGAAATCAATGTATCATATGACAGTATGGGAATTAATTAATTTTGTTCAGT 1342
QY 1321 GCAAAAGTGAAGTCTTATTCCTTCCCTTGTGATTTTTCAGATATAAAGT 1380
DB 1343 GCAAAAGTGAAGTCTTATTCCTTCCCTTGTGATTTTTCAGATATAAAGT 1402
QY 1381 TAAATGCTTAGCTTACTAGAGGTGTATACAGCAGCTCTCTCCCATCTCCAGC 1440
DB 1403 TAAATGCTTAGCTTACTAGAGGTGTATACAGCAGCTCTCTCCCATCTCCAGC 1462
QY 1441 CTATCTGTATGACCATCAACCCCTCCCATNTSACCTAAACAAATCTAATCTGTAAT 1500
DB 1463 CTATCTGTATGACCATCAACCCCTCCCATNTSACCTAAACAAATCTAATCTGTAAT 1522
QY 1501 CCTTGAACATGTCAGAGCAGATATCTTCTGCTGAGAAAGCTTCTCTGTCTT 1560
DB 1523 CCTTGAACATGTCAGAGCAGATATCTTCTGCTGAGAAAGCTTCTCTGTCTT 1582
QY 1561 AATCTAGATGATGTAAAGTTTGAATAGTATGATCTTCTCATGCAAAAGAGG 1620
DB 1583 AATCTAGATGATGTAAAGTTTGAATAGTATGATCTTCTCATGCAAAAGAGG 1642
QY 1621 ACACATATGATGATTCATCATGATGAGAGCAAGAAATCTAAAGTGAATTTGATATA 1680
DB 1643 ACACATATGATGATTCATCATGATGAGAGCAAGAAATCTAAAGTGAATTTGATATA 1702
QY 1681 AGAGTTAGATTAATTAATTAATGAATGCAAGAKCCACAGAGGATGTTTATGGGCGACTT 1740
DB 1703 AGAGTTAGATTAATTAATTAATGAATGCAAGAGCCACAGAGGATGTTTATGGGCGACTT 1762
QY 1741 TGTAAAGCTGGAGTGTGAAGMAAGGAGGAGCTCATAGTATCTTAATTAATTAATCTT 1800
DB 1763 TGTAAAGCTGGAGTGTGAAGMAAGGAGGAGCTCATAGTATCTTAATTAATTAATCTT 1822
QY 1801 CATTTCTATCTCTATTCACATATTCACACAGCTTTTCCAGAAATTCATGAGTGCAAA 1860
DB 1823 CATTTCTATCTCTATTCACATATTCACACAGCTTTTCCAGAAATTCATGAGTGCAAA 1882
QY 1861 TCCCAAGAGGTACCTTTATTCATTCATGAGGAGGCTTGAATTTTGGCAATCA 1920
DB 1883 TCCCAAGAGGTACCTTTATTCATTCATGAGGAGGCTTGAATTTTGGCAATCA 1942
QY 1921 TACTGTCACTATTCATCACTTTGAGATGTGTTGCTCTGTGATTAATTTGAAGAATA 1980
DB 1943 TACTGTCACTATTCATCACTTTGAGATGTGTTGCTCTGTGATTAATTTGAAGAATA 2002
QY 1981 GGGCACTCTTGTGAGCACTTTAGGTTACCTCTGGCAATTAAGATTTTACAAGA 2037
DB 2003 GGGCACTCTTGTGAGCACTTTAGGTTACCTCTGGCAATTAAGATTTTACAAGA 2059

RESULT 5
US-09-895-814-690
; Sequence 690, Application US/09895814
; Publication No. US20020193296A1
GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Devin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yugu
; APPLICANT: Kalos, Michael D.
; APPLICANT: Retler, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darick
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aljun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Vinals de Bassols, Carlota
; APPLICANT: Foy, Teresa
; APPLICANT: Fanger, Gary R.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
FILE REFERENCE: 210121.427C26
CURRENT APPLICATION NUMBER: US/09/895, 814
CURRENT FILING DATE: 2001-06-29
NUMBER OF SEQ ID NOS: 990
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 690
LENGTH: 3923
TYPE: DNA
ORGANISM: Homo sapien
US-09-895-814-690
Query Match 80.0%; Score 1629; DB 10; Length 3923;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 2029; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
QY 1 AGAAGCTGGCATCAGAAAACAGAGGGGAGATTTGTGTGCTGCACGCCGAGGAGACCG 60
DB 23 AGAAGCTGGCATCAGAAAACAGAGGGGAGATTTGTGTGCTGCACGCCGAGGAGACCG 82
QY 61 GAAGATCTGATGCTGGGGAAGGACCTGATGATACAGAGAAATTAACAACATATTAAGT 120
DB 83 GAAGATCTGATGCTGGGGAAGGACCTGATGATACAGAGAAATTAACAACATATTAAGT 142
QY 121 TGTTCATTAACCAACCAAGATTAATTAAGTAAGTAAGTATGCTGCTGATCTCCACAT 180
DB 143 TGTTCATTAACCAACCAAGATTAATTAAGTAAGTAAGTATGCTGCTGATCTCCACAT 202
QY 181 GACACAGGGGTGATCACCATCGACGCACTTTCTAGTACTAGTACGACGACAAAGAAAG 240
DB 203 GACACAGGGGTGATCACCATCGACGCACTTTCTAGTACTAGTACGACGACAAAGAAAG 262
QY 241 CTACACACATCTCAATATGAGGAGGCTGATGAATTAATTAACATCACTAGAAACAGCAAGATGACATA 300
DB 263 CTACACACATCTCAATATGAGGAGGCTGATGAATTAATTAACATCACTAGAAACAGCAAGATGACATA 322
QY 301 GGGCACACATCTCTGAATGGAATGAATTAATTAACATCACTAGAAACAGCAAGATGACATA 360
DB 323 GGGCACACATCTCTGAATGGAATGAATTAATTAACATCACTAGAAACAGCAAGATGACATA 382
QY 361 TAATGTCTAAGTATGATGATGTTTTCGACATTTCCAGCCCTTTAAATATCCACACACA 420
DB 383 TAATGTCTAAGTATGATGATGTTTTCGACATTTCCAGCCCTTTAAATATCCACACACA 442
QY 421 CAGGAAGCACAAAGAGACACAGAGATCCCTGGGAAATGCGCGGCCCATCTTGGG 480


```

: TYPE: DNA
: ORGANISM: Homo sapiens
US-10-144-678A-690

Query Match      80.0%; Score 1629; DB 12; Length 3923;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 2029; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 AGAAGCTGGCATCGAAGAAACAGAGGAGGAGATTGTGTGGCTGCAGCGGAGGAGACAG 60
DB 23 AGAAGCTGGCATCGAAGAAACAGAGGAGGAGATTGTGTGGCTGCAGCGGAGGAGACAG 82
QY 61 GAAGATCTGATGGTGGGAAGACCTGATGATACAGAGGATTACACACATATATCTTAG 120
DB 83 GAAGATCTGATGGTGGGAAGACCTGATGATACAGAGGATTACACACATATATCTTAG 142
QY 121 TGTATTAATGACACCAAGATTAATAATGTAAGAGCTAGTCCGTGAGATCTCTAGT 180
DB 143 TGTATTAATGACACCAAGATTAATAATGTAAGAGCTAGTCCGTGAGATCTCTAGT 202
QY 181 GACACAGGGCTGATCACCATCGACGCGACTTCTGATCTGACTGACGACGACAAAGAGA 240
DB 203 GACACAGGGCTGATCACCATCGACGCGACTTCTGATCTGACTGACGACGACAAAGAGA 262
QY 241 CTACAGACATCTCAATGGCAGGGGTGAGAAATGAAGAGGCTGCTGACTTTACCATCTGA 300
DB 263 CTACAGACATCTCAATGGCAGGGGTGAGAAATGAAGAGGCTGCTGACTTTACCATCTGA 322
QY 301 GGGCACACATCTGCTGAAATGAGATPATTAACATCTAGAAACAGACAGATGACATA 360
DB 323 GGGCACACATCTGCTGAAATGAGATPATTAACATCTAGAAACAGACAGATGACATA 382
QY 361 TAAATGCTAAGTAGTACATGTTTTTGGACATTTCCAGCCCTTTAAATATCCACACACA 420
DB 383 TAAATGCTAAGTAGTACATGTTTTTGGACATTTCCAGCCCTTTAAATATCCACACACA 442
QY 421 CAGGAAGCCAAAAAGAGACAGACAGATCCCTGGGAGAAATGCCCGGCCCATCTTGGG 480
DB 443 CAGGAAGCCAAAAAGAGACAGACAGATCCCTGGGAGAAATGCCCGGCCCATCTTGGG 502
QY 481 TCATCGTAGAGCTCGCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 540
DB 503 TCATCGTAGAGCTCGCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 562
QY 541 AATATGATGTTCTCTTAAGAGATGGCAGAGAAACAGATCTGTGTGATATTTATTTG 600
DB 563 AATATGATGTTCTCTTAAGAGATGGCAGAGAAACAGATCTGTGTGATATTTATTTG 622
QY 601 AACGGGATTACAGATTTGAAATGAAGTCAACAAAGTAGACATTTACCAATGAGAGAAACA 660
DB 623 AACGGGATTACAGATTTGAAATGAAGTCAACAAAGTAGACATTTACCAATGAGAGAAACA 682
QY 661 GAGCAGAAAAATCTTGATGGCTTCAACAAGACATGCAACAACAATAATGGAATAGTGTGATG 720
DB 683 GAGCAGAAAAATCTTGATGGCTTCAACAAGACATGCAACAACAATAATGGAATAGTGTGATG 742
QY 721 ACATGAGGACCCAGAGCTGGGAGAGATTAACACGGGGCAGAGGTCAGAGTTTGGCC 780
DB 743 ACATGAGGACCCAGAGCTGGGAGAGATTAACACGGGGCAGAGGTCAGAGTTTGGCC 802
QY 781 CTGCTGCTTAACCTGAGGCTTCAATACCAAAATGATTTCAATTTCTTAACCTTAACAA 840
DB 803 CTGCTGCTTAACCTGAGGCTTCAATACCAAAATGATTTCAATTTCTTAACCTTAACAA 862
QY 841 AGCTGTTGTAATATCTGATCTACAGTTCCTTCTGGGCCACACATTTCCATATATATCA 900
DB 863 AGCTGTTGTAATATCTGATCTACAGTTCCTTCTGGGCCACACATTTCCATATATATCA 922
QY 901 GCCACACTATTTTAAATATTAATTAATCCAGATCTGTACTGTGACCTTTCTACACGTGATG 960
DB 923 GCCACACTATTTTAAATATTAATTAATCCAGATCTGTACTGTGACCTTTCTACACGTGATG 982
QY 961 AATAACATATCATTTTGTTCAAAGACCTTGCTGTGCTGCTAATATGATGCTGACT 1020
```

```

|||||
DB 983 AATAACATATCATTTTGTTCAAAGACCTTGCTGTGCTGCTAATATGATGCTGACT 1042
QY 1021 GTTTTTCCTTAAGAGATTTCTGGCCAGGGGATCTGTGAACACAGCTGGGAGCATCTCAA 1080
DB 1043 GTTTTTCCTTAAGAGATTTCTGGCCAGGGGATCTGTGAACACAGCTGGGAGCATCTCAA 1102
QY 1081 GATCTTCCAGGGTTATCTTACTAGACACACAGATATCATTAACGAGGAAATTAATCTA 1140
DB 1103 GATCTTCCAGGGTTATCTTACTAGACACACAGATATCATTAACGAGGAAATTAATCTA 1162
QY 1141 ATCAACATCATCTCACTGCTCTTGGCCATACATGAAATTCATTTCCACTTTGTGCCCA 1200
DB 1163 ATCAACATCATCTCACTGCTCTTGGCCATACATGAAATTCATTTCCACTTTGTGCCCA 1222
QY 1201 TTCTCAAGACCTCAAAATGTCATTCATTAATATTCACAGATTAACCTTTTCTTAACC 1260
DB 1223 TTCTCAAGACCTCAAAATGTCATTCATTAATATTCACAGATTAACCTTTTCTTAACC 1282
QY 1261 TGGAGAAATTCATGTTACATTCAGCATATGGGAATTTAATACATATTTTGTTCAGT 1320
DB 1283 TGGAGAAATTCATGTTACATTCAGCATATGGGAATTTAATACATATTTTGTTCAGT 1342
QY 1321 GCAAAAGTACCTAAGTCTTTATCCCTCCCTTTGTTGATTTTTCAGTATAAGT 1380
DB 1343 GCAAAAGTACCTAAGTCTTTATCCCTCCCTTTGTTGATTTTTCAGTATAAGT 1402
QY 1381 TAAATGCTTAGGCTTGTACTGAGGCTGATATACAGACAGCCCTCCGCCATCCCTCAGC 1440
DB 1403 TAAATGCTTAGGCTTGTACTGAGGCTGATATACAGACAGCCCTCCGCCATCCCTCAGC 1462
QY 1441 CTATATCTATCACCATCAACCCCTCCCATATTAACCTTAACCTTAATCTGTAAT 1500
DB 1463 CTATATCTATCACCATCAACCCCTCCCATATTAACCTTAACCTTAATCTGTAAT 1522
QY 1501 CCTTGAACATGTAGGNCATACATTTCTCTTCTGCTGAGAAAGCTTCTCTTCTCTT 1560
DB 1523 CCTTGAACATGTAGGNCATACATTTCTCTTCTGCTGAGAAAGCTTCTCTTCTCTT 1582
QY 1561 AANTCTAGATGATGTAAGTTTGAATTAAGTGAATGATCTTACTCATGCAAGAAAGG 1620
DB 1583 AANTCTAGATGATGTAAGTTTGAATTAAGTGAATGATCTTACTCATGCAAGAAAGG 1642
QY 1621 ACACATATGATGATTCATCATCATGATGACAGCAAGAAATCTAATAATTTGATATATA 1680
DB 1643 ACACATATGATGATTCATCATCATGATGACAGCAAGAAATCTAATAATTTGATATATA 1702
QY 1681 AGAGTTAGATTAATATGAAATGCAACAKCCACAGAGGAAATGTTTATGGGGCAGCT 1740
DB 1703 AGAGTTAGATTAATATGAAATGCAACAGCCACAGAGGAAATGTTTATGGGGCAGCT 1762
QY 1741 TGTAAAGCTGGGATGTGAAGMAAAGCAGAGGAACCTCATAGTATCTTATATATATCTT 1800
DB 1763 TGTAAAGCTGGGATGTGAAGMAAAGCAGAGGAACCTCATAGTATCTTATATATATCTT 1822
QY 1801 CATTTCTATATCTATACAAATATCAACAAGCTTTTCAAGAAATTCATGCAATGCAANA 1860
DB 1823 CATTTCTATATCTATACAAATATCAACAAGCTTTTCAAGAAATTCATGCAATGCAANA 1882
QY 1861 TCCCAAGGTAACCTTATACATTCATGAGGAGGCTTTAGAAATTTTGGCAAAATCA 1920
DB 1883 TCCCAAGGTAACCTTATACATTCATGAGGAGGCTTTAGAAATTTTGGCAAAATCA 1942
QY 1921 TACTGTACTATATCAACATTTGAGATGTGTTTGCCTTGTAGTAAATTAAGAAATAA 1980
DB 1943 TACTGTACTATATCAACATTTGAGATGTGTTTGCCTTGTAGTAAATTAAGAAATAA 2002
QY 1981 GGGCACTCTTGTGAGCCACTTAAAGGTTCACTCTGCGCAATTAAGAAATTTTACAAGA 2037
DB 2003 GGGCACTCTTGTGAGCCACTTAAAGGTTCACTCTGCGCAATTAAGAAATTTTACAAGA 2059
```

RESULT 7


```
|||||
Db 1523 CCTGGAACATGTGAGACATACATATTCCTTGCCTGAGAGCTCTTCTGTCTT 1582
QY 1561 AATTCAGATGATGTAAGTTTGAATAGTGCATCTTCTTCAATGCAAGAAGG 1620
Db 1583 AATTCAGATGATGTAAGTTTGAATAGTGCATCTTCTTCAATGCAAGAAGG 1642
QY 1621 ACACATATGATGATTCATCATCATGAGACAGCAAACTACTAAAGTATTTGATATA 1680
Db 1643 ACACATATGATGATTCATCATCATGAGACAGCAAACTACTAAAGTATTTGATATA 1702
QY 1681 AGAGTTAGATTAATATATGAAATGCAAGACCAAGAGGAAATGTTTATGGGCACTT 1740
Db 1703 AGAGTTAGATTAATATATGAAATGCAAGACCAAGAGGAAATGTTTATGGGCACTT 1762
QY 1741 TGTAGAGCTGGATGTAAGAAAGGAGGAACTCATGATATCTATATATATATCTT 1800
Db 1763 TGTAGAGCTGGATGTAAGAAAGGAGGAACTCATGATATCTATATATATATCTT 1822
QY 1801 CATTTCTATCTCTATCATCAATATCCAAACAGCTTTTCACAGATTCATGAGTGCAAA 1860
Db 1823 CATTTCTATCTCTATCATCAATATCCAAACAGCTTTTCACAGATTCATGAGTGCAAA 1882
QY 1861 TCCCAAGGTAACCTTTATCCATTTTCATGAGTGAGTGCCTTTAGAAATTTGGCAATCA 1920
Db 1883 TCCCAAGGTAACCTTTATCCATTTTCATGAGTGAGTGCCTTTAGAAATTTGGCAATCA 1942
QY 1921 TACTGTCATCTATCTCAACTTTGAGATGTTTGTCTGTTGATTAATGAAGAATA 1980
Db 1943 TACTGTCATCTATCTCAACTTTGAGATGTTTGTCTGTTGATTAATGAAGAATA 2002
QY 1981 GGGCACTCTTGTAGCCACTTTAGGGTCACTCTGGCAATTAAGAATTTTACAAGA 2037
Db 2003 GGGCACTCTTGTAGCCACTTTAGGGTCACTCTGGCAATTAAGAATTTTACAAGA 2059

RESULT 8
US-10-205-823-316
: Sequence 316, Application US/10205823
: GENERAL INFORMATION:
: APPLICANT: Schlengel, Robert
: APPLICANT: Monahan, John E.
: APPLICANT: Endege, Wilson O.
: APPLICANT: Gannavarepu, Manjula
: APPLICANT: Gorbacheva, Belja
: APPLICANT: Hoersch, Sebastian
: APPLICANT: Kamatkar, Shubhangi
: APPLICANT: Monsey, Angela M.
: APPLICANT: Glatc, Karen
: APPLICANT: Zhao, Xumel
: APPLICANT: Anderson, Dustin
: TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
: THERAPY OF PROSTATE CANCER
: FILE REFERENCE: MRI-044
: CURRENT APPLICATION NUMBER: US/10/205,823
: CURRENT FILING DATE: 2002-07-25
: PRIOR APPLICATION NUMBER: 60/307,982
: PRIOR FILING DATE: 2001-07-25
: PRIOR APPLICATION NUMBER: 60/314,356
: PRIOR FILING DATE: 2001-08-22
: PRIOR APPLICATION NUMBER: 60/325,020
: PRIOR FILING DATE: 2001-09-25
: PRIOR APPLICATION NUMBER: 60/341,746
: PRIOR FILING DATE: 2001-12-12
: PRIOR APPLICATION NUMBER: 60/362,158
: PRIOR FILING DATE: 2002-03-05
: NUMBER OF SEQ ID NOS: 455
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 316
: LENGTH: 3923
: TYPE: DNA
```

```
: ORGANISM: Homo sapiens
US-10-205-823-316
Query Match 80.0%; Score 1629; DB 14; Length 3923;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 2029; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 AGAAGCTGGCATGAGAAAAACAGAGGGGACATTTGTGTGCTGACGCGGAGAGACAG 60
Db 23 AGAAGCTGGCATGAGAAAAACAGAGGGGACATTTGTGTGCTGACGCGGAGAGACAG 82
QY 61 GAAGATCTGCATGGTGGGAGAGACCTGATGATACAGAGAAATTAACAACATTAAGTAG 120
Db 83 GAAGATCTGCATGGTGGGAGAGACCTGATGATACAGAGAAATTAACAACATTAAGTAG 142
QY 121 TGTTCATGATTAACCAACAGATTAATAGTAAGTAAGTACAGTCCCTGCTGATCTCCACG 180
Db 143 TGTTCATGATTAACCAACAGATTAATAGTAAGTACAGTCCCTGCTGATCTCCACG 202
QY 181 GACACAGGCTGGATGACATCCATCGACGCACTTCTGATCTGATGATGACAGCAAGAAGA 240
Db 203 GACACAGGCTGGATGACATCCATCGACGCACTTCTGATCTGATGATGACAGCAAGAAGA 262
QY 241 CTACAGATCTCATATGCGAGGGGTGAGAAATTAAGAAAGGCTGCTGATTAACATCTGA 300
Db 263 CTACAGATCTCATATGCGAGGGGTGAGAAATTAAGAAAGGCTGCTGATTAACATCTGA 322
QY 301 GGGCACACATCTCTGAAATGGAGATTAATTAACATCTGTAAGAAACAGCAAGATGACAAAT 360
Db 323 GGGCACACATCTCTGAAATGGAGATTAATTAACATCTGTAAGAAACAGCAAGATGACAAAT 382
QY 361 TAATGCTTAAGTAGATGACATGTTTGTGCATTTCCAGCCCTTAATTAATTCACACACA 420
Db 383 TAATGCTTAAGTAGATGACATGTTTGTGCATTTCCAGCCCTTAATTAATTCACACACA 442
QY 421 CAGAGACACAAAAAGAGACAGACATCCTTGGGAGAAATGCCCGCGCCATCTTGGG 480
Db 443 CAGAGACACAAAAAGAGACAGACATCCTTGGGAGAAATGCCCGCGCCATCTTGGG 502
QY 481 TCATGATGAGCCTCGCCCTGTCCTGTCCTGTCCTGTCCTGTCCTGTCCTGTCCTGTCCTG 540
Db 503 TCATGATGAGCCTCGCCCTGTCCTGTCCTGTCCTGTCCTGTCCTGTCCTGTCCTGTCCTG 562
QY 541 AATTGATGTCCTTAAAGATGGCAGGAAAAAGATCTCTGTCCTGATTAATTTATTTG 600
Db 563 AATTGATGTCCTTAAAGATGGCAGGAAAAAGATCTCTGTCCTGATTAATTTATTTG 622
QY 601 AACGGATTCACATTTGAAATGAATGACCAAGTGACATTTCAATGAGAGAGAAACA 660
Db 623 AACGGATTCACATTTGAAATGAATGACCAAGTGACATTTCAATGAGAGAGAAACA 682
QY 661 GACGAGAAATCTTGAAGGCTTCACAAAGACATGCAACAAACAAATGAATTAAGTAG 720
Db 683 GACGAGAAATCTTGAAGGCTTCACAAAGACATGCAACAAACAAATGAATTAAGTAG 742
QY 721 ACATGAGGACCCAGCTGGGAGAGATTAACACAGGGGAGAGGTCAGAGTTCTGAGCC 780
Db 743 ACATGAGGACCCAGCTGGGAGAGATTAACACAGGGGAGAGGTCAGAGTTCTGAGCC 802
QY 781 CTGCTGCTTAAGTGTGCTTCAATTAACCAATCATTTATTTCTTAACCTCAAAACA 840
Db 803 CTGCTGCTTAAGTGTGCTTCAATTAACCAATCATTTATTTCTTAACCTCAAAACA 862
QY 841 AGCTGTTTAATTAATGATCTGACGTTCTGTCCTGAGGACCAATTCATATATATCA 900
Db 863 AGCTGTTTAATTAATGATCTGACGTTCTGTCCTGAGGACCAATTCATATATATCA 922
QY 901 GCCACATCAATTTTATATATTTAGTCCAGATCTGATGATGACCTTTCTACACTGAG 960
Db 923 GCCACATCAATTTTATATATTTAGTCCAGATCTGATGATGACCTTTCTACACTGAG 982
QY 961 AATTAACATTAATTTGTTCAAGACCTTCGTTGCTGCTTAATATGATGATGACT 1020
```

Db 983 AATAACATTACTGATTTTGTTCAAAGACCCTTGCTGTCGCTAATATGTAGCTGACT 1042
QY 1021 GTTTTCTTAAGGAGTGTTCGGCCAGGAGATCTGTACACAGCTGGGAACCATCTCA 1080
Db 1043 GTTTTCTTAAGGAGTGTTCGGCCAGGAGATCTGTACACAGCTGGGAACCATCTCA 1102
QY 1081 GATCTTTCCAGGGTATCTACTAGACACAGCATGTATTAAGAGGTGAATATCTA 1140
Db 1103 GATCTTTCCAGGGTATCTACTAGACACAGCATGTATTAAGAGGTGAATATCTA 1162
QY 1141 ATCAACATATCTCAGTGTCTTTGGCCAACTGTAATTCATTTTCCCACTTTTGCCCA 1200
Db 1163 ATCAACATATCTCAGTGTCTTTGGCCAACTGTAATTCATTTTCCCACTTTTGCCCA 1222
QY 1201 TTCTCAAGACCTCAAAAATGTGATTTTCAATTAATATACAGGATTAATTTTAAAC 1260
Db 1223 TTCTCAAGACCTCAAAAATGTGATTTTCAATTAATATACAGGATTAATTTTAAAC 1282
QY 1261 TGAAGAAATTCATGTATGATGACATGAGGATTTAATTCATATTTTGTTCAGT 1320
Db 1283 TGAAGAAATTCATGTATGATGACATGAGGATTTAATTCATATTTTGTTCAGT 1342
QY 1321 GCAAGAGATGACTAAGTCTTTATCCCTCCCTTTGTGATTTTTCACAGTAAAGT 1380
Db 1343 GCAAGAGATGACTAAGTCTTTATCCCTCCCTTTGTGATTTTTCACAGTAAAGT 1402
QY 1381 TAAATGCTTACCTGTGACGAGCTGTATACACAGGCTCTCCCATCCCTCCAGC 1440
Db 1403 TAAATGCTTACCTGTGACGAGCTGTATACACAGGCTCTCCCATCCCTCCAGC 1462
QY 1441 CTATCTGTCATGACCATCAACCCCTCCCATNYSACTAAACAAATCATCTGTAAT 1500
Db 1463 CTATCTGTCATGACCATCAACCCCTCCCATNYSACTAAACAAATCATCTGTAAT 1522
QY 1501 CTTGGAACATGTCAGGNCATACATTTCTCTCTGCTGAGAGGCTCTCTGCTCT 1560
Db 1523 CTTGGAACATGTCAGGNCATACATTTCTCTCTGCTGAGAGGCTCTCTGCTCT 1582
QY 1561 AANTCTAAGATGATTAAGTTTGAATTAAGTGTGATCTTACTTCAATGCAAAAGAG 1620
Db 1583 AANTCTAAGATGATTAAGTTTGAATTAAGTGTGATCTTACTTCAATGCAAAAGAG 1642
QY 1621 ACACATATGATGATTCATCATGACATGACAGCAATACTAAGTGAATTTGATTA 1680
Db 1643 ACACATATGATGATTCATCATGACATGACAGCAATACTAAGTGAATTTGATTA 1702
QY 1681 AGAGTTAGATTAATATGAAGATGCAAGACCAAGAGGAGTGTATGAGGACGTT 1740
Db 1703 AGAGTTAGATTAATATGAAGATGCAAGACCAAGAGGAGTGTATGAGGACGTT 1762
QY 1741 TGTAGGCTGGAGTGAAGAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1800
Db 1763 TGTAGGCTGGAGTGAAGAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1822
QY 1801 CATTTCTATCTATCATCAATATCAACAAAGCTTTTACAGAAATTCAGAGTCAAA 1860
Db 1823 CATTTCTATCTATCATCAATATCAACAAAGCTTTTACAGAAATTCAGAGTCAAA 1882
QY 1861 TCCTCCAAAGGATTAATTCATTCATTCATTCATTCATTCATTCATTCATTCAT 1920
Db 1883 TCCTCCAAAGGATTAATTCATTCATTCATTCATTCATTCATTCATTCATTCAT 1942
QY 1921 TACGTGTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCAT 1980
Db 1943 TACGTGTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCAT 2002
QY 1981 GGGGACCTGTTGAGCAGCTTTAGGCTTCACTCTGCAATTAAGATTTTACAAAGA 2037
Db 2003 GGGGACCTGTTGAGCAGCTTTAGGCTTCACTCTGCAATTAAGATTTTACAAAGA 2059

; Sequence 470, Application US/09759143
; Patent No. US2002022248A1
; GENERAL INFORMATION:
; APPLICANT: Xu, JIANGHUN
; APPLICANT: Dillon, David C.
; APPLICANT: Milham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuxui
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedrick, Thomas S.
; APPLICANT: Carter, Darick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yashir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C23
; CURRENT FILING DATE: 2001-01-12
; NUMBER OF SEQ ID NOS: 934
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 470
; LENGTH: 2426
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-759-143-470

Query Match 56.7%; Score 1154; DB 9; Length 2426;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 263 GGTGAATATGAAGAGGCTGCTGATTTACATCTGAGGCGCACATCTGCTGAATG 322
Db 1769 GGTGAATATGAAGAGGCTGCTGATTTACATCTGAGGCGCACATCTGCTGAATG 1710
QY 323 AGATATTAACATCACTAGAAACAGCAGATGACATATATATGCTAAGTAGACATGT 382
Db 1709 AGATATTAACATCACTAGAAACAGCAGATGACATATATATGCTAAGTAGACATGT 1650
QY 383 TTTTGACATTTTCCAGCCCTTTAATATCCACACAGAGAGAGAGAGAGAGAGAGAG 442
Db 1649 TTTTGACATTTTCCAGCCCTTTAATATCCACACAGAGAGAGAGAGAGAGAGAGAG 1590
QY 443 AGAGATCCCTGGGAGAAATGCCGCGCATCTTGGGTCATGATGAGAGCTCGCCCTGT 502
Db 1589 AGAGATCCCTGGGAGAAATGCCGCGCATCTTGGGTCATGATGAGAGCTCGCCCTGT 1530
QY 503 GCCTGCTCCGCTTGTGAGGAGAGACATTAAGAAATGAATGATGTCTTCTTAAAGA 562
Db 1529 GCCTGCTCCGCTTGTGAGGAGAGACATTAAGAAATGAATGATGTCTTCTTAAAGA 1470
QY 563 TGGGAG 622
Db 1469 TGGGAG 1410
QY 623 GAAGTCACAAAGTGAAGATTTACATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 682
Db 1409 GAAGTCACAAAGTGAAGATTTACATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1350
QY 683 CACAAGACATGCAACAAACAAATGATCTGTATGATGATGATGATGATGATGATGAT 742
Db 1349 CACAAGACATGCAACAAACAAATGATCTGTATGATGATGATGATGATGATGATGAT 1290
QY 743 AGAGATTAACAG 802
Db 1289 AGAGATTAACAG 1230

QY 803 ATACCAATCATTTATATTTCTAAACCTCAAAACAGCTTGTATATGTATCTC 862
Db 1229 ATACCAAAATCATTTATATTTCTAAACCTCAAAACAGCTTGTATATGTATCTC 1170
QY 863 TACGTTCTCTGGGCCCCAACATTCCTCATATATCAGCCACATCTTTTAATTTT 922
Db 1169 TACGTTCTCTGGGCCCCAACATTCCTCATATATCAGCCACATCTTTTAATTTT 1110
QY 923 AGTTCCAGATCTGTACTGTGACCTTTCACCTGTAGATTAACATTTACTATTTTTC 982
Db 1109 AGTTCCAGATCTGTACTGTGACCTTTCACCTGTAGATTAACATTTACTATTTTTC 1050
QY 983 AAGACCCCTTCTGTGTGCTGCTTAATATGTAGTACTGTGTTCCTAAGAGTGTCTG 1042
Db 1049 AAGACCCCTTCTGTGTGCTGCTTAATATGTAGTACTGTGTTCCTAAGAGTGTCTG 990
QY 1043 GCCCAGGGATCTGTAAACAGGCTGGGAAGCATCTCAAGATCTTCAGGGTATCTTA 1102
Db 989 GCCCAGGGATCTGTAAACAGGCTGGGAAGCATCTCAAGATCTTCAGGGTATCTTA 930
QY 1103 CTAGCACACAGCATGTATCTTAAGAGTGAATTAATCAACATCATCTCAGTCTC 1162
Db 929 CTAGCACACAGCATGTATCTTAAGAGTGAATTAATCAACATCATCTCAGTCTC 870
QY 1163 TTGCCCATCTGAATTCATTTCCACTTTTGTGCCCATCTCAAGACTCAAAATGTCA 1222
Db 869 TTGCCCATCTGAATTCATTTCCACTTTTGTGCCCATCTCAAGACTCAAAATGTCA 810
QY 1223 TTCCATTAATATACAGGATTAATCTTTTAACTGAGAGATTAATCAATGTATCATG 1282
Db 809 TTCCATTAATATACAGGATTAATCTTTTAACTGAGAGATTAATCAATGTATCATG 750
QY 1283 CAGCTATGGGAATTTATATATATATTTTTCACAGTGAAGATGACTAATCTCTTA 1342
Db 749 CAGCTATGGGAATTTATATATATATTTTTCACAGTGAAGATGACTAATCTCTTA 690
QY 1343 TCCCTCCCTTGTGTGATTTTTCACAGTGAAGATGACTAATCTCTTA 1402
Db 689 TCCCTCCCTTGTGTGATTTTTCACAGTGAAGATGACTAATCTCTTA 630
QY 1403 AGGCTGTATACAGC 1416
Db 629 AGGCTGTATACAGC 616

RESULT 10
US-09-780-669-470/c
; Sequence 470. Application US/09780669
; Patent No. US20020051977A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, David C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yugu
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedrick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aljun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; APPLICANT: Hurai, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C24

; CURRENT APPLICATION NUMBER: US/09/780, 669
; CURRENT FILING DATE: 2001-02-09
; NUMBER OF SEQ ID NOS: 943
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 470
; LENGTH: 2426
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-780-669-470

Query Match 56.7%; Score 1154; DB 9; Length 2426;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 263 GGTGAATAATGAAGAGGCTGCTGACTTTTACATCTGAGGCCACACATCTGCTGAATGG 322
Db 1769 GGTGAATAATGAAGAGGCTGCTGACTTTTACATCTGAGGCCACACATCTGCTGAATGG 1710
QY 323 AGATTAATTAACATCTAGTAAGACAGCAAGATGACAAATATATAGTCTAAGTAGTACATGT 382
Db 1709 AGATTAATTAACATCTAGTAAGACAGCAAGATGACAAATATATAGTCTAAGTAGTACATGT 1650
QY 383 TTTTGCACATTTCCAGCCCTTTAATATATCCACACACAGCAAGACAAAGAGAGCAC 442
Db 1649 TTTTGCACATTTCCAGCCCTTTAATATATCCACACACAGCAAGACAAAGAGAGCAC 1590
QY 443 AGATATCCCTGGGAGAAATCCCGCCGCAATCTGTGGATGATGATGAGCTGCGCCCTGT 502
Db 1589 AGATATCCCTGGGAGAAATCCCGCCGCAATCTGTGGATGATGATGAGCTGCGCCCTGT 1530
QY 503 GCTGTGCTCCGCTTGTGAGGGAAGACATTTAGAAATGAATGTATGTCTTAAAGGA 562
Db 1529 GCTGTGCTCCGCTTGTGAGGGAAGACATTTAGAAATGAATGTATGTCTTAAAGGA 1470
QY 563 TGGGCGAGAAACAGATCCGTGTGGATTTATTTGAACGGGATTAACATTTGAAT 622
Db 1469 TGGGCGAGAAACAGATCCGTGTGGATTTATTTGAACGGGATTTAAGATTTGAAT 1410
QY 623 GAAGTCAAAAGTACATTTACCAATGAGAGAAACAGACGAAATCTTGATGGCTT 682
Db 1409 GAAGTCAAAAGTACATTTACCAATGAGAGAAACAGACGAAATCTTGATGGCTT 1350
QY 683 CACAGACATGCAACAAACAAATGGAATGCTGTATGATGATGAGGACGCAAGCTGGGG 742
Db 1349 CACAGACATGCAACAAACAAATGGAATGCTGTATGATGATGAGGACGCAAGCTGGGG 1290
QY 743 AGGAGATTAACAGGAGGAGGAGGAGGATCTGAGCTGCGCTTAACATCTGGGCTC 802
Db 1289 AGGAGATTAACAGGAGGAGGAGGAGGATCTGAGCTGCGCTTAACATCTGGGCTC 1230
QY 803 ATACCAAAATCATTTATATTTCTAAACCTCAAAACAGCTTGTATATGTATCTC 862
Db 1229 ATACCAAAATCATTTATATTTCTAAACCTCAAAACAGCTTGTATATGTATCTC 1170
QY 863 TACGTTCTCTGGGCCCCAACATTCCTCATATATCAGCCACATCTTTTAATTTT 922
Db 1169 TACGTTCTCTGGGCCCCAACATTCCTCATATATCAGCCACATCTTTTAATTTT 1110
QY 923 AGTTCCAGATCTGTACTGTGACCTTTCACCTGTAGATTAACATTTACTATTTTTC 982
Db 1109 AGTTCCAGATCTGTACTGTGACCTTTCACCTGTAGATTAACATTTACTATTTTTC 1050
QY 983 AAGACCCCTTCTGTGTGCTGCTTAATATGTAGTACTGTGTTCCTAAGAGTGTCTG 1042
Db 1049 AAGACCCCTTCTGTGTGCTGCTTAATATGTAGTACTGTGTTCCTAAGAGTGTCTG 990
QY 1043 GCCCAGGGATCTGTAAACAGGCTGGGAAGCATCTCAAGATCTTCAGGGTATCTTA 1102
Db 989 GCCCAGGGATCTGTAAACAGGCTGGGAAGCATCTCAAGATCTTCAGGGTATCTTA 930
QY 1103 CTAGCACACAGCATGTATCTTAAGAGTGAATTAATCAACATCATCTCAGTCTC 1162
Db 929 CTAGCACACAGCATGTATCTTAAGAGTGAATTAATCAACATCATCTCAGTCTC 870

```

1  RESULT12
2  US-09-895-793-470/c
3  : Sequence 470, Application US/09895793A1
4  : Publication No. US20020192763A1
5  :
6  : GENERAL INFORMATION:
7  :
8  : APPLICANT: Xu, Jiangchun
9  :
10 : APPLICANT: Dillon, Devin C.
11 :
12 : APPLICANT: Mitcham, Jennifer L.
13 :
14 : APPLICANT: Harlocke, Susan L.
15 :
16 : APPLICANT: Jiang, Yugu
17 :
18 : APPLICANT: Kalos, Michael D.
19 :
20 : APPLICANT: Retter, Marc W.
21 :
22 : APPLICANT: Stolk, John A.
23 :
24 : APPLICANT: Day, Craig H.
25 :
26 : APPLICANT: Vedyck, Thomas S.
27 :
28 : APPLICANT: Carter, Darick
29 :
30 : APPLICANT: Li, Samuel X.
31 :
32 : APPLICANT: Wang, Aijun
33 :
34 : APPLICANT: Skeiky, Yasser A.W.
35 :
36 : APPLICANT: Hepfer, William T.

```

```

: APPLICANT: Henderson, Robert A.
: APPLICANT: Hural, John
: APPLICANT: McNeill, Patricia D.
: APPLICANT: Houghton, Raymond L.
: APPLICANT: Vinals de Bassols, Carlota
: APPLICANT: Foy, Teresa
: APPLICANT: Fanger, Gary R.
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
: TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
: FILE REFERENCE: 210121.534C2
: CURRENT APPLICATION NUMBER: US/09/895,793
: CURRENT FILING DATE: 2001-06-29
: NUMBER OF SEQ ID NOS: 982
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 470
: LENGTH: 2426
: TYPE: DNA
: ORGANISM: Homo sapiens
: US-09-895-793-470

Query Match      56.7%; Score 1154; DB 10; Length 2426;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 263 GGTGAAATTAAGAAAGGCTGCTGACTTACATCTGAGGCCACACATCTGCTGAATG 322
DB 1769 GGTGAAATTAAGAAAGGCTGCTGACTTACATCTGAGGCCACACATCTGCTGAATG 1710
QY 323 AGATAATTAACATCACTAGAAACAGCAAGATGACATATATATGCTAAGTAGCATGT 382
DB 1709 AGATAATTAACATCACTAGAAACAGCAAGATGACATATATATGCTAAGTAGCATGT 1650
QY 383 TTTTGACATTTTCACCCCTTTTAAATATCCACACACAGAGAAAGCAAAAGGAAGCAC 442
DB 1649 TTTTGACATTTTCACCCCTTTTAAATATCCACACACAGAGAAAGCAAAAGGAAGCAC 1590
QY 443 AAGATCCCTGGAGAAATCCCGGCCCATCTTGGGTATGATGAGCCTGCGCCTGT 502
DB 1589 AAGATCCCTGGAGAAATCCCGGCCCATCTTGGGTATGATGAGCCTGCGCCTGT 1530
QY 503 GCCTGGTCCCGCTTGTGAGGAAAGGACATTTAGAAATGATGTGTTCTTAAAGGA 562
DB 1529 GCCTGGTCCCGCTTGTGAGGAAAGGACATTTAGAAATGATGTGTTCTTAAAGGA 1470
QY 563 TGGGCAAGAAACAGATCCTGTTGTGATATTTTGAACGGGATTACAGATTTGAAT 622
DB 1469 TGGGCAAGAAACAGATCCTGTTGTGATATTTTGAACGGGATTACAGATTTGAAT 1410
QY 623 GAAGTACAAAGTGACATTTACCAATGAGAGAAACACAGGAAATCTTGATGGCTT 682
DB 1409 GAAGTACAAAGTGACATTTACCAATGAGAGAAACACAGGAAATCTTGATGGCTT 1350
QY 683 CACAAGACATGCAACAAACAAATGGAATCTGTGATGACATGAGGACCAAGCTGGGG 742
DB 1349 CACAAGACATGCAACAAACAAATGGAATCTGTGATGACATGAGGACCAAGCTGGGG 1290
QY 743 AAGAGATTAACCAAGGGGCAAGAGGTCAGATTCCTGCTGCTTAAACTGTGGCTT 802
DB 1289 AAGAGATTAACCAAGGGGCAAGAGGTCAGATTCCTGCTGCTTAAACTGTGGCTT 1230
QY 803 ATTAACCAATCATTTTCAATTTCTTAACCTCAAAACAAAGCTTGTATATCTGATC 862
DB 1229 ATTAACCAATCATTTTCAATTTCTTAACCTCAAAACAAAGCTTGTATATCTGATC 1170
QY 863 TAGGTTCTTCTGGGCCCAACATTCCTCATATATCCACACACATTTTAAATAT 922
DB 1169 TAGGTTCTTCTGGGCCCAACATTCCTCATATATCCACACACATTTTAAATAT 1110
QY 923 AGTCCAGATCTGTAAGTGAACCTTTGACACTGTAGAATAACATTTACTATTTTGTTC 982
DB 1109 AGTCCAGATCTGTAAGTGAACCTTTGACACTGTAGAATAACATTTACTATTTTGTTC 1050
QY 983 AAGAGCCCTTGTGCTGCTAATATGATGACTGCTGTTTCTTAAAGAGTGTTCG 1042
```

```

|||||
DB 1049 AAGAGCCCTTGTGCTGCTAATATGATGACTGTTTCTTAAAGAGTGTTCG 990
QY 1043 GCCAGGAGATCTGTGAACAGGCTGGGAAGCATCTCAAGATCTTTCAGAGTTATCTTA 1102
DB 989 GCCAGGAGATCTGTGAACAGGCTGGGAAGCATCTCAAGATCTTTCAGAGTTATCTTA 930
QY 1103 CTAGCACACAGCATGATCATTTAGGAGTGAATATATCAATCAATCATCTCAGTGTCT 1162
DB 929 CTAGCACACAGCATGATCATTTAGGAGTGAATATATCAATCAATCATCTCAGTGTCT 870
QY 1163 TTGCCATGATGAAATTTCAATTTCCCATTTTGTGGCCATTTCTAAGACCTCAAAATGTA 1222
DB 869 TTGCCATGATGAAATTTCAATTTCCCATTTTGTGGCCATTTCTAAGACCTCAAAATGTA 810
QY 1223 TTCCATTAATATACAGATTAATCTTTTAACTGAGAAATTCATGTTACATG 1282
DB 809 TTCCATTAATATACAGATTAATCTTTTAACTGAGAAATTCATGTTACATG 750
QY 1283 CAGCTATGGAAATTTATATACATATTTGTTTCCAGTGCAGAAAGATGACTAAGCTCTTA 1342
DB 749 CAGCTATGGAAATTTATATACATATTTGTTTCCAGTGCAGAAAGATGACTAAGCTCTTA 690
QY 1343 TCCCTCCCTTTGTTGATTTTTCAGATTAAGTTAAATGCTTAGCCTTGATG 1402
DB 689 TCCCTCCCTTTGTTGATTTTTCAGATTAAGTTAAATGCTTAGCCTTGATG 630
QY 1403 AGGCTGATACAGC 1416
DB 629 AGGCTGATACAGC 616

RESULT 13
US-09-895-814-470/c
: Sequence 470, Application US/09895814
: Publication No. US20020193296A1
: GENERAL INFORMATION:
: APPLICANT: Xu, Jiangchun
: APPLICANT: Dillon, Davin C.
: APPLICANT: Mitcham, Jennifer L.
: APPLICANT: Harlocker, Susan L.
: APPLICANT: Jiang, Yuguu
: APPLICANT: Kalos, Michael D.
: APPLICANT: Retter, Marc W.
: APPLICANT: Stolk, John A.
: APPLICANT: Day, Craig H.
: APPLICANT: Vedvick, Thomas S.
: APPLICANT: Carter, Derrick
: APPLICANT: Li, Samuel X.
: APPLICANT: Wang, Aljun
: APPLICANT: Skelky, Yasir A.W.
: APPLICANT: Hepler, William T.
: APPLICANT: Henderson, Robert A.
: APPLICANT: Hural, John
: APPLICANT: McNeill, Patricia D.
: APPLICANT: Houghton, Raymond L.
: APPLICANT: Vinals de Bassols, Carlota
: APPLICANT: Foy, Teresa
: APPLICANT: Fanger, Gary R.
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
: TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
: FILE REFERENCE: 210121.427C26
: CURRENT APPLICATION NUMBER: US/09/895,814
: CURRENT FILING DATE: 2001-06-29
: NUMBER OF SEQ ID NOS: 990
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 470
: LENGTH: 2426
: TYPE: DNA
: ORGANISM: Homo sapiens
: US-09-895-814-470

Query Match      56.7%; Score 1154; DB 10; Length 2426;
```


QY 503 GCCTGCTCCCGCTTGTGAGGAAAGACATTAGAAAAATGATGTGTCCTTAAAGGA 562
DB 1529 GCTTGTGCTCCCGCTTGTGAGGAAAGACATTAGAAAAATGATGTGTCCTTAAAGGA 1470
QY 563 TGGGCAAGGAAAGACATGCTGTGATATTTATTTGAAAGGATTTACGATTTGAAAT 622
DB 1469 TGGGCAAGGAAAGACATGCTGTGATATTTATTTGAAAGGATTTACGATTTGAAAT 1410
QY 623 GAAGTCACAAAGTACATTTACCAATGAGAGAAAACAGAGAAAATCTTGATGGCTT 682
DB 1409 GAAGTCACAAAGTACATTTACCAATGAGAGAAAACAGAGAAAATCTTGATGGCTT 1350
QY 683 CACAAACATGCAACAAACAAATGCAATATCTGTATGACATGAGCCAGCAAGCTGGGG 742
DB 1349 CACAAACATGCAACAAACAAATGCAATATCTGTATGACATGAGCCAGCAAGCTGGGG 1290
QY 743 AGGAGATTAACCAAGGGGCAAGAGGATGAGATTTGAGCCCTGCTTAAACCTGGCTTC 802
DB 1289 AGGAGATTAACCAAGGGGCAAGAGGATGAGATTTGAGCCCTGCTTAAACCTGGCTTC 1230
QY 803 ATTAACCAATTCATTTCTATTTCTTAAACCTCAAAACAAAGCTGTGTAATATCTGATCTC 862
DB 1229 ATTAACCAATTCATTTCTATTTCTTAAACCTCAAAACAAAGCTGTGTAATATCTGATCTC 1170
QY 863 TAGGTTCCCTTGGGGCCCAACATTTCTCAATATATCCAGCCACACATCTTTTAATATT 922
DB 1169 TAGGTTCCCTTGGGGCCCAACATTTCTCAATATATCCAGCCACACATCTTTTAATATT 1110
QY 923 AGTTCCAGATCTGTACTGTGACCTTCTTCACTGTAGATAATACATTTACTTGTGTC 982
DB 1109 AGTTCCAGATCTGTACTGTGACCTTCTTCACTGTAGATAATACATTTACTTGTGTC 1050
QY 983 AAGACCTTTCCTGTGTGCTGCTTAATATGTAGCTGACTGTTTCTTAAGAGAGTGTCTG 1042
DB 1049 AAGACCTTTCCTGTGTGCTGCTTAATATGTAGCTGACTGTTTCTTAAGAGAGTGTCTG 990
QY 1043 GCCCAGGGATCTGTAAACAGCTGGGAAGCATCTCAAAATCTTCCAGGCTTAACTTA 1102
DB 989 GCCCAGGGATCTGTAAACAGCTGGGAAGCATCTCAAAATCTTCCAGGCTTAACTTA 930
QY 1103 CTAGCACACAGCATGATCTTACGAGTGAATATATCTTAATCAACATCTCTAGTGTCT 1162
DB 929 CTAGCACACAGCATGATCTTACGAGTGAATATATCTTAATCAACATCTCTAGTGTCT 870
QY 1163 TTGCCCATCTGAAATTTCACTTTCCTGCTGCTTCCATCTCAAGACCTCAAAATGTCA 1222
DB 869 TTGCCCATCTGAAATTTCACTTTCCTGCTGCTTCCATCTCAAGACCTCAAAATGTCA 810
QY 1223 TTCCATTAAATACAGATTAACATTTTCTTTTAAACCTGGAAGATTTCAATCTTCAATG 1282
DB 809 TTCCATTAAATACAGATTAACATTTTCTTTTAAACCTGGAAGATTTCAATCTTCAATG 750
QY 1283 CAGCATATGGGAATTAATTAATATTTTCTTCCAGTCAAGATGACTAAGTCTTTA 1342
DB 749 CAGCATATGGGAATTAATTAATATTTTCTTCCAGTCAAGATGACTAAGTCTTTA 690
QY 1343 TCCCTCCCTTGTGATTTTCTTCCAGTCAAGATGACTAAGTCTTTA 1402
DB 689 TCCCTCCCTTGTGATTTTCTTCCAGTCAAGATGACTAAGTCTTTA 630
QY 1403 AGGCTGTATACAGC 1416
DB 629 AGGCTGTATACAGC 616

RESULT 15

US-10-012-896-470/C

; Sequence 470, Application US/10012896

; Publication No. US20020183251A1

; GENERAL INFORMATION:

; APPLICANT: Xu, Jiangchun

; APPLICANT: Dillon, David C.

; APPLICANT: Mitcham, Jennifer L.

APPLICANT: Harlocker, Susan L.
APPLICANT: Jiang, Yugu
APPLICANT: Kalos, Michael D.
APPLICANT: Retter, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Day, Craig H.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Darrick
APPLICANT: Wang, Samuel X.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Hepler, William T.
APPLICANT: Henderson, Robert A.
APPLICANT: Hural, John
APPLICANT: McNeill, Patricia D.
APPLICANT: Houghton, Raymond L.
APPLICANT: Vinals de Bassols, Carlota
APPLICANT: Foy, Teresa
APPLICANT: Fanger, Gary R.
APPLICANT: Wantanabe, Yoshihiro
APPLICANT: Meagher, Madeleine Joy
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427C27
CURRENT FILING DATE: 05/10/012, 896
CURRENT APPLICATION NUMBER: 2001-12-10
SOFTWARE: FastSeq for Windows Version 3.0
SEQUENCE ID NO 470
LENGTH: 2426
TYPE: DNA
ORGANISM: Homo sapiens
US-10-012-896-470

Query Match 56.7%; Score 1154; DB 13; Length 2426;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 263 GGTGAGAAATTAAGAAAGGCTGTGACTTTCATCTGAGGCGCACATCTGTAATG 322
DB 1769 GGTGAGAAATTAAGAAAGGCTGTGACTTTCATCTGAGGCGCACATCTGTAATG 1710
QY 323 AGATTAATTAACATCACTAATAACAGCAATGCAATATTAATGTCTAAGTACATGT 382
DB 1709 AGATTAATTAACATCACTAATAACAGCAATGCAATATTAATGTCTAAGTACATGT 1650
QY 383 TTTTGACATTTCCAGCCCTTTAATATCCACACACAGAGAGCAAAAGGAAGCAC 442
DB 1649 TTTTGACATTTCCAGCCCTTTAATATTCACACACAGAGAGCAAAAGGAAGCAC 1590
QY 443 AGAGATCCCTGGGAGAAATGCCCCGCCCATCTTGGATCATGATGAGCTCGCCCTGT 502
DB 1589 AGAGATCCCTGGGAGAAATGCCCCGCCCATCTTGGATCATGATGAGCTCGCCCTGT 1530
QY 503 GCCTGCTCCCGCTTGTGAGGAAAGACATTTAATAATGAAATGATGTGTTCTTAAAGGA 562
DB 1529 GCCTGCTCCCGCTTGTGAGGAAAGACATTTAATAATGAAATGATGTGTTCTTAAAGGA 1470
QY 563 TGGGCAAGGAAAGACATCTCTGTGATATTTATTTTGAACGGATTTACAGATTTGAAAT 622
DB 1469 TGGGCAAGGAAAGACATCTCTGTGATATTTATTTTGAACGGATTTACAGATTTGAAAT 1410
QY 623 GAAGTCACAAAGTACATTTACCAATGAGAGAAAACAGAGAAAATCTTGATGGCTT 682
DB 1409 GAAGTCACAAAGTACATTTACCAATGAGAGAAAACAGAGAAAATCTTGATGGCTT 1350
QY 683 CACAAACATGCAACAAACAAATGCAATATCTGTATGACATGAGCCAGCAAGCTGGGG 742
DB 1349 CACAAACATGCAACAAACAAATGCAATATCTGTATGACATGAGCCAGCAAGCTGGGG 1290
QY 743 AGGAGATTAACCAAGGGGCAAGAGGATGAGATTTGAGCCCTGCTTAAACCTGGCTTC 802
DB 1289 AGGAGATTAACCAAGGGGCAAGAGGATGAGATTTGAGCCCTGCTTAAACCTGGCTTC 1230

QY 803 ATACCAATCATTTTCATATTTCTAACCCCTCAAAAACAAGCTGTGTATATATCTGATCTC 862
 |||||||
 Db 1229 ATACCAATCATTTTCATATTTCTAACCCCTCAAAAACAAGCTGTGTATATCTGATCTC 1170
 QY 863 TACGGTTCCTCTGGGCCCAACATTCACATATATCCAGCCACACTCATTTTATATATTT 922
 |||||||
 Db 1169 TACGGTTCCTCTGGGCCCAACATTCACATATATCCAGCCACACTCATTTTATATATTT 1110
 QY 923 AGTCCCAAGATCTTACTGACCTTCTACACTGTAGAAATACATTACTCATTTTGTTC 982
 |||||||
 Db 1109 AGTCCCAAGATCTTACTGACCTTCTACACTGTAGAAATACATTACTCATTTTGTTC 1050
 QY 983 AAAGACCCCTGTGTGTGCTGCTATATATAGTACCTGACTGTTTCCCTAGGAGGTCTG 1042
 |||||||
 Db 1049 AAAGACCCCTGTGTGTGCTGCTATATATAGTACCTGACTGTTTCCCTAGGAGGTCTG 990
 QY 1043 GCCCAGGGGATCTGTGTAACAGGCTGGGAAGCATCTCAAGATCTTCCAGGGTTATCTTA 1102
 |||||||
 Db 989 GCCCAGGGGATCTGTGTAACAGGCTGGGAAGCATCTCAAGATCTTCCAGGGTTATCTTA 930
 QY 1103 CTAGCACACAGCATGATCATTTAGGAGTGAATATCTATACACATCATCTCAGTGTCT 1162
 |||||||
 Db 929 CTAGCACACAGCATGATCATTTAGGAGTGAATATCTATACACATCATCTCAGTGTCT 870
 QY 1163 TTGCCCATAGTGAATTCATTTCCCACTTTTGTGCCCATCTCAAGACCTCAAAATGTCA 1222
 |||||||
 Db 869 TTGCCCATAGTGAATTCATTTCCCACTTTTGTGCCCATCTCAAGACCTCAAAATGTCA 810
 QY 1223 TTCCATTATATCAGAGATTAATCTTTTAACTGGAGAGATTCATGTACATG 1282
 |||||||
 Db 809 TTCCATTATATCAGAGATTAATCTTTTAACTGGAGAGATTCATGTACATG 750
 QY 1283 CAGCTATGGGAATTAATTAATATATTTTGTTCAGTGCNAAGATGACTAAGTCTTTA 1342
 |||||||
 Db 749 CAGCTATGGGAATTAATTAATATATTTTGTTCAGTGCNAAGATGACTAAGTCTTTA 690
 QY 1343 TCCCTCCCTTGTGTGATTTTTCAGTATAAAGTTAAATGCTTAGCCTGTACTG 1402
 |||||||
 Db 689 TCCCTCCCTTGTGTGATTTTTCAGTATAAAGTTAAATGCTTAGCCTGTACTG 630
 QY 1403 AGGCTGTATACAGC 1416
 |||||||
 Db 629 AGGCTGTATACAGC 616

Search completed: September 27, 2003, 12:16:05
 Job time : 477.057 secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 26, 2003, 21:39:38 : Search time 4274.73 Seconds
(without alignments)
11581.589 Million cell updates/sec

Title: US-09-402-713A-1
Perfect score: 2037
Sequence: 1 agaaagctgcacacagaataa.....caataaagaattacaaga 2037

Scoring table:
OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 22781392 seqs, 12152238056 residues

Word size : 0

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

EST:*
1: em_estbda:*
2: em_esthum:*
3: em_estln:*
4: em_estnu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hlc:*
9: gb_est1:*
10: gb_est2:*
11: gb_hlc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: em_gss_hum:*
18: em_gss_liv:*
19: em_gss_pln:*
20: em_gss_vrt:*
21: em_gss_fun:*
22: em_gss_man:*
23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_rtd:*
26: em_gss_phg:*
27: em_gss_vrl:*
28: gb_gss1:*
29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	367	18.0	402	9	AA578773
2	238	11.7	290	10	BF373619
3	222	10.9	654	28	AQ319247
4	214	10.5	226	10	BF858371

C	5	214	10.5	394	28	AQ206972	AQ206972 HS_3238_B
C	6	213	10.5	332	10	BF858286	BF858286 RC5-FT019
C	7	198	9.7	282	10	BF373581	BF373581 MRO-FT017
C	8	167	8.2	167	10	BF373406	BF373406 IL2-FT015
C	9	147	7.2	856	9	AT557225	AT557225 PT2.1-15-
C	10	124	6.1	441	10	BF858890	BF858890 RC5-FT019
C	11	99	4.9	572	13	BQ292550	BQ292550 PMO-AN008
C	12	86	4.2	657	9	AT557495	AT557495 PT2.1.7_H
C	13	43	2.1	451	28	AQ246715	AQ246715 HS_2059_B
C	14	26	1.3	305	14	RO1974	RO1974 Y685F01.r1
C	15	26	1.3	371	14	T79384	T79384 Yd74g09.r1
C	16	26	1.3	378	14	R24922	R24922 Yh38g05.r1
C	17	26	1.3	435	10	BE763909	BE763909 RC4-NT005
C	18	26	1.3	437	10	BE763867	BE763867 RC4-NT005
C	19	26	1.3	448	14	T83051	T83051 Yd43d10.r1
C	20	26	1.3	594	12	BM761346	BM761346 K-EST0042
C	21	26	1.3	613	10	AW969419	AW969419 EST381496
C	22	26	1.3	644	12	BM843410	BM843410 K-EST0121
C	23	26	1.3	647	12	BI604102	BI604102 603244033
C	24	26	1.3	691	12	BM761207	BM761207 K-EST0041
C	25	26	1.3	726	9	AT084676	AT084676 o278h07.x
C	26	26	1.3	766	13	BU623156	BU623156 UT-H-FL1-
C	27	26	1.3	823	10	BG715096	BG715096 602676034
C	28	26	1.3	840	9	AL545416	AL545416 AL545416
C	29	26	1.3	847	9	AL530074	AL530074 AL530074
C	30	26	1.3	876	12	BM453922	BM453922 AGENCOURT
C	31	26	1.3	931	12	BM047350	BM047350 603628473
C	32	26	1.3	938	13	BQ226375	BQ226375 AGENCOURT
C	33	26	1.3	943	9	AL540648	AL540648 AL540648
C	34	26	1.3	950	13	BX433585	BX433585 BX433585
C	35	26	1.3	961	13	BU174024	BU174024 AGENCOURT
C	36	26	1.3	984	12	BI517827	BI517827 603042086
C	37	26	1.3	1021	12	BM924430	BM924430 AGENCOURT
C	38	26	1.3	1043	12	BM919376	BM919376 AGENCOURT
C	39	26	1.3	1059	12	BM546894	BM546894 AGENCOURT
C	40	26	1.3	1201	9	AL517341	AL517341 AL517341
C	41	26	1.3	1201	9	AL530467	AL530467 AL530467
C	42	26	1.3	1201	13	BX361048	BX361048 BX361048
C	43	26	1.3	1414	11	BC015146	BC015146 SP_1025_L
C	44	25	1.2	472	28	AZ194043	AZ194043 SP_1025_L
C	45	23	1.1	510	10	BE239955	BE239955 EST404004

ALIGNMENTS

RESULT 1
AA578773
LOCUS
DEFINITION nh24a04.e1 NCI_CGAP_Prl Homo sapiens cdna clone IMAGE:953262, mRNA
ACCESSION AA578773
VERSION AA578773.1
KEYWORDS GI:2356957
SOURCE
ORGANISM Homo sapiens (human)

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: W. Marston Linehan, M.D., Rodrigo Chuquai, M.D.
Michael Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: David B. Kitzman, Ph.D.
CDNA Library Arrayed by: Genome Systems Inc., Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/dbrrp/image/image.html

Insert Length: 565 Std Error: 0.00
 Seq primer: -40ml3 fwd. ET from Amersham
 High quality sequence stop: 373.
 Location/Qualifiers
 1.402

/organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:953262"
 /sex="Male"
 /dev_stage="45 years old"
 /lab_host="DH10B"
 /clone_lib="NCL_CGAP_Prl"
 /note="Vector: PAMP10; Site.1: NotI; Site.2: EcoRI; 1st strand cDNA was primed with oligo(dT)17 on 50 ng of DNase-treated, total cellular RNA obtained from 5,000-10,000 microdissected, histologically normal prostate epithelial cells. Double-stranded cDNA was ligated to EcoRI adaptors, 5 cycles of PCR applied to the cDNA with an adaptor-specific primer, and the resulting PCR product subcloned into PAMP10 by the UDG-cloning method (Life Technologies). Average insert size is 600 bp. NOTE: Not directionally cloned. This library was constructed by David Krizman."

BASE COUNT 128 a 86 c 84 g 104 t

ORIGIN

Query Match 18.0%; Score 367; DB 9; Length 402;
 Best Local Similarity 100.0%; Pred.No.3.4e-147;

Matches 367; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

595 TATTTGACGGATTACAGATTGAAATGATGACAAAGTGACATTACCATGAGAG 654
 |||||||
 36 TATTTGACGGATTACAGATTGAAATGATGACAAAGTGACATTACCATGAGAG 95
 |||||||
 655 AAACGAGAGAGAAATCTTGATGCTTCAACAAGACATGCAACAAACAAATGAAAT 714
 |||||||
 96 AAACGAGAGAGAAATCTTGATGCTTCAACAAGACATGCAACAAACAAATGAAAT 155
 |||||||
 715 GTGATGATGAGAGCGACAGCTGGGAGGAGATTAACAGGGGAGAGGGTCAGAGATT 774
 |||||||
 156 GTGATGATGAGAGCGACAGCTGGGAGGAGATTAACAGGGGAGAGGGTCAGAGATT 215
 |||||||
 775 GTGGCCCTGCTGCTTAACCTGTCATTAACCAATCATTTTCTTAACCTCA 834
 |||||||
 216 GTGGCCCTGCTGCTTAACCTGTCATTAACCAATCATTTTCTTAACCTCA 275
 |||||||
 835 AAACAAAGCTGTTGATATCTGATCTGACGTTCTTCTGGGCCCAACATTTCCAT 894
 |||||||
 276 AAACAAAGCTGTTGATATCTGATCTGACGTTCTTCTGGGCCCAACATTTCCAT 335
 |||||||
 895 TATCCAGCCACATCTATTTTAAATATTTAGTCCAGATCTGACTGTGACCTTTTACA 954
 |||||||
 336 TATCCAGCCACATCTATTTTAAATATTTAGTCCAGATCTGACTGTGACCTTTTACA 395
 |||||||
 955 CTGTAGA 961
 |||||||
 396 CTGTAGA 402

RESULT 2
 BF373619 290 bp mRNA linear EST 24-NOV-2000

LOCUS BF373619
 DEFINITION MR0-FT0175-310800-106-h09 FT0175 Homo sapiens cDNA, mRNA sequence.

ACCESSION BF373619
 VERSION BF373619.1 GI:11335644

KEYWORDS EST.
 SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Cranialia; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 290)
 Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,

TITLE
 JOURNAL
 MEDLINE
 PUBMED

COMMENT

Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
 Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H.,
 Brunstein,A., deoliveira,P.S., Bucher,P., Jongeel,C.V., O'hare,
 M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
 Simpson,A.U.
 Shotgun sequencing of the human transcriptome with ORF expressed
 sequence tags
 Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
 20202663
 10737800
 Contact: Simpson A.J.G.
 Laboratory of Cancer Genetics
 Ludwig Institute for Cancer Research
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
 Brazil
 Tel: +55-11-2704922
 Fax: +55-11-2707001
 Email: asimpson@ludwig.org.br
 This sequence was derived from the FAPESP/LICR Human Cancer Genome
 Project. This entry can be seen in the following URL
 (<http://www.ludwig.org.br/scripts/gethtml2.pl?l=MR0&t=MR0-FT0175-310800-106-h09&t3=2000-08-31&t4=1>)
 Seq primer: puc 18 forward
 High quality sequence stop: 290.
 Location/Qualifiers
 1.290

FEATURES
 source

/organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /dev_stage="Adult"
 /clone_lib="FT0175"
 /note="Organ: prostate.tumor; Vector: puc18; Site.1: SmaI; Site.2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

BASE COUNT 78 a 73 c 53 g 86 t

ORIGIN

Query Match 11.7%; Score 238; DB 10; Length 290;
 Best Local Similarity 100.0%; Pred.No.1.6e-91;

Matches 238; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

740 GGGAGAGATTAACCAAGGGGAGAGGCTAGAGATTCTGGCCCTGCTTAACCTGTGG 799
 |||||||
 21 GGGAGAGATTAACCAAGGGGAGAGGCTAGAGATTCTGGCCCTGCTTAACCTGTGG 80
 |||||||
 800 TTCAATACCAAAATCATTTTCTATTTCTAACCCCAAAACAAAGCTTTGTAATATCTGAT 859
 |||||||
 81 TTCAATACCAAAATCATTTTCTATTTCTAACCCCAAAACAAAGCTTTGTAATATCTGAT 140
 |||||||
 860 CTCTACGGTTCCTTCTGGGCCCAACATTCCTCATATATCCAGCCACACATCTTTAATA 919
 |||||||
 141 CTCTACGGTTCCTTCTGGGCCCAACATTCCTCATATATCCAGCCACACATCTTTAATA 200
 |||||||
 920 TTTAGTCCAGATCTGATCTGACCTTTCTACACTGTAGATAATACATTAATCTATT 977
 |||||||
 201 TTTAGTCCAGATCTGATCTGACCTTTCTACACTGTAGATAATACATTAATCTATT 258

RESULT 3
 A0319247/c 654 bp DNA linear GSS 06-MAY-1999

LOCUS A0319247
 DEFINITION RPII11-108L4.TV RPII-11 Homo sapiens genomic clone RPII-11-108L4,
 genomic survey sequence.

ACCESSION A0319247
 VERSION A0319247.1 GI:4052212

KEYWORDS GSS.
 SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Cranialia; Vertebrata; Euteleostomi;

REFERENCE	TITLE	JOURNAL	COMMENT
1 (Pages 1 to 654)	Mammalia: Eutheria: Primates: Catarrhini; Hominoidea; Homo		
Adams M.D., Rounsley S.D., Zhao S., Linher K., Golden K., Berry K., Granger D., Shih E., Wible C., de Jong P and Venter J.C	Use of human BAC End Sequences for Sequence Ready Map Building		
Unpublished			
Contact: Shaying Zhao, William Nierman, Mark Adams			

FEATURES	Location/Qualifiers
source	1. .654

BASE COUNT ORIGIN	213 a	100 c	139 g	202 t
----------------------	-------	-------	-------	-------

Query Match	10.9%;	Score 222;	DB 28;	Length 654;
Best Local Similarity	100.0%;	Pred. NO. 1.1e-84;		
Matches 222;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

QY	1195	TGCCATTTCACACCCCAAAAGTCACTTCATTAATATACAGAGTTAACTTTTTTTT	125
Db	654	TGCCATTTCACACCTCCAAAATGTCTATTCATTAAATATCACAGAGTTAACTTTTTTTT	595
QY	1255	TTAACTCGGAAGATTCAATGTTACATGACAGCTATGGGAATTTAATACATATTTGTTT	1314
Db	594	TTAACTCGGAAGATTCAATGTTACATGACAGCTATGGGAATTTAATACATATTTGTTT	535
QY	1315	TCCAGTGCAAAGATGACTAAGTCCCTTAATCCCTCCCTTTGTTGATTTTTTTTTCCAGTA	137
Db	534	TCCAGTGCAAAGATGACTAAGTCCCTTAATCCCTCCCTTTGTTGATTTTTTTTTCCAGTA	475
QY	1375	TTAAGTTAAATGCTTAGCCCTTGACACAGAGCTGATACAGC	1416
Db	474	TTAAGTTAAATGCTTAGCCCTTGACACAGAGCTGATACAGC	433

[illegible]

REFERENCE
AUTHORS

1 (bases 1 to 226)
Dias Neto, E., Garcia Correa, R., Veijovskí-Almeida, S., Briones, M. R., Nagai, M. A., da Silva, W. Jr., Zago, M. A., Bordin, S., Costa, F. F., Goldman, G. H., Carvalho, A. F., Matsukuma, A., Babi, G. S., Simpson, D. H., Brunstein, A., deOliveira, P. S., Bucher, P., Jongeneel, C. V., O'Hare

TITLE	M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.
JOURNAL	Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
MEDLINE	Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
PUBMED	20202663
COMMENT	10737800 Contact: Simpson A.J.G.

FEATURES	Location/Qualifiers
source	1. .226

BASE COUNT	79 a	29 c	59 g	59 t
ORIGIN				

Query Match	10.5%;	Score 214;	DB 10;	Length 226;
Best Local Similarity	100.0%;	Pred. No. 3.7e-81;		
Matches 214;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0

QY	846
787	CTTAAACGTGCGTTCCATACCAGTAATCAATTTTCATATTTTCTAAACCTCAAAACAAAGCGT
Db	226 CCTAAACGTGCGTTCCATACCAGTAATCAATTTTCTAAACCTCAAAACAAAGCGT 167
QY	847 TGTATATCTGATCTCTACGGTCCCTTCTGGGCCCAACATCTTCCATATATTCAGCCACA 906
Db	166 TGTATATCTGATCTCTACGGTCTCTTCTGGGCCCAACATCTTCCATATATTCAGCCACA 107
QY	907 CTCATTTTTAAATATTTAGTTCCTCCAGATCTGTACTGTGACCTTTCTACACTGTAGATAAC 966
Db	106 CTCATTTTTAAATATTTAGTTCCTCCAGATCTGTACTGTGACCTTTCTACACTGTAGATAAC 47
QY	967 ATTACTCATTTTGTTCNAAAGACCCCTGCTGTGGC 1000
Db	46 ATTACTCATTTTGTTCNAAAGACCCCTGCTGTGGC 13

LOCUS	DEFINITION	394 bp	DNA	linear	GSS 17-SEP-1991
AQ206972/c	AQ206972	HS_3238_B1_G11_MR	CIT	Approved Human Genomic Sperm Library	D Homo sapiens genomic clone Plate=3238 Col=21 Row=N, genomic survey sequence.

SOURCE	ORGANISM
REFERENCE	Homo sapiens (human)
1 (bases 1 to 394)	Homo sapiens
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.

AUTHORS Mahatras,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T., Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and Hood,L.

TITLE Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)

MEDLINE 99380589

PUBMED 10449764

COMMENT Contact: Mahatras GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Sequence Tagged Connector
Plate: 3238 row: N column: 21
Class: BAC ends
High quality sequence stop: 394.
Location/Qualifiers
1. .394
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/clone="Plate=3238 Col=21 Row=N"
/sex="male"
/clone_lib="CIR Approved Human Genomic Sperm Library D"
/note="Organ: sperm; Vector: pBelOBAC11; BAC Clones in E-Coli DH10B"

BASE COUNT 134 a 62 c 93 g 103 t 2 others

ORIGIN

Query Match 10.5%; Score 214; DB 28; Length 394;
Best Local Similarity 99.4%; Pred. No. 3,4e-81;
Matches 314; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 883 ACATTTCATATATCCAGCACATCTTTTAAATTTAGTCCAGATCTGTACTGT 942
|||||
DB 381 ACATTTCATATATCCAGCACATCTTTTAAATTTAGTCCAGATCTGTACTGT 322
|||||

QY 943 GACCTTTCATACCTAGATATACATTTTCTTCAAGACCCCTCGTGTGCTG 1002
|||||
DB 321 GACCTTTCATACCTAGATATACATTTTCTTCAAGACCCCTCGTGTGCTG 262
|||||

QY 1003 CCTAATATAGTACTGCTGTTTTCCTAAGAGAGTCTTGCCAGGGATCTGTGACA 1062
|||||
DB 261 CCTAATATAGTACTGCTGTTTTCCTAAGAGAGTCTTGCCAGGGATCTGTGACA 202
|||||

QY 1063 GGCTGGGAGCATCTCAAGATCTTTCAGAGGTTATCTACTAGCACACAGCATGATCAT 1122
|||||
DB 201 GGCTGGGAGCATCTCAAGATCTTTCAGAGGTTATCTACTAGCACACAGCATGATCAT 142
|||||

QY 1123 TACGAGTGAATATATCAATCAACATCATCTCAGTGTCTTGCCTACTAGTAATTCAT 1182
|||||
DB 141 TACGAGTGAATATATCAATCAACATCATCTCAGTGTCTTGCCTACTAGTAATTCAT 82
|||||

QY 1183 TTCCCACTTTGTGCC 1198
|||||
DB 81 TTCCCACTTTGTGCC 66
|||||

RESULT 6
BF858286 332 bp mRNA linear EST 16-JAN-2001
LOCUS BF858286
DEFINITION RC5-FT0193-201100-012-D06 FT0193 Homo sapiens cDNA, mRNA sequence.
ACCESSION BF858286
VERSION BF858286.1 GI:12246030
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 332)

AUTHORS Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.

TITLE Shotgun sequencing of the human transcriptome with ORF expressed sequence tags

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

MEDLINE 20202663

PUBMED 10737800

COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=RC5&t2=RC5-FT0193-201100-012-D06&t3=2000-11-20&t4=1)
Seq primer: puc 18 forward
High quality sequence stop: 332.
Location/Qualifiers
1. .332
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="FT0193"
/note="Organ: prostate,tumor; Vector: puc18; Site:1; Smai; Site:2; Smai; A mini-library was made by cloning products derived from OREGENS PCR (U.S. Letters Patent application No.196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

BASE COUNT 90 a 84 c 64 g 94 t

ORIGIN

Query Match 10.5%; Score 213; DB 10; Length 332;
Best Local Similarity 100.0%; Pred. No. 9,5e-81;
Matches 213; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 741 GGAGGAGTATACACGGGGGAGGGGACAGATTCGCGCCCTGCTTAATGTGGCGT 800
|||||
DB 61 GGAGGAGTATACACGGGGGAGGGGACAGATTCGCGCCCTGCTTAATGTGGCGT 120
|||||

QY 801 TCATTAACCAATCATTTCTATATTTCTAACCCCTCAAAACAAAGCTGTGTATATCTGATC 860
|||||
DB 121 TCATTAACCAATCATTTCTATATTTCTAACCCCTCAAAACAAAGCTGTGTATATCTGATC 180
|||||

QY 861 TCTACGCTTCTTCTGGGCCCAACATTTCTCAATATATCCAGCACACTATTTTATAT 920
|||||
DB 181 TCTACGCTTCTTCTGGGCCCAACATTTCTCAATATATCCAGCACACTATTTTATAT 240
|||||

QY 921 TTAGTCCAGATCTGACTGACCTTCTAC 953
|||||
DB 241 TTAGTCCAGATCTGACTGACCTTCTAC 273
|||||

RESULT 7
BF373581 282 bp mRNA linear EST 24-NOV-2000
LOCUS BF373581
DEFINITION MRO-FT0175-210800-101-d05 FT0175 Homo sapiens cDNA, mRNA sequence.
ACCESSION BF373581
VERSION BF373581.1 GI:11335606
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

SOURCE	ORGANISM	Hom sapiens (human)
REFERENCE	AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 167) Das Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bata, G.S., Simpson, D.H., Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.J. Shotgun sequencing of the human transcriptome with ORF expressed sequence tags Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
JOURNAL	MEDLINE	20202663
PUBMED		10737800
COMMENT		Contact: Simpson A.J.J. Laboratory of Cancer Genetics Ludwig Institute for Cancer Research Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil Tel: +55-11-2704922 Fax: +55-11-2707001 Email: asimpson@ludwig.org.br This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=IL2&t2=IL2-FT0159-070800-120-H01&t3=2000-08-07&t4=1) Seq primer: puc 18 forward High quality sequence stop: 167. Location/Qualifiers 1. 167 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /def_stage="Adult" /clone_lib="FT0159" /note="Organ: prostate,tumor; Vector: puc18, Site_1: Sma1; Site_2: Sma1; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the puc 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
BASE COUNT		47 a 38 c 49 g 33 t
ORIGIN		
Query Match		8.2%; Score 167; DB 10; Length 167;
Best Local Similarity		100.0%; Pred. No. 7,2e-61;
Matches 167;	Conservative 0;	Mismatches 0; Indels 0; Gaps 0;
QY	419 CACAGGAGCACAAGGAGACACAGAGATCCCTGGGAGAAATGCCCGGCCCATCTTG	478
Db	1 CACGAGGAGCCACAAGGAGGAGACACAGAGATCCCTGGGAGAAATCCCGGCCCATCTTG	60
OY	479 GGCATGATGATGAGCCTCGCCTGTGCGCTGGCGCCGCTTGAGAGGAGGACATAGAAAA	538
Db	61 GGCATGATGATGAGCCTCGCCTGTGCGCTGGCGCTTGAGAGGAGGACATAGAAAA	120
OY	539 TGAATGATGATGATCTTAAAGAGATGGGAGGAGAAACAGATCCCTGT	585
Db	121 TGAATGATGATGATCTTAAAGAGATGGGAGGAGAAACAGATCCCTGT	167
RESULT 9		
LOCUS	AI557225	856 bp mRNA linear EST 09-AUG-1999
DEFINITION	PT.1.15_B05.r tumor2 Homo sapiens CDNA 3', mRNA sequence.	
ACCESSION	AI557225	
VERSION	AI557225.1	GI:4489588
KEYWORDS	EST.	
SOURCE	Homo sapiens (human)	
ORGANISM	Homo sapiens	

Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpsoneludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=PMO&tc2=PMO-AN0087-240501-019-a06&tc3=2001-05-24&tc4=1)
Seq primer: puc 18 forward
High quality sequence stop: 572.

FEATURES

source

1. 572
Location/Qualifiers

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/dev_stage="Adult"

/clone_id="AN0087"

/note="Organ: amnion-normal; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

BASE COUNT

150 a 90 c 169 g 163 t

ORIGIN

Query Match

Best Local Similarity 100.0%; Score 99; DB 13; Length 572;
Pred. No. 1.3e-31;

Matches 99; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY

1 AGAAGCTGCATCGAAGAAACAGAGGAGATTTGTGCTGCAGCCGAGGAGACAC 60

Db

116 AGAAGCTGCATCGAAGAAACAGAGGAGATTTGTGCTGCAGCCGAGGAGACAC 175

QY

61 GAAGATCTGCATGCTGGGAAAGACCTGATACACAG 99

Db

176 GAAGATCTGCATGCTGGGAAAGACCTGATACACAG 214

RESULT 12

AI557495 657 bp mRNA linear EST 09-AUG-1999

LOCUS

PT2.1.7.H12.r tumor2 Homo sapiens cDNA 3', mRNA sequence.

ACCESSION

AI557495

VERSION

AI557495.1 GI:4489858

KEYWORDS

EST.

SOURCE

Homo sapiens (human)

ORGANISM

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE

1 (bases 1 to 657)
Huang, G.M., Ng, W.L., Parkas, J., He, L., Liang, H.A., Gordon, D., Yu, J.

AUTHORS

Prostate cancer expression profiling by cDNA sequencing analysis
Genomics 59 (2), 178-186 (1999)

TITLE

Prostate cancer expression profiling by cDNA sequencing analysis

JOURNAL

Genomics 59 (2), 178-186 (1999)

MEDLINE

99339982

PUBMED

10409429

COMMENT

Contact: Guyang Matthew Huang
Leroy Hood
University of Washington
Department of Molecular Biotechnology, Box 357730, University of
Washington, Seattle, WA 98195
Tel: 5106280100
Fax: 5106280108
Email: huangm@yahoo.com.

FEATURES

Location/Qualifiers

source

1. 657

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone_id="tumor2"

/note="Organ: prostate; Vector: pBluescript; Directional

BASE COUNT

179 a 112 c 153 g 166 t 47 others

ORIGIN

Query Match
Best Local Similarity 100.0%; Score 86; DB 9; Length 657;
Pred. No. 5.3e-26;

Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY

13 CAGAAAACAGAGGAGATTTGTGCTGCAGCCGAGGAGACCGAAGATCTGCAT 72

Db

14 CAGAAAACAGAGGAGATTTGTGCTGCAGCCGAGGAGACCGAAGATCTGCAT 73

QY

73 GGTCGAAGACCTGATACACAG 98

Db

74 GGTCGAAGACCTGATACACAG 99

RESULT 13

AQ246715 451 bp DNA linear GSS 06-OCT-1998

LOCUS

HS-2059_B2_E08_T7 CIT Approved Human Genomic Sperm Library D Homo

DEFINITION

sapiens genomic clone Plate=2059 Col=16 Row=J, genomic survey

ACCESSION

AQ246715

VERSION

AQ246715.1 GI:3696897

KEYWORDS

GSS.

SOURCE

Homo sapiens (human)

ORGANISM

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE

1 (bases 1 to 451)
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

AUTHORS

Mahairas, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T.,
Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D., and
Hood, L.

TITLE

Sequence-tagged connectors: A sequence approach to mapping and
scanning the human genome

JOURNLT

Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)

MEDLINE

99380589

PUBMED

10449764

COMMENT

Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Sequence Tagged Connector
Plate: 2059 row: J column: 16
Class: BAC ends
High quality sequence stop: 451.

FEATURES

Location/Qualifiers

source

1. 451

/organism="Homo sapiens"

/mol_type="genomic DNA"

/db_xref="taxon:9606"

/clone="Plate=2059 Col=16 Row=J"

/sex="male"

/clone_id="CIT"

/note="Organ: sperm; Vector: pBeloBAC11; BAC Clones in
E-Coli DH10B"

BASE COUNT

133 a 101 c 86 g 130 t 1 others

ORIGIN

Query Match
Best Local Similarity 100.0%; Score 43; DB 28; Length 451;
Pred. No. 2e-07;

Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY

1910 TTGGCAATCATCTGCTCACTTATCTCACTTGAAGATCTGT 1952

Db

26 TTGGCAATCATCTGCTCACTTATCTCACTTGAAGATCTGT 68

```

RESULT 14
R01974      305 bp      mRNA      linear      EST 31-MAR-1995
LOCUS       ye85f01.r1 Soares fetal liver spleen INFUS Homo sapiens cDNA clone
DEFINITION  IMAGE:124537 5', mRNA sequence.
ACCESSION   R01974
VERSION     R01974.1 GI:751710
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
ORGANISM    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE   1 (bases 1 to 305)
AUTHORS     Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman
             M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Maria,M., Parsons,J.,
             Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevasakis,E., Waterston
             R., Williamson,A., Wohldmann,P. and Wilson,R.
             The WashU-Merck EST Project
TITLE       Unpublished
JOURNAL
COMMENT     Contact: Wilson RK
             Washington University School of Medicine
             4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
             Tel: 314 286 1800
             Fax: 314 286 1810
             Email: est@watson.wustl.edu
             Insert Size: 864
             High quality sequence stops: 200 Source: IMAGE Consortium, LNL
             This clone is available royalty-free through LNL; contact the
             IMAGE Consortium (info@image.llnl.gov) for further information.
             Insert Length: 864 Std Error: 0.00
             Seq primer: M13Rpl
             High quality sequence stop: 200.
             Location/Qualifiers
               1..305
               /organism="Homo sapiens"
               /mol_type="mRNA"
               /db_xref="GDB:477082"
               /db_xref="taxon:9606"
               /clone="IMAGE:124537"
               /sex="male"
               /dev_stage="20 week-post conception fetus"
               /lab_host="DH10B (ampicillin resistant)"
               /clone_lib="Soares fetal liver spleen INFUS"
               /note="Organ: Liver and Spleen; Vector: pT73D (Pharmacia)
               with a modified polylinker; Site_1: Pac I; Site_2: Eco RI;
               1st strand cDNA was primed with a Pac I - oligo(dT) primer
               [5' AACGAGAGAAATTAATTAAGATCTTTTCTTTTCTTTT 3'],
               double-stranded cDNA was ligated to Eco RI adaptors
               (Pharmacia), digested with Pac I and cloned into the Pac I
               and Eco RI sites of the modified pT73 vector. Library
               went through one round of normalization. Library
               constructed by Bento Soares and M.Patima Bonaldo."
BASE COUNT  76 a      68 c      69 g      86 t      6 others
ORIGIN
Query Match 1.3%; Score 26; DB 14; Length 305;
Best Local Similarity 100.0%; Pred. No. 4.4;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1142 TCACATCATCTCTCAGTGTCTTGGC 1167
|||||
Db 20 TCACATCATCTCTCAGTGTCTTGGC 45

RESULT 15
T79384      371 bp      mRNA      linear      EST 15-MAR-1995
LOCUS       yd74g09.r1 Soares fetal liver spleen INFUS Homo sapiens cDNA clone
DEFINITION  IMAGE:114016 5', mRNA sequence.
ACCESSION   T79384
VERSION     T79384.1 GI:697893
KEYWORDS    EST.

```

```

SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE   1 (bases 1 to 371)
AUTHORS     Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman
             M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Maria,M., Parsons,J.,
             Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevasakis,E., Waterston
             R., Williamson,A., Wohldmann,P. and Wilson,R.
             The WashU-Merck EST Project
TITLE       Unpublished
JOURNAL
COMMENT     Other_ESTS: yd74g09.s1
             Contact: Wilson RK
             Washington University School of Medicine
             4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
             Tel: 314 286 1800
             Fax: 314 286 1810
             Email: est@watson.wustl.edu
             Insert Size: 1236
             High quality sequence stops: 275 Source: IMAGE Consortium, LNL
             This clone is available royalty-free through LNL; contact the
             IMAGE Consortium (info@image.llnl.gov) for further information.
             Insert Length: 1236 Std Error: 0.00
             Seq primer: M13Rpl
             High quality sequence stop: 275.
             Location/Qualifiers
               1..371
               /organism="Homo sapiens"
               /mol_type="mRNA"
               /db_xref="GDB:469633"
               /db_xref="taxon:9606"
               /clone="IMAGE:114016"
               /sex="male"
               /dev_stage="20 week-post conception fetus"
               /lab_host="DH10B (ampicillin resistant)"
               /clone_lib="Soares fetal liver spleen INFUS"
               /note="Organ: Liver and Spleen; Vector: pT73D (Pharmacia)
               with a modified polylinker; Site_1: Pac I; Site_2: Eco RI;
               1st strand cDNA was primed with a Pac I - oligo(dT) primer
               [5' AACGAGAGAAATTAATTAAGATCTTTTCTTTTCTTTT 3'],
               double-stranded cDNA was ligated to Eco RI adaptors
               (Pharmacia), digested with Pac I and cloned into the Pac I
               and Eco RI sites of the modified pT73 vector. Library
               went through one round of normalization. Library
               constructed by Bento Soares and M.Patima Bonaldo."
BASE COUNT  105 a     81 c     70 g     113 t     2 others
ORIGIN
Query Match 1.3%; Score 26; DB 14; Length 371;
Best Local Similarity 100.0%; Pred. No. 4.3;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1142 TCACATCATCTCTCAGTGTCTTGGC 1167
|||||
Db 127 TCACATCATCTCTCAGTGTCTTGGC 152

```

Search completed: September 27, 2003, 11:35:43
 Job time : 4278.73 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: September 26, 2003, 19:57:16 ; Search time 3185 Seconds

(without alignments)
655,068 Million cell updates/sec

Title: US-09-402-713a-2

Perfect score: 51

Sequence: 1 MFHHSPPFYPHPTQEAQKE.....HGGSSMLACIVPIVREGH 51

Scoring table:
OLIGO
Xgapop 60.0 , Xgapext 60.0
Ygapop 60.0 , Ygapext 60.0
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2888711 segs, 20454813386 residues

Word size: 1

Total number of hits satisfying chosen parameters: 5773124

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Command line parameters:

-MODEL=frame+g2n.model -DEV=xlh
-O=/cgn2_1/USPRO.spool/US09402713/runat_26092003_143059_16960/app-query.fasta_1.199
-DB=genfmb1 -QPM=fastap -SUFFIX=olig.rge -MINMATCH=0.1 -LOOPEL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=oligo -TRANS=human40.cdi -LIST=45
-DOCLIGN=200 -THR.SCORE=quality -THR.MIN=1 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc
-NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09402713_ECGN_1_1_3508_6runat_26092003_143059_16960 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEOBJECT -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV.TIMEOUT=120 -WARN.TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7

Database :

Genfmb1:*
1: gb_ba:*
2: gb_hlg:*
3: gb_in:*
4: gb_cm:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
21: em_or:*
22: em_ov:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sts:*
28: em_un:*

29: em_vi:*
30: em_htg_hum:*
31: em_htg_inv:*
32: em_htg_other:*
33: em_htg_mus:*
34: em_htg_pln:*
35: em_htg_rtd:*
36: em_htg_mam:*
37: em_htg_vrt:*
38: em_sy:*
39: em_htgo_hum:*
40: em_htgo_mus:*
41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	51	100.0	812	6	AR261039 Sequence
2	51	100.0	812	6	AR278570 Sequence
3	51	100.0	812	6	AX1065207 Sequence
4	51	100.0	812	6	AX106690 Sequence
5	51	100.0	812	6	AX140981 Sequence
6	51	100.0	812	6	AX200841 Sequence
7	51	100.0	812	6	AX267497 Sequence
8	51	100.0	820	6	BD082484 PCA3, PCA
9	51	100.0	1872	6	BD082483 PCA3, PCA
10	51	100.0	2037	6	BD082482 PCA3, PCA
11	51	100.0	2229	6	AR261037 Sequence
12	51	100.0	2229	6	AR278568 Sequence
13	51	100.0	2229	6	AX1066205 Sequence
14	51	100.0	2229	6	AX106688 Sequence
15	51	100.0	2229	6	AX140979 Sequence
16	51	100.0	2229	6	AX200839 Sequence
17	51	100.0	2229	6	AX267495 Sequence
18	51	100.0	2426	6	AR261038 Sequence
19	51	100.0	2426	6	AR278569 Sequence
20	51	100.0	2426	6	AX1066206 Sequence
21	51	100.0	2426	6	AX106689 Sequence
22	51	100.0	2426	6	AX140980 Sequence
23	51	100.0	2426	6	AX200840 Sequence
24	51	100.0	2426	6	AX267496 Sequence
25	51	100.0	3112	6	AR261036 Sequence
26	51	100.0	3112	6	AR278567 Sequence
27	51	100.0	3112	6	AX1066204 Sequence
28	51	100.0	3112	6	AX106687 Sequence
29	51	100.0	3112	6	AX140978 Sequence
30	51	100.0	3112	6	AX200838 Sequence
31	51	100.0	3112	6	AX267494 Sequence
32	51	100.0	3582	6	BD082485 PCA3, PCA
33	51	100.0	3923	6	AR261166 Sequence
34	51	100.0	3923	6	AR278697 Sequence
35	51	100.0	3923	6	AX200888 Sequence
36	51	100.0	3923	6	AX267716 Sequence
37	51	100.0	3923	9	AF103907 Homo sapi
38	43	84.3	718	6	AR260894 Sequence
39	43	84.3	718	6	AR278425 Sequence
40	43	84.3	718	6	AX106603 Sequence
41	43	84.3	718	6	AX106532 Sequence
42	43	84.3	718	6	AX140823 Sequence
43	43	84.3	718	6	AX200683 Sequence
44	43	84.3	718	6	AX267339 Sequence
45	43	84.3	718	6	AX267339 Sequence

RESULT 1

ALIGNMENTS

AR261039/c
LOCUS AR261039 812 bp DNA linear PAT 29-JAN-2003
DEFINITION Sequence 471 from patent US 6321716.
ACCESSION AR261039
VERSION AR261039.1 GI:28071802
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 812)
AUTHORS Mashiki,Z. and Harada,J.
TITLE Negative pressure control apparatus for engine mounted in vehicle
JOURNAL Patent: US 6321716-A 471 27-NOV-2001;
FEATURES
source Location/Qualifiers
1. 812
BASE COUNT 198 a 189 c 169 g 256 t
ORIGIN

Alignment Scores:
Pred. No.: 2.37e-44 Length: 812
Score: 51.00 Matches: 51
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: Gaps: 0

US-09-402-713A-2 (1-51) x AR261039 (1-812)

QY 1 MetPheLeuHisIleSerSerProphelysTyrrProHisThrGlnGluAaGlnLysGlu 20
Db 604 ATGTTTTTGACATTTTCACAGCCCTTTAAATATCCACACACAGAGAACAAAAAGGAA 545

QY 21 AlaGlnArgSerLeuGlyGluMetProGlyArgHisLeuGlySerSerMetSerLeuAla 40
Db 544 GCACAGAGATCCCTGGGAGAAATGCCCGCCGCATCTTGATCATCATGAGACCTCGCC 485

QY 41 LeuCysLeuValProLeuValArgGluGlyHis 51
Db 484 CTGTGCTGCTGCCCTGTGTGAGGAGAGACAT 452

RESULT 2
AR278570/c
LOCUS AR278570 812 bp DNA linear PAT 10-APR-2003
DEFINITION Sequence 471 from patent US 6512094.
ACCESSION AR278570
VERSION AR278570.1 GI:29712816
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 812)
AUTHORS Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y.,
Kalis,M.D., Fanger,G.R., Better,M.W., Stolk,J.A., Day,C.H.,
Vedick,T.S., Carter,D., Li,S.X., Wang,A., Skeiky,Y.A.W.,
Hepler,W.T. and Henderson,R.A.
TITLE Compositions and methods for the therapy and diagnosis of prostate
cancer
JOURNAL Patent: US 6512094-A 471 28-JAN-2003;
FEATURES
source Location/Qualifiers
1. 812
BASE COUNT 198 a 189 c 169 g 256 t
ORIGIN

Alignment Scores:
Pred. No.: 2.37e-44 Length: 812
Score: 51.00 Matches: 51
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: Gaps: 0

US-09-402-713A-2 (1-51) x AR278570 (1-812)

QY 1 MetPheLeuHisIleSerSerProphelysTyrrProHisThrGlnGluAaGlnLysGlu 20
Db 604 ATGTTTTTGACATTTTCACAGCCCTTTAAATATCCACACACAGAGAACAAAAAGGAA 545

QY 21 AlaGlnArgSerLeuGlyGluMetProGlyArgHisLeuGlySerSerMetSerLeuAla 40
Db 544 GCACAGAGATCCCTGGGAGAAATGCCCGCCGCATCTTGATCATCATGAGACCTCGCC 485

QY 41 LeuCysLeuValProLeuValArgGluGlyHis 51
Db 484 CTGTGCTGCTGCCCTGTGTGAGGAGAGACAT 452

RESULT 3
AX106207/c
LOCUS AX106207 812 bp DNA linear PAT 30-APR-2001
DEFINITION Sequence 345 from Patent WO0125273.
ACCESSION AX106207
VERSION AX106207.1 GI:13921896
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Skeiky,Y.A., Xu,J., Cheever,M.A. and Reed,S.G.
TITLE Compositions and methods for wtl specific immunotherapy
JOURNAL Patent: WO 0125273-A 345 12-APR-2001;
CORIXA CORPORATION (US)
FEATURES
source Location/Qualifiers
1. 812
BASE COUNT 198 a 189 c 169 g 256 t
ORIGIN

Alignment Scores:
Pred. No.: 2.37e-44 Length: 812
Score: 51.00 Matches: 51
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: Gaps: 0

US-09-402-713A-2 (1-51) x AX106207 (1-812)

QY 1 MetPheLeuHisIleSerSerProphelysTyrrProHisThrGlnGluAaGlnLysGlu 20
Db 604 ATGTTTTTGACATTTTCACAGCCCTTTAAATATCCACACACAGAGAACAAAAAGGAA 545

QY 21 AlaGlnArgSerLeuGlyGluMetProGlyArgHisLeuGlySerSerMetSerLeuAla 40
Db 544 GCACAGAGATCCCTGGGAGAAATGCCCGCCGCATCTTGATCATCATGAGACCTCGCC 485

QY 41 LeuCysLeuValProLeuValArgGluGlyHis 51
Db 484 CTGTGCTGCTGCCCTGTGTGAGGAGAGACAT 452

RESULT 4
AX106690/c
LOCUS AX106690 812 bp DNA linear PAT 30-APR-2001
DEFINITION Sequence 471 from Patent WO0125272.
ACCESSION AX106690
VERSION AX106690.1 GI:13922355
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Xu,J., Skeiky,Y.A., Reed,S.G. and Cheever,M.A.
TITLE Compositions and methods for wtl specific immunotherapy
JOURNAL Patent: WO 0125272-A 471 12-APR-2001;
CORIXA CORPORATION (US)
FEATURES
source Location/Qualifiers
1. 812
BASE COUNT 198 a 189 c 169 g 256 t
ORIGIN

Alignment Scores:
Pred. No.: 2.37e-44 Length: 812
Score: 51.00 Matches: 51
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: Gaps: 0

TITLE Compositions and methods for therapy and diagnosis of prostate cancer
JOURNAL Patent: WO 0125272-A 471 12-APR-2001;
CORIXA CORPORATION (US)
FEATURES location/Qualifiers
source 1..812
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
BASE COUNT 198 a 189 c 169 g 256 t
ORIGIN

Alignment Scores:
Pred. No.: 2.37e-44 Length: 812
Score: 51.00 Matches: 51
Percent Similarity: 100.00% Conservatave: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-09-402-713A-2 (1-51) x AX106690 (1-812)

QY 1 MetPheLeuHisIleSerSerProPheLysTyrProHisThrGlnGluAlaGlnLysGlu 20
Db 604 ATGTTTTCACATTTCCAGCCCTTTAAATATCCACACACAGAGAGCAACAAAGGAA 545

QY 21 AlaGlnArgSerLeuGlyGluMetProGlyArgHisLeuGlySerSerMetSerLeuAla 40
Db 544 GCACAGAGATCCCTGGGAGAAATGCCCGCCCATCTTGGTGATCATGATGAGCCTCC 485

QY 41 LeuCysLeuValProLeuValArgGluLysHis 51
Db 484 CTGTGCTGTGTCCTGCTGTGAGGAGAGACAT 452

RESULT 5
AX140981 812 bp DNA linear PAT 31-MAY-2001
LOCUS AX140981
DEFINITION Sequence 471 from Patent WO0134802.
ACCESSION AX140981
VERSION AX140981.1 GI:14281078
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
AUTHORS Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y.,
Reed,S.G., Kalos,M.D., Retter,M.W., Stolk,J.A., Day,C.H.,
Skelky,Y.A. and Wang,A.
TITLE Compositions and methods for the therapy and diagnosis of prostate cancer
JOURNAL Patent: WO 0134802-A 471 17-MAY-2001;
CORIXA CORPORATION (US)
FEATURES location/Qualifiers
source 1..812
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
BASE COUNT 198 a 189 c 169 g 256 t
ORIGIN

Alignment Scores:
Pred. No.: 2.37e-44 Length: 812
Score: 51.00 Matches: 51
Percent Similarity: 100.00% Conservatave: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-09-402-713A-2 (1-51) x AX140981 (1-812)

QY 1 MetPheLeuHisIleSerSerProPheLysTyrProHisThrGlnGluAlaGlnLysGlu 20
Db 604 ATGTTTTCACATTTCCAGCCCTTTAAATATCCACACACAGAGAGCAACAAAGGAA 545

QY 21 AlaGlnArgSerLeuGlyGluMetProGlyArgHisLeuGlySerSerMetSerLeuAla 40
Db 544 GCACAGAGATCCCTGGGAGAAATGCCCGCCCATCTTGGTGATCATGATGAGCCTCC 485

QY 41 LeuCysLeuValProLeuValArgGluLysHis 51
Db 484 CTGTGCTGTGTCCTGCTGTGAGGAGAGACAT 452

RESULT 7
AX267497 812 bp DNA linear PAT 26-OCT-2001
LOCUS AX267497
DEFINITION Sequence 471 from Patent WO0173032.
ACCESSION AX267497
VERSION AX267497.1 GI:16516261
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
AUTHORS Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y.,
Reed,S.G., Kalos,M.D., Retter,M.W., Stolk,J.A., Day,C.H.,
Fanger,G.R., Fanger,G.R., Retter,M.W., Stolk,J.A., Day,C.H.,

Db 604 ATGTTTTCACATTTCCAGCCCTTTAAATATCCACACACAGAGAGCAACAAAGGAA 545

QY 21 AlaGlnArgSerLeuGlyGluMetProGlyArgHisLeuGlySerSerMetSerLeuAla 40
Db 544 GCACAGAGATCCCTGGGAGAAATGCCCGCCCATCTTGGTGATCATGATGAGCCTCC 485

QY 41 LeuCysLeuValProLeuValArgGluLysHis 51
Db 484 CTGTGCTGTGTCCTGCTGTGAGGAGAGACAT 452

RESULT 6
AX200841 812 bp DNA linear PAT 29-AUG-2001
LOCUS AX200841
DEFINITION Sequence 471 from Patent WO0151633.
ACCESSION AX200841
VERSION AX200841.1 GI:15390744
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
AUTHORS Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y.,
Reed,S.G., Kalos,M.D., Fanger,G.R., Day,C.H., Retter,M.W.,
Stolk,J.A., Skelky,Y.A., Wang,A. and Mesgher,M.J.
TITLE Compositions and methods for the therapy and diagnosis of prostate cancer
JOURNAL Patent: WO 0151633-A 471 19-JUL-2001;
CORIXA CORPORATION (US)
FEATURES location/Qualifiers
source 1..812
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
BASE COUNT 198 a 189 c 169 g 256 t
ORIGIN

Alignment Scores:
Pred. No.: 2.37e-44 Length: 812
Score: 51.00 Matches: 51
Percent Similarity: 100.00% Conservatave: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-09-402-713A-2 (1-51) x AX200841 (1-812)

QY 1 MetPheLeuHisIleSerSerProPheLysTyrProHisThrGlnGluAlaGlnLysGlu 20
Db 604 ATGTTTTCACATTTCCAGCCCTTTAAATATCCACACACAGAGAGCAACAAAGGAA 545

QY 21 AlaGlnArgSerLeuGlyGluMetProGlyArgHisLeuGlySerSerMetSerLeuAla 40
Db 544 GCACAGAGATCCCTGGGAGAAATGCCCGCCCATCTTGGTGATCATGATGAGCCTCC 485

QY 41 LeuCysLeuValProLeuValArgGluLysHis 51
Db 484 CTGTGCTGTGTCCTGCTGTGAGGAGAGACAT 452

RESULT 7
AX267497 812 bp DNA linear PAT 26-OCT-2001
LOCUS AX267497
DEFINITION Sequence 471 from Patent WO0173032.
ACCESSION AX267497
VERSION AX267497.1 GI:16516261
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
AUTHORS Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y.,
Reed,S.G., Kalos,M.D., Retter,M.W., Stolk,J.A., Day,C.H.,
Fanger,G.R., Fanger,G.R., Retter,M.W., Stolk,J.A., Day,C.H.,

TITLE Vedicik,T.S., Carter,D., Li,S.X., Wang,A., Skeiky,Y.A., Hepler,W.T.
and Henderson,R.A.
Compositions and methods for the therapy and diagnosis of prostate
cancer
JOURNAL Patent: WO 0173032-A 471 04-Oct-2001;
CORIXA CORPORATION (US)

FEATURES
source 1. .812
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

BASE COUNT 198 a 189 c 169 g 256 t
ORIGIN

Alignment Scores:

Pred. No.: 2.37e-44 Length: 812
Score: 51.00 Matches: 51
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-09-402-713a-2 (1-51) x AX267497 (1-812)

OY 1 MetPheLeuHisIleSerSerProPheLysTYrProHisThrGlnGluAglInySglu 20
|||||

DB 604 ATGTTTTCACATTTCCAGCCCTTTAAATATCCACACACAGAGAGCAAAAGAA 545
|||||

OY 21 AlaGlnArgSerLeuGluMetProGlyArgHisLeuGlySerSerMetSerLeuAla 40
|||||

DB 544 GCACAGAGATCCCTGGAGAAATGCCGCGGCATCTGGGTATGATGAGACCTCGCC 485
|||||

OY 41 LeuCysLeuValProLeuValArgGluGlnHis 51
|||||

DB 484 CTGTGCTGTGCTCCGCTTGTGAGAGAGACAT 452
|||||

RESULT 8
BD082484 820 bp DNA linear PAT 27-AUG-2002
LOCUS

DEFINITION PCA3, PCA3 genes, and methods of use.
BD082484

ACCESSION BD082484.1 GI:22628094
VERSION

KEYWORDS JP 2001522240-A/3.
SOURCE

ORGANISM Mastadenovirus
Mastadenovirus
Virus; dsDNA viruses, no RNA stage; Adenoviridae.

REFERENCE 1 (bases 1 to 820)
AUTHORS Bussemakers,M.J.G.
TITLE PCA3, PCA3 genes, and methods of use
JOURNAL Patent: JP 2001522240-A 3 13-NOV-2001;
DIAGNOCURE INC

COMMENT
PN JP 2001522240-A/3
PD 13-NOV-2001
PF 09-APR-1998 JP 1998542194
PR 10-APR-1997 US 60/041836
PI MARION J G BUSSEMAKERS
PC C12N15/00,C12N15/12,C12N5/12,C12N1/21,C07K14/47,C07K16/18, PC
C1201/68,
PC G01N33/577,A61K39/395,A01K67/027
CC Strandedness: Double;
CC Topology: Linear;
FH Key

FEATURES
source 1. .820
Location/Qualifiers
/organism="Mastadenovirus"
/mol_type="genomic DNA"
/db_xref="taxon:10509"

BASE COUNT 262 a 169 c 191 g 198 t
ORIGIN

Alignment Scores:

Pred. No.: 2.38e-44 Length: 820
Score: 51.00 Matches: 51

Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-09-402-713a-2 (1-51) x BD082484 (1-820)

OY 1 MetPheLeuHisIleSerSerProPheLysTYrProHisThrGlnGluAglInySglu 20
|||||

DB 214 ATGTTTTCACATTTCCAGCCCTTTAAATATCCACACACAGAGAGCAAAAGAA 273
|||||

OY 21 AlaGlnArgSerLeuGluMetProGlyArgHisLeuGlySerSerMetSerLeuAla 40
|||||

DB 274 GCACAGAGATCCCTGGAGAAATGCCGCGGCATCTGGGTATGATGAGACCTCGCC 333
|||||

OY 41 LeuCysLeuValProLeuValArgGluGlnHis 51
|||||

DB 334 CTGTGCTGTGCTCCGCTTGTGAGAGAGACAT 366
|||||

RESULT 9
BD082483 1872 bp DNA linear PAT 27-AUG-2002
LOCUS

DEFINITION PCA3, PCA3 genes, and methods of use.
BD082483

ACCESSION BD082483.1 GI:22628093
VERSION

KEYWORDS JP 2001522240-A/2.
SOURCE

ORGANISM Mastadenovirus
Mastadenovirus
Virus; dsDNA viruses, no RNA stage; Adenoviridae.

REFERENCE 1 (bases 1 to 1872)
AUTHORS Bussemakers,M.J.G.
TITLE PCA3, PCA3 genes, and methods of use
JOURNAL Patent: JP 2001522240-A 2 13-NOV-2001;
DIAGNOCURE INC

COMMENT
PN JP 2001522240-A/2
PD 13-NOV-2001
PF 09-APR-1998 JP 1998542194
PR 10-APR-1997 US 60/041836
PI MARION J G BUSSEMAKERS
PC C12N15/00,C12N15/12,C12N5/12,C12N1/21,C07K14/47,C07K16/18, PC
C1201/68,
PC G01N33/577,A61K39/395,A01K67/027
CC Strandedness: Double;
CC Topology: Linear;
FH Key

FEATURES
source 1. .1872
Location/Qualifiers
/organism="Mastadenovirus"
/mol_type="genomic DNA"
/db_xref="taxon:10509"

BASE COUNT 567 a 389 c 369 g 539 t 8 others
ORIGIN

Alignment Scores:

Pred. No.: 4.51e-44 Length: 1872
Score: 51.00 Matches: 51
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-09-402-713a-2 (1-51) x BD082483 (1-1872)

OY 1 MetPheLeuHisIleSerSerProPheLysTYrProHisThrGlnGluAglInySglu 20
|||||

DB 214 ATGTTTTCACATTTCCAGCCCTTTAAATATCCACACACAGAGAGCAAAAGAA 273
|||||

OY 21 AlaGlnArgSerLeuGluMetProGlyArgHisLeuGlySerSerMetSerLeuAla 40
|||||

DB 274 GCACAGAGATCCCTGGAGAAATGCCGCGGCATCTGGGTATGATGAGACCTCGCC 333
|||||

OY 41 LeuCysLeuValProLeuValArgGluGlnHis 51
|||||

DB 334 CTGTGCTGTGTCGCCGCTTGTGAGGAGACAT 366

RESULT 10
BD082482

LOCUS BD082482 2037 bp DNA linear PAT 27-AUG-2002

DEFINITION PC3, PC3 genes, and methods of use.

ACCESSION BD082482

VERSION BD082482.1 GI:22628092

KEYWORDS JP 2001522240-A/1.

SOURCE Mastadenovirus

ORGANISM Mastadenovirus

REFERENCE 1 (bases 1 to 2037)
Virus; dsDNA viruses, no RNA stage; Adenoviridae.
AUTHORS Bussemakers, M.J.G.
TITLE PC3, PC3 genes, and methods of use
JOURNAL DIAGNOSTIC INC SECRETARY OF THE DEPARTMENT OF HEALTH HUMAN SERVICES
COMMENT PN JP 200152240-A/1
PD 13-NOV-2001
PF 09-APR-1998 JP 1998542194
PR 10-APR-1997 US 60/041836
PI MARION J G BUSSEMAKERS
PC C12N15/00, C12N15/12, C12N5/12, C12N1/21, C07K14/47, C07K16/18, PC C12Q1/68
PC G01N33/577, A61K39/395, A01K67/027
CC Strandedness: Double;
CC Topology: Linear;
FH key Location/Qualifiers
FT CDS Location/Qualifiers
1. 2037
/organism="Mastadenovirus"
/mol_type="genomic DNA"
/db_xref="taxon:10509"

BASE COUNT 622 a 426 c 406 g 575 t 8 others

ORIGIN

Alignment Scores:
Pred. No.: 4.82e-44 Length: 2037
Score: 51.00 Matches: 51
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 0

US-09-402-713a-2 (1-51) x BD082482 (1-2037)

QY 1 MetPheLeuHisIleSerSerProPheLysTyrProHisThrGlnGluAlaGlnLysGlu 20
|||||
DB 379 ATGTTTGGACATTTCCAGCCCTTTAAATATCCACACACAGAGAACAAAGAA 438

QY 21 AlaGlnArgSerLeuGlyGluMetProGlyArgHisLeuGlySerSerMetSerLeuAla 40
|||||
DB 439 GCACAGAGATCCCTGGGAGAAATGCCGCCCATCTTGGTCAATCATGATGAGCCTCGCC 498

QY 41 LeuCysLeuValProLeuValArgGlnGlyHis 51
|||||
DB 499 CTGTGCTGTGTCGCCGCTTGTGAGGAGACAT 531

RESULT 11
AR261037 2229 bp DNA linear PAT 29-JAN-2003

LOCUS AR261037

DEFINITION Sequence 469 from patent US 6321716.

ACCESSION AR261037

VERSION AR261037.1 GI:28071800

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 2229)
Mashiki, Z., and Harada, J.
TITLE Negative pressure control apparatus for engine mounted in vehicle
JOURNAL Patent: US 6321716-A 469 27-NOV-2001;

FEATURES
source Location/Qualifiers
1. 2229
/organism="unknown"

BASE COUNT 654 a 447 c 481 g 647 t

ORIGIN

Alignment Scores:
Pred. No.: 5.17e-44 Length: 2229
Score: 51.00 Matches: 51
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 0

US-09-402-713a-2 (1-51) x AR261037 (1-2229)

QY 1 MetPheLeuHisIleSerSerProPheLysTyrProHisThrGlnGluAlaGlnLysGlu 20
|||||
DB 1659 ATGTTTGGACATTTCCAGCCCTTTAAATATCCACACACAGAGAACAAAGAA 1600

QY 21 AlaGlnArgSerLeuGlyGluMetProGlyArgHisLeuGlySerSerMetSerLeuAla 40
|||||
DB 1599 GCACAGAGATCCCTGGGAGAAATGCCGCCCATCTTGGTCAATCATGATGAGCCTCGCC 1540

QY 41 LeuCysLeuValProLeuValArgGlnGlyHis 51
|||||
DB 1539 CTGTGCTGTGTCGCCGCTTGTGAGGAGACAT 1507

RESULT 12
AR278568 2229 bp DNA linear PAT 10-APR-2003

LOCUS AR278568

DEFINITION Sequence 469 from patent US 6512094.

ACCESSION AR278568

VERSION AR278568.1 GI:29712814

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 2229)
XU, J., DILLON, D. C., MITCHAM, J. L., HARLOCKER, S. L., JIANG, Y.,
KALOS, M. D., FANGER, G. R., RETTER, M. W., STOLK, J. A., DAY, C. H.,
VEDVICK, T. S., CARTER, D., LI, S. X., WANG, A., SKEIKY, Y. A. W.,
HEPLER, W. T., and HENDERSON, R. A.
TITLE Compositions and methods for the therapy and diagnosis of prostate
cancer
JOURNAL Patent: US 6512094-A 469 28-JAN-2003;
FEATURES
source Location/Qualifiers
1. 2229
/organism="unknown"

BASE COUNT 654 a 447 c 481 g 647 t

ORIGIN

Alignment Scores:
Pred. No.: 5.17e-44 Length: 2229
Score: 51.00 Matches: 51
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 0

US-09-402-713a-2 (1-51) x AR278568 (1-2229)

QY 1 MetPheLeuHisIleSerSerProPheLysTyrProHisThrGlnGluAlaGlnLysGlu 20
|||||
DB 1659 ATGTTTGGACATTTCCAGCCCTTTAAATATCCACACACAGAGAACAAAGAA 1600

QY 21 AlaGlnArgSerLeuGlyGluMetProGlyArgHisLeuGlySerSerMetSerLeuAla 40
|||||
DB 1599 GCACAGAGATCCCTGGGAGAAATGCCGCCCATCTTGGTCAATCATGATGAGCCTCGCC 1540

QY 41 LeuCysLeuValProLeuValArgGlnGlyHis 51
|||||
DB 1539 CTGTGCTGTGTCGCCGCTTGTGAGGAGACAT 1507

```
RESULT 13
LOCUS AX106205 2229 bp DNA linear PAT 30-APR-2001
DEFINITION Sequence 343 from Patent WO0125273.
ACCESSION AX106205
VERSION AX106205.1 GI:13921894
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE
AUTHORS Skelky,Y.A., Xu,J., Cheever,M.A. and Reed,S.G.
TITLE Compositions and methods for wt1 specific immunotherapy
JOURNAL Patent: WO 0125273-A 343 12-APR-2001;
CORIXA CORPORATION (US)
FEATURES
source 1..2229
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
BASE COUNT 654 a 447 c 481 g 647 t
ORIGIN
Alignment Scores:
Pred. No.: 5.17e-44 Length: 2229
Score: 51.00 Matches: 51
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 0
DB: 6

US-09-402-713a-2 (1-51) x AX106205 (1-2229)
QY 1 MetPhleuHisIleSerSerProphelysTYrProHisThrgInuIaGInuysgu 20
DB 1659 ATGTTTTCACATTTCCAGCCCCCTTAATATCCACACACAGGAGCAAAAGGAA 1600
QY 21 AlaGlnArgSerLeuGlyMetProGlyArgHisLeuGlySerSerMetSerLeuAla 40
DB 1599 GCACAGAGATCCCTGGAGAAATGCCGGCCGCACATCTGGTGCATGATGAGCCTCGCC 1540
QY 41 LeuCysLeuValProLeuValArgGluGlyHis 51
DB 1539 CTGTGCTGTGTCCTGCTGTGAGGAGAGACAT 1507

RESULT 14
LOCUS AX106688/c 2229 bp DNA linear PAT 30-APR-2001
DEFINITION Sequence 469 from Patent WO0125272.
ACCESSION AX106688
VERSION AX106688.1 GI:13922353
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE
AUTHORS Xu,J., Skelky,Y.A., Reed,S.G. and Cheever,M.A.
TITLE Compositions and methods for therapy and diagnosis of prostate
cancer
JOURNAL Patent: WO 0125272-A 469 12-APR-2001;
CORIXA CORPORATION (US)
FEATURES
source 1..2229
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
BASE COUNT 654 a 447 c 481 g 647 t
ORIGIN
Alignment Scores:
Pred. No.: 5.17e-44 Length: 2229
Score: 51.00 Matches: 51
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 0
DB: 6

US-09-402-713a-2 (1-51) x AX106688 (1-2229)
QY 1 MetPhleuHisIleSerSerProphelysTYrProHisThrgInuIaGInuysgu 20
DB 1659 ATGTTTTCACATTTCCAGCCCCCTTAATATCCACACACAGGAGCAAAAGGAA 1600
QY 21 AlaGlnArgSerLeuGlyMetProGlyArgHisLeuGlySerSerMetSerLeuAla 40
DB 1599 GCACAGAGATCCCTGGAGAAATGCCGGCCGCACATCTGGTGCATGATGAGCCTCGCC 1540
QY 41 LeuCysLeuValProLeuValArgGluGlyHis 51
DB 1539 CTGTGCTGTGTCCTGCTGTGAGGAGAGACAT 1507

FEATURES
source 1..2229
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
BASE COUNT 654 a 447 c 481 g 647 t
ORIGIN
```

```
Pred. No.: 5.17e-44 Length: 2229
Score: 51.00 Matches: 51
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 0
DB: 6

US-09-402-713a-2 (1-51) x AX106688 (1-2229)
QY 1 MetPhleuHisIleSerSerProphelysTYrProHisThrgInuIaGInuysgu 20
DB 1659 ATGTTTTCACATTTCCAGCCCCCTTAATATCCACACACAGGAGCAAAAGGAA 1600
QY 21 AlaGlnArgSerLeuGlyMetProGlyArgHisLeuGlySerSerMetSerLeuAla 40
DB 1599 GCACAGAGATCCCTGGAGAAATGCCGGCCGCACATCTGGTGCATGATGAGCCTCGCC 1540
QY 41 LeuCysLeuValProLeuValArgGluGlyHis 51
DB 1539 CTGTGCTGTGTCCTGCTGTGAGGAGAGACAT 1507

FEATURES
source 1..2229
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
BASE COUNT 654 a 447 c 481 g 647 t
ORIGIN
Alignment Scores:
Pred. No.: 5.17e-44 Length: 2229
Score: 51.00 Matches: 51
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 0
DB: 6

US-09-402-713a-2 (1-51) x AX140979 (1-2229)
QY 1 MetPhleuHisIleSerSerProphelysTYrProHisThrgInuIaGInuysgu 20
DB 1659 ATGTTTTCACATTTCCAGCCCCCTTAATATCCACACACAGGAGCAAAAGGAA 1600
QY 21 AlaGlnArgSerLeuGlyMetProGlyArgHisLeuGlySerSerMetSerLeuAla 40
DB 1599 GCACAGAGATCCCTGGAGAAATGCCGGCCGCACATCTGGTGCATGATGAGCCTCGCC 1540
QY 41 LeuCysLeuValProLeuValArgGluGlyHis 51
DB 1539 CTGTGCTGTGTCCTGCTGTGAGGAGAGACAT 1507

REFERENCE
AUTHORS Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y.,
Reed,S.G., Kalos,M.D., Retter,M.W., Stolk,J.A., Day,C.H.,
Skelky,Y.A. and Wang,A.
TITLE Compositions and methods for the therapy and diagnosis of prostate
cancer
JOURNAL Patent: WO 0134802-A 469 17-MAY-2001;
CORIXA CORPORATION (US)
FEATURES
source 1..2229
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
BASE COUNT 654 a 447 c 481 g 647 t
ORIGIN
Alignment Scores:
Pred. No.: 5.17e-44 Length: 2229
Score: 51.00 Matches: 51
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 0
DB: 6

US-09-402-713a-2 (1-51) x AX140979 (1-2229)
QY 1 MetPhleuHisIleSerSerProphelysTYrProHisThrgInuIaGInuysgu 20
DB 1659 ATGTTTTCACATTTCCAGCCCCCTTAATATCCACACACAGGAGCAAAAGGAA 1600
QY 21 AlaGlnArgSerLeuGlyMetProGlyArgHisLeuGlySerSerMetSerLeuAla 40
DB 1599 GCACAGAGATCCCTGGAGAAATGCCGGCCGCACATCTGGTGCATGATGAGCCTCGCC 1540
QY 41 LeuCysLeuValProLeuValArgGluGlyHis 51
DB 1539 CTGTGCTGTGTCCTGCTGTGAGGAGAGACAT 1507

FEATURES
source 1..2229
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
BASE COUNT 654 a 447 c 481 g 647 t
ORIGIN
```

Search completed: September 26, 2003, 21:01:01
Job time : 3188 secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: September 26, 2003, 19:55:06 ; Search time 301 Seconds
(without alignments)
457.380 Million cell updates/sec

Title: US-09-402-713A-2

Perfect score: 51
Sequence: 1 MFLHSSPFKYPHTQEAQKE.....HLGSSMSLALCVPLVREGH 51

Scoring table:
OLIGO
Xgapop 60.0 , Xgapext 60.0
Ygapop 60.0 , Ygapext 60.0
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2552756 segs, 1349719017 residues

Word size: 1

Total number of hits satisfying chosen parameters: 5103471

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Command line parameters:

-MODE=frame-p2n model -DEV=xlh
-Q=/cgn2_1/USP10.spool/US09402713/runat_26092003_143059_16949/app_query.fasta.1.199
-DB=V_Geneseq.19Jun03 -QPM=fastlap -SUFFIX=oligo.rng -MINMATCH=0.1 -LOOPEL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=oligo -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR.SCORE=quality -THR.MIN=1 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptio -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09402713.ecgn.1.1.0.grunat_26092003_143059_16949 -NCPU=6 -ICPU=3
-DEV.TIMEOUT=120 -WARP.TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FCGAPOP=6
-FCGAPEXT=7 -YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7

Database :

N_Geneseq.19Jun03: *
1: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1980.DAT: *
2: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT: *
3: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1982.DAT: *
4: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1983.DAT: *
5: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1984.DAT: *
6: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1985.DAT: *
7: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1986.DAT: *
8: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1987.DAT: *
9: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1988.DAT: *
10: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1989.DAT: *
11: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1990.DAT: *
12: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1991.DAT: *
13: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1992.DAT: *
14: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1993.DAT: *
15: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1994.DAT: *
16: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1995.DAT: *
17: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1996.DAT: *
18: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1997.DAT: *
19: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1998.DAT: *
20: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1999.DAT: *
21: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA2000.DAT: *
22: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT: *
23: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT: *
24: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT: *
25: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA2003.DAT: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,

and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match Length	DB ID	Description
c 1	51	100.0	812 21	AAA06690 Human immunogenic
c 2	51	100.0	812 22	AA563899 Human prostate CDN
c 3	51	100.0	812 22	AAH93806 Human prostate-spe
c 4	51	100.0	812 22	AAH85120 Human prostate-spe
c 5	51	100.0	812 22	AAH02871 Prostate tumour an
c 6	51	100.0	812 22	AAH69949 Human P710P invent
c 7	51	100.0	812 25	ABL95270 Human P710P CDNA s
c 8	51	100.0	812 25	ACA59707 Prostate cancer th
c 9	51	100.0	820 19	AAV62429 Prostate cancer an
c 10	51	100.0	876 24	AAD38815 Human PSNA CDNA, p
c 11	51	100.0	1872 19	AAV62428 Prostate cancer an
c 12	51	100.0	2037 19	AAV62427 Prostate cancer an
c 13	51	100.0	2229 21	AAA06688 Human immunogenic
c 14	51	100.0	2229 22	AA563897 Human prostate CDN
c 15	51	100.0	2229 22	AAH93804 Human prostate-spe
c 16	51	100.0	2229 22	AAH85118 Human prostate-spe
c 17	51	100.0	2229 22	AAH02869 Prostate tumour an
c 18	51	100.0	2229 22	AAH69947 Human P710P invent
c 19	51	100.0	2229 24	ABL95268 Human P710P CDNA s
c 20	51	100.0	2229 25	ACA59705 Prostate cancer th
c 21	51	100.0	2426 21	AAA06689 Human immunogenic
c 22	51	100.0	2426 22	AA563898 Human prostate CDN
c 23	51	100.0	2426 22	AAH93805 Human prostate-spe
c 24	51	100.0	2426 22	AAH85119 Human prostate-spe
c 25	51	100.0	2426 22	AAH02870 Prostate tumour an
c 26	51	100.0	2426 22	AAH69948 Human P710P invent
c 27	51	100.0	2426 24	ABL95269 Human P710P CDNA s
c 28	51	100.0	2426 25	ACA59706 Prostate cancer th
c 29	51	100.0	3112 21	AAA06687 Human immunogenic
c 30	51	100.0	3112 22	AA563896 Human prostate CDN
c 31	51	100.0	3112 22	AAH93803 Human prostate-spe
c 32	51	100.0	3112 22	AAH85117 Human prostate-spe
c 33	51	100.0	3112 22	AAH02868 Prostate tumour an
c 34	51	100.0	3112 22	AAH69947 Human P710P invent
c 35	51	100.0	3112 24	ABL95267 Human P710P CDNA s
c 36	51	100.0	3112 25	ACA59704 Prostate cancer th
c 37	51	100.0	3582 19	AAV62430 Prostate cancer an
c 38	51	100.0	3923 22	AA564026 Human CDNA encodin
c 39	51	100.0	3923 22	AAH93861 Gene D33 CDNA sequ
c 40	51	100.0	3923 24	ABK92196 Prostate cancer-as
c 41	51	100.0	3923 24	ABL95397 Human D33 CDNA seq
c 42	51	100.0	3923 25	ACA59834 Prostate cancer th
c 43	46	90.2	449 23	ABV36763 Human prostate exp
c 44	46	90.2	550 23	ABV49867 Human immunogenic
c 45	43	84.3	718 21	AAA06545

RESULT 1
ID AAA06690/c
AAA06690 standard; CDNA; 812 BP.

ALIGNMENTS
ID AAA06690;
AC AAA06690;
DE 13-JUN-2000 (first entry)
DF Human immunogenic prostate tumour protein CDNA sequence SEQ ID NO:471.
DE Human immunogenic prostate tumour protein CDNA sequence SEQ ID NO:471.
KW Human; prostate cancer; diagnosis; tumour; gene therapy; detection;
KW immunogenic; cytostatic; vaccine; ss.
XX
XX Homo sapiens.
OS
XX
XX
XX WO200004149-A2.
XX

PD 27-JAN-2000.
XX
XX 14-JUL-1999; 99MO-US15838.
XX
PR 14-JUL-1998; 98US-0115453.
PR 14-JUL-1998; 98US-0116134.
PR 23-SEP-1998; 98US-0159812.
PR 23-SEP-1998; 98US-0159812.
PR 15-JAN-1999; 99US-0232149.
PR 15-JAN-1999; 99US-0232880.
PR 09-APR-1999; 99US-0288946.
XX
XX (CORI-) CORIXA CORP.
XX
XX Dillon DC, Harlocker SL, Yugu J, Xu J, Mitcham JL;
XX WPI; 2000-171268/15.
XX
XX New polypeptide useful for treating and diagnosing prostate cancer
PT comprises an immunogenic portion of prostate tumor protein -
XX
XX
XX Claim 1; Page 262; 263pp; English.
XX
XX The present invention describes isolated polypeptides, comprising an
CC immunogenic portion of a prostate tumor protein (PTP). The polypeptides
CC and polynucleotides encoding them have cytostatic activity and can be
CC used in vaccines and in gene therapy. The polypeptides and
CC polynucleotides encoding them, antigen presenting cells which express
CC the polypeptides, antibodies against the polypeptides and vaccines
CC comprising them can be used for inhibiting the development of prostate
CC cancer in a patient. The polypeptides can be used to generate antibodies
CC or anti-idiotypic antibodies for passive immuno therapy. A portion of
CC the polynucleotides encoding the polypeptides can be used as a probe or
CC to modulate the expression of the polypeptides. AA06241 to AA06691 and
CC AA82000 to AA82020 represent sequences used in the exemplification of
CC the present invention.
XX
XX Sequence 812 BP; 198 A; 189 C; 169 G; 256 T; 0 other;
SQ
Alignment Scores:
Pred. No.: 7.03e-44 Length: 812
Score: 51.00 Matches: 51
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 21 Gaps: 0
XX
US-09-402-713A-2 (1-51) x AA06690 (1-812)
OY 1 MetPheLeuHisIleSerSerProPheIysTYrProHisThrgIngluAlaInIysglu 20
DB 604 ATGTTTTTGCACATTTCCAGCCCTTTAAATATCCACACACAGGAAACACAAAAGGAA 545
OY 21 AlaGlnArgSerLeuGlyLysMetProGlyArgHisLeuGlySerSerMetSerLeuAla 40
DB 544 GCACAGAGATCCCTGGGAGAAATGCCCGGCCGCCCACTTGGGTCAATCGATGAGCCTCGCC 485
OY 41 LeuCysLeuValProLeuValArgGluGlnHis 51
DB 484 CTGTGCCTGTCCCGCTGTGAGGGAAGACAT 452
RESULT 2
AA863899/c
ID AA863899 standard; cDNA; 812 BP.
XX
XX AA863899;
XX
XX 29-JAN-2002 (first entry)
XX
XX Human prostate cDNA sequence #433.
DE
XX
XX Human; prostate cancer; ss; cytostatic; immunostimulant; tumour.
XX

OS Homo sapiens.
XX
XX PN WO200173032-A2.
XX
XX 04-OCT-2001.
XX
XX 27-MAR-2001; 2001MO-US09919.
XX
XX 27-MAR-2000; 2000US-0536857.
PR 09-MAY-2000; 2000US-0568100.
PR 12-MAY-2000; 2000US-0570737.
PR 13-JUN-2000; 2000US-0593793.
PR 27-JUN-2000; 2000US-0605783.
PR 10-AUG-2000; 2000US-0636215.
PR 29-AUG-2000; 2000US-0651236.
PR 06-SEP-2000; 2000US-0657279.
PR 02-OCT-2000; 2000US-0679426.
PR 10-OCT-2000; 2000US-0685166.
XX
XX (CORI-) CORIXA CORP.
XX
XX
XX Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Kalos MD;
PI Fanger GR, Retter MW, Stolk JA, Day CH, Vedrick TS, Carter D;
PI Li SX, Wang A, Skelky YAW, Hepler WT, Henderson RA;
XX WPI; 2001-639232/73.
XX
XX New human prostate-specific polypeptides and polynucleotides useful for
PT the diagnosis and treatment of cancer, especially prostate cancer -
XX
XX
XX Claim 1; Page 386-387; 579pp; English.
XX
XX The invention relates to isolated prostate-specific
CC polynucleotides, polypeptides, fusion proteins of the polypeptides,
CC antibodies raised against the polypeptides (or antigenic epitopes
CC derived from them) and antigen presenting cells expressing the
CC polypeptides. The antibodies are useful for detecting the presence of
CC cancer, especially prostate cancer. The polypeptides, polynucleotides and
CC the antigen-presenting cells are useful for stimulating and/or expanding
CC T cells specific for a tumour protein, and for inhibiting the development
CC of cancer especially prostate cancer. Compositions comprising the
CC polynucleotide and/or polypeptide are useful for stimulating an immune
CC response, and for treating cancer. The oligonucleotide is useful for
CC detecting cancer. The present sequence is a prostate specific
CC polynucleotide of the invention.
XX
SQ Sequence 812 BP; 198 A; 189 C; 169 G; 256 T; 0 other;
Alignment Scores:
Pred. No.: 7.03e-44 Length: 812
Score: 51.00 Matches: 51
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 22 Gaps: 0
XX
US-09-402-713A-2 (1-51) x AA863899 (1-812)
OY 1 MetPheLeuHisIleSerSerProPheIysTYrProHisThrgIngluAlaInIysglu 20
DB 604 ATGTTTTTGCACATTTCCAGCCCTTTAAATATCCACACACAGGAAACACAAAAGGAA 545
OY 21 AlaGlnArgSerLeuGlyLysMetProGlyArgHisLeuGlySerSerMetSerLeuAla 40
DB 544 GCACAGAGATCCCTGGGAGAAATGCCCGGCCGCCCACTTGGGTCAATCGATGAGCCTCGCC 485
OY 41 LeuCysLeuValProLeuValArgGluGlnHis 51
DB 484 CTGTGCCTGTCCCGCTGTGAGGGAAGACAT 452
RESULT 3
AA893806/c
ID AA893806 standard; cDNA; 812 BP.
XX


```

XX AH93806;
AC
XX 04-OCT-2001 (first entry)
DT
XX Human prostate-specific cDNA sequence P710P #4.
DE
XX Human prostate cancer; prostate-specific; diagnosis; vaccine;
KW cyrostatic; gene therapy; metastasis; ss.
XX
OS Homo sapiens.
XX WO200151633-A2.
XX
XX 19-JUL-2001.
XX
XX 16-JAN-2001; 2001WO-US01574.
XX
XX 14-JAN-2000; 2000US-0483672.
XX
XX (CORI-) CORIXA CORP.
XX
XX Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Reed SG;
PI Kalos MD, Fanger GR, Day CH, Retter MW, Stolk JA, Skelky YAW;
PI Wang A, Meagher MJ;
XX
XX WPI; 2001-425873/45.
XX
XX New polynucleotide encoding a prostate-specific protein, for
PT diagnosing, monitoring and treating prostate cancer in a patient and
PT for use in vaccines -
XX
XX
XX Claim 1; Page 385; 543pp; English.
XX
XX The present invention describes polynucleotide sequences (I) which encode
CC prostate-specific proteins (II). (I) and (II) have cytostatic activity,
CC and can be used in vaccine production and gene therapy. (I), (II),
CC antibodies to (II), fusion proteins comprising (II), and isolated
CC T cells prepared using (I) or (II) are used to treat cancer in a patient.
CC (I) and the antibodies are also used in the detection of cancer in a
CC patient. The cancer that is diagnosed or treated is particularly
CC prostate cancer. (I) and (II) can be used in vaccines. The antibodies or
CC (I) can be used for monitoring the progression of cancer in a patient.
CC (I) and (II) can also be used to improve diagnosis and therapeutic
CC methods for prostate cancer. They can indicate the level of metastasis
CC as well as the prostate volume. AAH93357 to AAH93944 and AAH01115 to
CC AAH01318 represent polynucleotide and amino acid sequences used in the
CC exemplification of the present invention.
XX
XX Sequence 812 BP; 198 A; 189 C; 169 G; 256 T; 0 other;
SQ

```

```

Alignment Scores:
Pred. No.: 7.03e-44 Length: 812
Score: 51.00 Matches: 51
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 22 Gaps: 0

```

US-09-402-713a-2 (1-51) x AAH93806 (1-812)

```

QY 1 MetPheLeuHsIleSerProPhelystyrProHsthrGlnGluAlaGlnLysGlu 20
DB 604 ATGTTTTCACATTTTCACGCCCTTTAAATATCCACACACAGAAACAAAGAA 545
QY 21 AlaGlnArgSerLeuGlyGluMetProGlyArgHisLeuGlySerSerMetSerLeuAla 40
DB 544 GCACAGAGATCCCGGAGAAATGCCCGGCCCATCTTGCGTCATGATGAGCGCTCGCC 485
QY 41 LeucysLeuValProLeuValArgGluGlyHis 51
DB 484 CTGTGCTGGTCCCGCTTGAGGAGAAAGACAT 452

```

```

RESULT 4
ID AAH85120/c
XX AAH85120 standard; cDNA; 812 BP.
XX
XX AAH85120;
AC
XX 25-SEP-2001 (first entry)
DT
XX Human prostate-specific cDNA sequence P710P #4.
DE
XX Human prostate cancer; therapy; diagnosis; cat eye syndrome;
KW chromosome 22q11.2; prostate-specific protein; chromosome 1;
KW prostate specific antigen; PSA; ss.
XX
XX Homo sapiens.
XX
XX WO200134802-A2.
XX
XX 17-MAY-2001.
XX
XX 09-NOV-2000; 2000WO-US30904.
XX
XX 12-NOV-1999; 99US-0439313.
XX
XX 18-NOV-1999; 99US-0443686.
XX
XX (CORI-) CORIXA CORP.
XX
XX Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Reed SG;
PI Kalos MD, Retter MW, Stolk JA, Day CH, Skelky YAW, Wang A;
XX
XX WPI; 2001-308785/32.
XX
XX
XX Isolated polypeptide comprising at least an immunogenic portion of a
PT prostate-specific protein, useful in the diagnosis and therapy of a
PT prostate cancer -
XX
XX Claim 5; Page 284-285; 325pp; English.
XX
XX The present invention describes an isolated polypeptide (P1) comprising
CC at least an immunogenic portion of a prostate-specific protein, or its
CC variant. Also described are polynucleotides (N1) encoding (P1), (P1) and
CC (N1) have cytostatic activity and can be used in vaccine production.
CC The polypeptides, nucleic acids and antibodies from the present
CC invention are useful in the diagnosis and therapy of prostate cancer.
CC Prostate specific genes P704P, P712P, P774P, P775P and B305D are located
CC in a genomic region on chromosome 22q11.2 known as the Cat Eye Syndrome
CC region. Prostate specific antigen (PSA) P501S was located on
CC chromosome 1. AAH84671 to AAH85143 and AAC99000 to AAC99077 represent
CC polynucleotide and polypeptide sequences used in the exemplification
CC of the present invention.
XX
XX Sequence 812 BP; 198 A; 189 C; 169 G; 256 T; 0 other;
SQ

```

```

Alignment Scores:
Pred. No.: 7.03e-44 Length: 812
Score: 51.00 Matches: 51
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 22 Gaps: 0

```

US-09-402-713a-2 (1-51) x AAH85120 (1-812)

```

QY 1 MetPheLeuHsIleSerProPhelystyrProHsthrGlnGluAlaGlnLysGlu 20
DB 604 ATGTTTTCACATTTTCACGCCCTTTAAATATCCACACACAGAAACAAAGAA 545
QY 21 AlaGlnArgSerLeuGlyGluMetProGlyArgHisLeuGlySerSerMetSerLeuAla 40
DB 544 GCACAGAGATCCCGGAGAAATGCCCGGCCCATCTTGCGTCATGATGAGCGCTCGCC 485
QY 41 LeucysLeuValProLeuValArgGluGlyHis 51

```

Db	484	CTGTGCTGTGCTCCGCTTGTGAGGAGACAT	452
Db	AAH02871/c		
XX	ID	AAH02871 standard; cDNA; 812 BP.	
XX	AC		
XX	AAH02871;		
XX	14-JUN-2001	(first entry)	
XX	Prostate tumour antigen cDNA sequence for P710P #4.		
XX	Human; prostate tumour antigen; prostate tumour; therapy; diagnosis;		
XX	prostate cancer; immunogenic; cytostatic; vaccine; ss.		
XX	Homo sapiens.		
XX	W0200125272-A2.		
XX	12-APR-2001.		
XX	04-OCT-2000; 2000MO-US27464.		
XX	04-OCT-1999; 99US-0157455.		
XX	(CORI-) CORIXA CORP.		
XX	Xu J, Skeiky YAM, Reed SG, Cheever MA;		
XX	WPI: 2001-245062/25.		
XX	Prostate specific protein and its encoding polynucleotide, useful for		
XX	the treatment and diagnosis of prostate cancer -		
XX	Claim 4; Page 267; 276pp; English.		
XX	The present invention describes an isolated polypeptide (I) comprising		
XX	at least an immunogenic portion of a prostate tumour antigen protein or		
XX	its variant. (I) have cytostatic activity and can be used in vaccine		
XX	production. (II) prostate tumour antigen polynucleotides, an antigen		
XX	presenting cell (APC e.g. a dendritic cell) that expresses (I), and a		
XX	pharmaceutical composition containing (I) are useful for inhibiting the		
XX	development of cancer in a patient. Antibodies specific for prostate		
XX	specific proteins and oligonucleotides that hybridize to a		
XX	polynucleotide that encodes a prostate specific protein are useful		
XX	for detecting the presence or absence of a cancer or monitoring the		
XX	progression the progression of a cancer, especially prostate cancer.		
XX	AAH02422 to AAH2872, AAB74798 to AAB74821 and AAB74830 are sequences		
XX	used in the exemplification of the present invention.		
XX	Sequence 812 BP; 198 A; 189 C; 169 G; 256 T; 0 other;		
XX	Alignment Scores:		
XX	Pred. NO.:	7.03e-44	Length: 812
XX	Score:	51.00	Matches: 51
XX	Percent Similarity:	100.00%	Conservative: 0
XX	Best local Similarity:	100.00%	Mismatches: 0
XX	Query Match:	100.00%	Indels: 0
XX	DB:	22	Gaps: 0
XX	US-09-402-713A-2 (1-51) x AAH02871 (1-812)		
XX	0Y	1 MetPheLeuHisIleSerSerProPheLysTYrProHISThrGlnGluAlaGlnLysGlu	20
XX	Db	TTTTTGCACATTTCCAGCCCTTTAAATATTCACACACACAGGACCAAAAGAA	545
XX	0Y	21 AlaGlnArgSerLeuGlyGluMetProGlnArgHisLeuGlySerSerMetSerLeuAla	40
XX	Db	544 GCACAGAGATCCCTGGAGAAATGCCGCGCCCATCTTGGGTATCATGATAGCCCTGCC	485
XX	0Y	41 LeuGlyLeuValProLeuValArgGlnGlnHis	51
XX	Db	CTGTGCTGTGCTCCGCTTGTGAGGAGACAT	452

Seq ID	Seq Name	Seq Length	Seq Description
1	AAAF86949/c	812	AAAF86949 standard; cDNA; 812 BP.
2	AAAF86949	812	AAAF86949 (first entry)
3	Human P710P	812	Human P710P inventive antigen coding sequence SEQ ID NO: 345.
4	Human	812	Human; mouse; immunotherapy; cancer; leukaemia; WT1; Wilm's tumour gene; chromosome 11p13; zinc finger transcription factor; ss.
5	Homo sapiens	812	Homo sapiens.
6	WO200125273-A2	812	WO200125273-A2.
7	12-APR-2001	812	12-APR-2001.
8	04-OCT-2000	812	04-OCT-2000; 2000WO-US27465.
9	04-OCT-1999	812	04-OCT-1999; 99US-0157459.
10	(CORI-) CORIXA CORP.	812	(CORI-) CORIXA CORP.
11	Skelky YAM, Xu J, Cheever MA, Reed SG	812	Skelky YAM, Xu J, Cheever MA, Reed SG; WPI: 2001-328324/34.
12	Polypeptide comprising part of the Wilm's Tumour gene product sequence	812	Polypeptide comprising part of the Wilm's Tumour gene product sequence is used in the diagnosis and treatment of malignant diseases e.g. leukemia and cancer associated with WT1 -
13	Disclosure; Page 220; 228pp; English.	812	Disclosure; Page 220; 228pp; English.
14	The present invention describes compositions comprising peptides derived from the Wilm's tumour protein WT1 and methods for their use in treating malignant diseases. Peptides derived from both the murine and human WT1 proteins are provided. The human WT1 gene is found on chromosome 11p13, and the protein was shown to be a zinc finger transcription factor. The immunogenic peptides of the invention are particularly useful in the diagnosis and treatment of cancer and leukaemia. The present sequence is a coding sequence used in the exemplification of the invention.	812	
15	Sequence 812 BP; 198 A; 189 C; 169 G; 256 T; 0 other	812	
16	Alignment Scores:	812	
17	Pred. No.:	7.03e-44	
18	Score:	51.00	
19	Percent Similarity:	100.00%	
20	Best local Similarity:	100.00%	
21	Query Match:	22	
22		Matches:	812
23		Conservative:	51
24		Mismatches:	0
25		Indels:	0
26		Gaps:	0
27	US-09-402-713A-2 (1-51) x AAFF86949 (1-812)	812	
28	1 MetPheLeuHisIleSerSerProPheLeuTYRProHisThrGlnGluAlaGlnLeuGlu	812	
29	604 ATGTTTTCGACATTTCCAGCCCTTTAAATATCCACACACAGAGACACAAAGGAA	812	
30	21 AAGLARGSerLeuGluMetProGlyArgHisLeuGlySerMetSerLeuAla	812	
31	544 GCACAGAGATCCCTGGGAGAAATGCCCGGCCCATCTTGGGTGATGATAGCCTGCC	812	
32	41 LeucysLeuValProLeuValArgGlnGlyHis	812	
33	484 CTCTGCGTGGTCCCTCTGTGAGGAGACAT	812	
34	RESULT 7	812	
35	ABL95270/c	812	
36	ID ABL95270 standard; cDNA; 812 BP.	812	

AC ABL95270;
XX
XX 19-JUL-2002 (first entry)
XX
DE Human P710P cDNA sequence SEQ ID NO 471.
XX
XX Human; cancer; prostate cancer; vaccine; cytostatic; immunostimulant;
KW gene therapy; gene; ss.
XX
XX Homo sapiens.
XX US2002022248-A1.
XX
XX 21-FEB-2002.
XX
XX 12-JAN-2001; 2001US-0759143.
XX
XX 25-FEB-1997; 97US-0806099.
XX 01-AUG-1997; 97US-0904804.
XX 09-FEB-1998; 98US-0020956.
XX 25-FEB-1998; 98US-0030607.
XX 14-JUL-1998; 98US-0115453.
XX 23-SEP-1998; 98US-0139812.
XX 15-JAN-1999; 99US-0232149.
XX 09-APR-1999; 99US-0288946.
XX 13-JUL-1999; 99US-0352616.
XX 12-NOV-1999; 99US-0439313.
XX 18-NOV-1999; 99US-0443686.
XX 14-JAN-2000; 2000US-0483672.
XX 27-MAR-2000; 2000US-0536857.
XX 09-MAY-2000; 2000US-0568100.
XX 12-MAY-2000; 2000US-0570737.
XX 13-JUN-2000; 2000US-0593793.
XX 27-JUN-2000; 2000US-0605783.
XX 10-AUG-2000; 2000US-0636215.
XX 29-AUG-2000; 2000US-0651236.
XX 06-SEP-2000; 2000US-0657279.
XX 02-OCT-2000; 2000US-0679426.
XX 10-OCT-2000; 2000US-0685166.
XX
XX (XUJ/) XU J.
XX (DILL/) DILLON D C.
XX (MITC/) MITCHAM J L.
XX (HARL/) HARLOCKER S L.
XX (JIAN/) JIANG Y.
XX (KALO/) KALOS M D.
XX (FANG/) FANGER G R.
XX (RETT/) RETTER M W.
XX (STOL/) STOLK J A.
XX (DAYC/) DAY C H.
XX (VEDV/) VEDVICK T S.
XX (CART/) CARTER D.
XX (LISX/) LI S X.
XX (WANG/) WANG A.
XX (SKEI/) SKEIKY Y A W.
XX (HEPL/) HEPLER W T.
XX (HEND/) HENDERSON R A.
XX
XX Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Kalos MD;
XX Fanger GR, Retter MW, Stolk JA, Day CH, Vedvick TS, Carter D;
XX Li SX, Wang A, Skeiky YAW, Hepler WT, Henderson RA;
XX WPT; 2002-255649/30.
XX
XX New prostate-specific polynucleotides for diagnosing and treating
XX diseases, in particular prostate cancer, and as markers for the
XX progression of cancer
XX
XX Claim 1: SEQ ID NO 471; 87pp; English.
XX
XX The present invention provides prostate-specific coding sequences and
XX their encoded proteins. These can be used in the diagnosis and treatment
XX of cancers, particularly prostate cancer. The present sequence is a cDNA

CC described in the invention.
XX
XX SQ Sequence 812 BP; 198 A; 189 C; 169 G; 256 T; 0 other;
XX
XX Alignment Scores:
XX Pred. No.: 7,03e-44 Length: 812
XX Score: 51.00 Matches: 51
XX Percent Similarity: 100.00% Conservative: 0
XX Best Local Similarity: 100.00% Mismatches: 0
XX Query Match: 100.00% Indels: 0
XX DB: 24 Gaps: 0
XX
XX US-09-402-713A-2 (1-51) x ABL95270 (1-812)
XX
XX QY 1 MetPheLeuHisIleSerSerProPheIysTrpProHisThrGlnGluAlaGlnIysGlu 20
XX DB 604 ATGTTTGGACATTTCAGCCCTTTAAATTCACACACACAGAGGACCAAAAGGAA 545
XX QY 21 AlaGlnArgSerLeuGlyGluMetProGlyArgHisLeuGlySerSerMetSerLeuAla 40
XX DB 544 GCACAGACATCCCTGGAGAAATGCCCGCCCATCTTGGTCTATCATGAGCTCCGC 485
XX QY 41 LeuCysLeuValProLeuValArgGluGlnHis 51
XX DB 484 CTGTGCTGTGTCCTGCTGTGTGAGGAGAGGACAT 452
XX
XX RESULT 8
XX ACA59707/c
XX ID ACA59707 standard; cDNA; 812 BP.
XX
XX AC ACA59707;
XX
XX DT 10-JUN-2003 (first entry)
XX
XX DE Prostate cancer therapy associated cDNA #450.
XX
XX KW Prostate cancer; vaccine; gene therapy; cytostatic; fusion protein;
XX immunogen; cancer; prostate specific antigen; PSA;
XX KW prostatic acid phosphatase; PAP; prostate specific membrane antigen;
XX PSMA; gene; ss.
XX
XX OS Homo sapiens.
XX
XX PN US2002192763-A1.
XX
XX PD 19-DEC-2002.
XX
XX PF 29-JUN-2001; 2001US-0895793.
XX
XX PR 17-APR-2000; 2000US-157455P.
XX PR 04-OCT-2000; 2000US-0679272.
XX PR 28-MAR-2001; 2001US-0822827.
XX
XX (XUJ/) XU J.
XX (DILL/) DILLON D C.
XX (MITC/) MITCHAM J L.
XX (HARL/) HARLOCKER S L.
XX (JIAN/) JIANG Y.
XX (KALO/) KALOS M D.
XX (FANG/) FANGER G R.
XX (RETT/) RETTER M W.
XX (STOL/) STOLK J A.
XX (DAYC/) DAY C H.
XX (VEDV/) VEDVICK T S.
XX (CART/) CARTER D.
XX (LISX/) LI S X.
XX (WANG/) WANG A.
XX (SKEI/) SKEIKY Y A W.
XX (HEPL/) HEPLER W T.
XX (HEND/) HENDERSON R A.
XX (MCNE/) MCNEILL P D.
XX (HOUG/) HOUGHTON R L.

PA (DBAS/) Y DE BASSOLS C V.
PA (FOYT/) FOY T M.
XX
XX Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Kalos MD;
PI Fanger GR, Retten MW, Stolk JA, Day CH, Vedvick TS, Carter D;
PI Li SX, Wang A, Skeiky YAM, Hepler W, Henderson RA, Hural J;
PI McNeill PD, Houghton RL, Y De Bassols CV, Foy TM;
XX
DR WPI: 2003-352711/33.
XX
XX
PT New fusion protein comprising prostate-specific polypeptides, or its
PT immunogenic portions, useful for diagnosing, preventing and/or treating
PT cancer, particularly prostate cancer
XX
PS Example 16: SEQ ID NO 471: 85bp; English.
XX
XX The invention describes a fusion protein comprising at least one amino
CC acid sequence of immunogenic portions of any of the 3 sequences not
CC defined in the specification, or sequences having at least 70 or 90 %
CC sequence identity to any one of the 35 sequences defined in the USPTO
CC web site, which is encoded by any of the 4 nucleotide sequences not
CC defined in the specification. The fusion protein, composition and
CC methods are useful for diagnosing, preventing and/or treating cancer,
CC particularly prostate cancer. The proteins are useful as markers to
CC indicate the presence or absence of cancer. This sequence
CC represents a prostate cancer therapy associated cDNA.
CC Note: The sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
CC from the US patent office at
XX seqdata.uspto.gov/sequence.html?DocID=US20020192763.
XX
SQ Sequence 812 BP: 198 A; 189 C; 169 G; 256 T; 0 other:

Alignment Scores:
Pred. No.: 7.03e-44 Length: 812
Score: 51.00 Matches: 51
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 25 Gaps: 0

US-09-402-713A-2 (1-51) x ACA59707 (1-812)
OY 1 MetPheLeuHisIleSerSerProPheLysTyrProHisThrGlnuAaGlnLysGlu 20
DB 604 ATGTTTTCACATTTCCAGCCCTTTAATATCCACACACAGGAAAGCAAAAGGAA 545
OY 21 AlaGlnArgSerLeuGluMetProGlyArgHisLeuGlySerSerMetSerLeuAla 40
DB 544 GCACAGAGATCCCTGGGAGAAATGCCCGGCCCATCTTGATGATGAGACCTCGCC 485
OY 41 LeuCysLeuValProLeuValArgGluGlyHis 51
DB 484 CTGTGCTGGTCCCGCTTGTGAGAGGAAGACAT 452
RESULT 9
ID AAV62429 standard; cDNA: 820 BP.
XX
AC AAV62429;
XX
DT 30-DEC-1998 (first entry)
XX
DE Prostate cancer antigen (PCA3) cDNA splice variant 3.
XX
XX Prostate cancer antigen cDNA splice variant 3; PCA3; prostatic cancer;
KM PC; ds.
XX
XX Homo sapiens.
OS
XX
PN MO9845420-A1.
XX
PD 15-OCT-1998.

XX
PF 09-APR-1998; 98WO-CA00346.
XX
XX
PR 10-APR-1997; 97US-0041836.
XX
XX (DIAG-) DIAGNOCURE INC.
XX
XX Bussemakers MJG;
XX
DR WPI: 1998-568347/48.
XX
XX
PT New nucleic acid encoding prostate cancer antigen 3 - for diagnosis,
PT prevention and treatment of prostatic cancer
XX
PS Claim 4: Pages 77-78; 11pp; English.
XX
XX The present sequence represents the prostate cancer antigen (PCA3)
CC cDNA splice variant 3 sequence comprising of exons 1, 3, and 4a
CC of the PCA3 gene. The PCA3 cDNA splice variant 3 sequence,
CC isolated from a human primary prostatic tumour tissue cDNA library,
CC was found in approximately 15% of the cDNA clones isolated. The
CC invention claims for PCA3 cDNA variants and the proteins they encode.
CC The invention also claims for antibodies against PCA3 protein. The
CC antibodies are claimed to be useful for detecting PCA3 protein in
CC immunoassay tests, for diagnosing, assessing and prognosing of
CC prostatic cancer (PC). Antibodies, optionally coupled to a cytotoxin
CC or radioisotope, and nucleic acids antisense to PCA3 cDNA are claimed
CC to be useful for treating PC, while determining elevated levels of
CC PCA3 (as RNA or protein) is useful for detecting a predisposition
CC to development of PC, e.g. in prenatal tests. Detecting PCA3 protein
CC allows differentiation between malignant and benign prostatic disease,
CC and the level of PCA3 expression allows correlation with the grade of
CC tumour. PCA3 protein and its fragments are also claimed to be useful
CC in vaccines for preventing PC; in drug screens for identifying
CC specific (ant)agonists (potentially useful therapeutically) and for
XX studying protein-DNA interactions.
XX
SQ Sequence 820 BP: 262 A; 169 C; 191 G; 198 T; 0 other:

Alignment Scores:
Pred. No.: 7.09e-44 Length: 820
Score: 51.00 Matches: 51
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 19 Gaps: 0

US-09-402-713A-2 (1-51) x AAV62429 (1-820)
OY 1 MetPheLeuHisIleSerSerProPheLysTyrProHisThrGlnuAaGlnLysGlu 20
DB 214 ATGTTTTCACATTTCCAGCCCTTTAATATCCACACACAGGAAAGCAAAAGGAA 273
OY 21 AlaGlnArgSerLeuGluMetProGlyArgHisLeuGlySerSerMetSerLeuAla 40
DB 274 GCACAGAGATCCCTGGGAGAAATGCCCGGCCCATCTTGATGATGAGACCTCGCC 333
OY 41 LeuCysLeuValProLeuValArgGluGlyHis 51
DB 334 CTGTGCTGGTCCCGCTTGTGAGAGGAAGACAT 366
RESULT 10
ID AAD38815 standard; cDNA: 876 BP.
XX
AC AAD38815;
XX
DT 23-SEP-2002 (first entry)
XX
XX Human PSNA cDNA, Pro123.
DE
XX
XX Human; prostate specific protein; PSP; prostate specific nucleic acid;
KM vaccine; transgenic; prostate cancer; gene therapy; transgenic animal;
KW

XX	15-Oct-1998.
PD	
XX	09-APR-1998; 98MO-CA00346.
PF	
XX	10-APR-1997; 97US-0041836.
PR	
XX	(DIAG-) DIAGNOCURE INC.
PA	
XX	Bussemakers MUG;
PI	
XX	WPI: 1998-568347/48.
DR	
XX	New nucleic acid encoding prostate cancer antigen 3 - for diagnosis,
PT	prevention and treatment of prostatic cancer
XX	
PS	Claim 4; Pages 76-77; 11pp; English.
XX	
XX	The present sequence represents the prostate cancer antigen (PCa3)
CC	CDNA splice variant 2 sequence comprising of exons 1, 3, 4a and
CC	4b of the PCa3 gene. The PCa3 CDNA splice variant 2 sequence,
CC	isolated from a human primary prostatic tumour tissue cDNA library,
CC	was found in approximately 65% of the cDNA clones isolated. The
CC	invention claims for PCa3 cDNA variants and the proteins they encode.
CC	The invention also claims for antibodies against PCa3 protein. The
CC	antibodies are claimed to be useful for detecting PCa3 protein in
CC	immunoassay tests, for diagnosing, assessing and prognosing of
CC	prostatic cancer (PC). Antibodies, optionally coupled to a cytotoxin
CC	or radioisotope, and nucleic acids antisense to PCa3 cDNA are claimed
CC	to be useful for treating PC, while determining elevated levels of
CC	PCa3 (as RNA or protein) is useful for detecting a predisposition
CC	to development of PC, e.g. in prenatal tests. Detecting PCa3 protein
CC	allows differentiation between malignant and benign prostatic disease,
CC	and the level of PCa3 expression allows correlation with the grade of
CC	tumour. PCa3 protein and its fragments are also claimed to be useful
CC	in vaccines for preventing PC; in drug screens for identifying
CC	specific (ant)agonists (potentially useful therapeutically) and for
CC	studying protein-DNA interactions.
CC	
XX	Sequence 1872 BP; 567 A; 389 C; 369 G; 539 T; 8 other;
SO	
	Alignment Scores:
	Pred. No.: 1.55e-43 Length: 1872
	Score: 51.00 Matches: 51
	Percent Similarity: 100.00% Conservative: 0
	Best Local Similarity: 100.00% Mismatches: 0
	Query Match: 100.00% Indels: 0
	DB: 19 Gaps: 0
	US-09-402-713A-2 (1-51) x AAV62428 (1-1872)
OY	1 Merpheuenuflileseerprophelystyrproh1stphnglualaglnlyglu 20
DB	214 ATGTTTTTGACATTTCCAGCCCCCTTTAAATTCACACACACAGAAAGCA 273
OY	21 AlaglnarserleuglyglumetpProglYAqhlslaglylserSerMetSerLeuAla 40
DB	274 GCACAGAGATCCCTGGGAGAAATAGCCGCCCCCACTTTGGGTATCATAGAGCTTGGCC 333
OY	41 LeucysleuValProleuValAArglgllyhlsl 51
DB	334 CTGTGCTGTGCTCCGCTGTGAGAGGAGACAT 366
RESULT 12	
AAV62427	
ID	AAV62427 standard; cDNA; 2037 BP.
XX	
AC	AAV62427;
XX	
DT	30-DEC-1998 (first entry)
XX	
DE	Prostate cancer antigen (PCa3) cDNA splice variant 1.

KW Prostate cancer antigen CDNA splice variant 1; PCA3; prostatic cancer;
PC; ds.
XX Homo sapiens.
OS
FH Key Location/Qualifiers
FT CDS 379..534
FT CD5 /*tag= a
FT /*product= "PCA3 protein variant 1"
FT 2019..2024
FT /*tag= b
XX
XX
PN W09845420-A1.
XX
XX 15-OCT-1998.
XX
XX 09-APR-1998; 98WO-CA00346.
XX
XX 10-APR-1997; 97US-0041836.
XX
XX (DIAG-) DIAGNOCURE INC.
XX
XX Bussemakers MJG;
XX
XX WPI: 1998-568347/48.
XX P-PSDB; AAW79736.
XX
XX New nucleic acid encoding prostate cancer antigen 3 - for diagnosis,
XX prevention and treatment of prostatic cancer
XX
XX Claim 3: Fig 2B-2J; 11pp: English.
XX
XX The present sequence represents the prostate cancer antigen (PCA3)
XX CDNA splice variant 1 sequence comprising of exons 1, 2, 3, 4a and
XX 4b of the PCA3 gene. The PCA3 CDNA splice variant 1 sequence,
XX isolated from a human primary prostatic tumour tissue CDNA library,
XX was found in approximately 5% of the CDNA clones isolated. The
XX invention claims for PCA3 CDNA variants and the proteins they encode.
XX The invention also claims for antibodies against PCA3 protein. The
XX antibodies are claimed to be useful for detecting PCA3 protein in
XX immunoassay tests, for diagnosing, assessing and prognosing of
XX prostatic cancer (PC). Antibodies, optionally coupled to a cytotoxin
XX or radioisotope, and nucleic acids antisense to PCA3 CDNA are claimed
XX to be useful for treating PC, while determining elevated levels of
XX PCA3 (as RNA or protein) is useful for detecting a predisposition
XX to development of PC, e.g. in prenatal tests. Detecting PCA3 protein
XX allows differentiation between malignant and benign prostatic disease,
XX and the level of PCA3 expression allows correlation with the grade of
XX tumour. PCA3 protein and its fragments are also claimed to be useful
XX in vaccines for preventing PC; in drug screens for identifying
XX specific (ant)agonists (potentially useful therapeutically) and for
XX studying protein-DNA interactions.
XX
XX Sequence 2037 BP; 622 A; 426 C; 406 G; 575 T; 8 other;
SQ
Alignment Scores:
Pred. No.: 1,67e-43 Length: 2037
Score: 51.00 Matches: 51
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 19 Gaps: 0
US-09-402-713A-2 (1-51) x AAV62427 (1-2037)
QY 1 MetPheLeuHisIleSerSerProPheLysTyrProHisThrGlnGluAlaGlnLysGlu 20
Db 379 AAGTTTTCACACTTTCCAGCCCTTTAAATATCCACACACAGAGAGACACAAAAGGAA 438
QY 21 AlaGlnArgSerLeuGlyGluMetProGlyArgHisLeuGlySerSerMetSerLeuAla 40
Db 439 GCACAGAGATCCCTGGAGAAATAGCCGCGCCGACATCTTGCGTCAATGAGACCTCGCC 498

QY 41 LeuCysLeuValProLeuValArgGluGlyHis 51
Db 499 CTGTGCTGTGTCCTGCTGTGAGGAGAGACAT 531
RESULT 13
ID AAA06688 standard; cDNA; 2229 BP.
XX
XX AAA06688;
AC
XX
XX 13-JUN-2000 (first entry)
DE Human immunogenic prostate tumour protein CDNA sequence SEQ ID NO:469.
XX
XX Human: prostate cancer; diagnosis; tumour; gene therapy; detection;
XX immunogenic; cytostatic; vaccine; ss.
XX
XX Homo sapiens.
XX
XX W0200004149-A2.
XX
XX 27-JAN-2000.
XX
XX 14-JUL-1999; 99WO-US15838.
XX
XX 14-JUL-1998; 98US-0115453.
XX 14-JUL-1998; 98US-0116134.
XX 23-SEP-1998; 98US-0159812.
XX 23-SEP-1998; 98US-0159822.
XX 15-JAN-1999; 99US-0232149.
XX 15-JAN-1999; 99US-0232860.
XX 09-APR-1999; 99US-0288946.
XX
XX (CORI-) CORIXA CORP.
XX
XX Dillion DC, Harlocker SL, Yugu J, Xu J, Mitcham JL;
XX
XX WPI: 2000-171268/15.
XX
XX New polypeptide useful for treating and diagnosing prostate cancer
XX comprises an immunogenic portion of prostate tumor protein -
XX
XX Claim 1; Page 260-261; 263pp: English.
XX
XX The present invention describes isolated polypeptides, comprising an
XX immunogenic portion of a prostate tumour protein (PTP). The polypeptides
XX and polynucleotides encoding them have cytostatic activity and can be
XX used in vaccines and in gene therapy. The polypeptides and
XX polynucleotides encoding them, antigen presenting cells which express
XX the polypeptides, antibodies against the polypeptides and vaccines
XX comprising them can be used for inhibiting the development of prostate
XX cancer in a patient. The polypeptides can be used to generate antibodies
XX or anti-idiotypic antibodies for passive immuno therapy. A portion of
XX the polynucleotides encoding the polypeptides can be used as a probe or
XX to modulate the expression of the polypeptides. AAA06241 to AAA06691 and
XX AAA82000 to AA182020 represent sequences used in the exemplification of
XX the present invention.
XX
XX Sequence 2229 BP; 654 A; 447 C; 481 G; 647 T; 0 other;
SQ
Alignment Scores:
Pred. No.: 1,82e-43 Length: 2229
Score: 51.00 Matches: 51
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 21 Gaps: 0
US-09-402-713A-2 (1-51) x AAA06688 (1-2229)
QY 1 MetPheLeuHisIleSerSerProPheLysTyrProHisThrGlnGluAlaGlnLysGlu 20
Db 1659 AAGTTTTCACACTTTCCAGCCCTTTAAATATCCACACACAGAGAGACACAAAAGGAA 1600

```

Qy      21 AlaGlnArgSerLeuGlyGluMetProGlyArgHisIleuGlySerSerMetSerLeuAla 40
Db      1599 GCACAGAGATCCCTCGGAGAAATGCCGCGCCATCTTGGTCATGATGAGCTCGCC 1540
Qy      41 LeuCysLeuValProLeuValArgGluGlyHis 51
Db      1539 CTGTGCTGTGCTCGCTTGTGAGGAAAGACAT 1507

RESULT 14
AAS63897/C
ID      AAS63897 standard; cDNA; 2229 BP.
XX
AC      AAS63897;
XX
DT      29-JAN-2002 (first entry)
XX
DE      Human prostate cDNA sequence #431.
XX
KW      Human; prostate cancer; ss; cytostatic; immunostimulant; tumour.
XX
OS      Homo sapiens.
XX
PN      MO200173032-A2.
XX
PD      04-OCT-2001.
XX
PF      27-MAR-2001; 2001WO-US09919.
XX
PR      27-MAR-2000; 2000US-0536857.
PR      09-MAY-2000; 2000US-0568100.
PR      12-MAY-2000; 2000US-0570737.
PR      13-JUN-2000; 2000US-0593783.
PR      27-JUN-2000; 2000US-0605783.
PR      10-AUG-2000; 2000US-0636215.
PR      29-AUG-2000; 2000US-0651236.
PR      06-SEP-2000; 2000US-0657279.
PR      02-OCT-2000; 2000US-0679426.
PR      10-OCT-2000; 2000US-0685166.
XX
PA      (CORI-) CORIXA CORP.
XX
PI      Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Kalos MD;
PI      Fanger GR, Retter MW, Stolk JA, Day CH, Vedvick JS, Carter D;
PI      Li SX, Wang A, Skeiky YAM, Hepler WT, Henderson RA;
XX
DR      WPI; 2001-639232/73.
XX
PT      New human prostate-specific polypeptides and polynucleotides useful for
PT      the diagnosis and treatment of cancer, especially prostate cancer -
PS      Claim 1; Page 385; 579pp; English.
XX
XX      The invention relates to isolated prostate-specific
XX      polynucleotides, polypeptides, fusion proteins of the polypeptides,
XX      antibodies raised against the polypeptides (or antigenic epitopes
XX      derived from them) and antigen-presenting cells expressing the
XX      polypeptides. The antibodies are useful for detecting the presence of
XX      cancer, especially prostate cancer. The polypeptides, polynucleotides and
XX      the antigen-presenting cells are useful for stimulating and/or expanding
XX      T cells specific for a tumour protein, and for inhibiting the development
XX      of cancer especially prostate cancer. Compositions comprising the
XX      polynucleotide and/or polypeptide are useful for stimulating an immune
XX      response, and for treating cancer. The oligonucleotide is useful for
XX      detecting cancer. The present sequence is a prostate specific
XX      polynucleotide of the invention.
XX
SQ      Sequence 2229 BP; 654 A; 447 C; 481 G; 647 T; 0 other;

Alignment Scores:
Pred. No.:      1.82e-43      Length:      2229
Score:          51.00      Matches:      51
Percent Similarity: 100.00%      Conservative: 0

```

```

Best Local Similarity: 100.00%      Mismatches: 0
Query Match:          100.00%      Indels: 0
DB:                   22      Gaps: 0

US-09-402-713a-2 (1-51) x AAS63897 (1-2229)

Qy      1 MethLeuHisIleSerSerProPheIysIyrProHisIhrGlnJuaGlnItyGlu 20
Db      1659 ATGTGTTTGCACATTTCCAGCCCTTTAAATATCCACACACACAGAAACAAAGGAA 1600
Qy      21 AlaGlnArgSerLeuGlyGluMetProGlyArgHisIleuGlySerSerMetSerLeuAla 40
Db      1599 GCACAGAGATCCCTCGGAGAAATGCCGCGCCATCTTGGTCATGATGAGCTCGCC 1540
Qy      41 LeuCysLeuValProLeuValArgGluGlyHis 51
Db      1539 CTGTGCTGTGCTCGCTTGTGAGGAAAGACAT 1507

RESULT 15
AAH93804/C
ID      AAH93804 standard; cDNA; 2229 BP.
XX
AC      AAH93804;
XX
DT      04-OCT-2001 (first entry)
XX
DE      Human prostate-specific cDNA sequence P710P #2.
XX
KW      Human; prostate cancer; prostate-specific; diagnosis; vaccine;
KW      cytostatic; gene therapy; metastasis; ss.
XX
OS      Homo sapiens.
XX
PN      MO200151633-A2.
XX
PD      19-JUL-2001.
XX
PF      16-JAN-2001; 2001WO-US01574.
XX
PR      14-JAN-2000; 2000US-0483672.
XX
PA      (CORI-) CORIXA CORP.
XX
PI      Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Reed SG;
PI      Kalos MD, Fanger GR, Day CH, Retter MW, Stolk JA, Skeiky YAM;
PI      Wang A, Meagher MJ;
XX
DR      WPI; 2001-425873/45.
XX
PT      New polynucleotide encoding a prostate-specific protein, for
PT      diagnosing, monitoring and treating prostate cancer in a patient and
PT      for use in vaccines -
PS      Claim 1; Page 383-384; 543pp; English.
XX
XX      The present invention describes polynucleotide sequences (I) which encode
XX      prostate-specific proteins (II). (I) and (II) have cytostatic activity,
XX      and can be used in vaccine production and gene therapy. (I), (II),
XX      antibodies to (II), fusion proteins comprising (II), and isolated
XX      T cells prepared using (I) or (II) are used treat cancer in a patient.
XX      (I) and the antibodies are also used in the detection of cancer in a
XX      patient. The cancer that is diagnosed or treated is particularly
XX      prostate cancer. (I) and (II) can be used in vaccines. The antibodies or
XX      (I) can be used for monitoring the progression of cancer in a patient.
XX      (I) and (II) can also be used to improve diagnostic and therapeutic
XX      methods for prostate cancer. They can indicate the level of metastasis
XX      as well as the prostate volume. AAH93357 to AAH93944 and AAH01115 to
XX      AAH01318 represent polynucleotide and amino acid sequences used in the
XX      exemplification of the present invention.
XX

SQ      Sequence 2229 BP; 654 A; 447 C; 481 G; 647 T; 0 other;

Alignment Scores:

```


Pred. No.: 1 82e-43
 Score: 51.00
 Percent Similarity: 100.00%
 Best Local Similarity: 100.00%
 Query Match: 100.00%
 DB: 22
 Matches: 2229
 Conservative: 51
 Mismatches: 0
 Indels: 0
 Gaps: 0

US-09-402-713A-2 (1-51) x AAH93804 (1-2229)

QY 1 MetPheLeuHisIleSerSerProPheLysTyrProHisThrGlnGluAlaGlnLysGlu 20
 DB 1659 ATGTTTTCACATTTCCAGCCCTTTAAATATCCACACACAGAGAGCAAAAGGA 1600
 QY 21 AlaGlnArgSerLeuGluMetProGlyArgHisLeuGlySerSerMetSerLeuAla 40
 DB 1599 GCACAGAGATCCCTGGGAGAAATGCCGCCCATCTTGCGTCATCGATGAGAGCTCGCC 1540
 QY 41 LeuCysLeuValProLeuValArgGlnGlyHis 51
 DB 1539 CTGTGCCCTGGTCCCGCTGTGAGGAGAGACAT 1507

Search completed: September 26, 2003, 20:07:46
 Job time : 303 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: September 26, 2003, 20:02:42; Search time 278 Seconds

(without alignments)
456.705 Million cell updates/sec

Title: US-09-402-713A-2

Perfect score: 51

Sequence: 1 MFLHISPFKPHPTQEAQKE.....HLGSSMLALCTPLVLRGH 51

Scoring table:

OLIGO
Xgapop 60.0, Xgapext 60.0
Ygapop 60.0, Ygapext 60.0
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 1678620 seqs, 1244745471 residues

Word size: 1

Total number of hits satisfying chosen parameters: 3352635

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Command line parameters:

-MODE=frame+g2n.model -DEV=x1h
-O=/cgn2_1/USPTO_spool/US09402713/runat_26092003_143100_17023/app-query.fasta.1.199
-DB=Published.Applications_NA -OPMT=fastlap -SUFFIX=olig.rmpb -MINMATCH=0.1
-LOOCEL=0 -LOOEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=oligo
-TRANS=human40.cdi -LIST=45 -DOCALLIGN=200 -THR SCORE=QUALITY -THR MIN=1
-ALIGN=15 -MODE=LOCAL -OUTFMT=pro -NORM=ext -HEADSIZE=500 -MINLEN=0
-MAXLEN=2000000000 -USER=US09402713 @CGN_1_1_265 @runat_26092003_143100_17023
-NCPU=6 -TCPU=3 -NO_MMAP -LARGEOUTERT -NEG_SCORES=0 -WAIT -DSBLOCK=100
-LONGLOG -DEVTIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60
-EGADOP=6 -EGAPEXT=7 -YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7

Database: Published.Applications_NA.*

1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq.*
2: /cgn2_6/ptodata/2/pubpna/PC1_NEW_PUB.seq.*
3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq.*
4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq.*
5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq.*
6: /cgn2_6/ptodata/2/pubpna/PCRUS_PUBCOMB.seq.*
7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq.*
8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq.*
9: /cgn2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq.*
10: /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq.*
11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq.*
12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq.*
13: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq.*
14: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq.*
15: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq.*
16: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq.*
17: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Length	ID	Description
c 1	51	100.0	812 9	US-09-759-143-471 Sequence 471, App

c 2	51	100.0	812 9	US-09-780-669-471 Sequence 471, App
c 3	51	100.0	812 9	US-09-822-827-471 Sequence 471, App
c 4	51	100.0	812 10	US-09-895-793-471 Sequence 471, App
c 5	51	100.0	812 10	US-09-895-814-471 Sequence 471, App
c 6	51	100.0	812 12	US-10-144-678A-471 Sequence 471, App
c 7	51	100.0	812 13	US-10-012-896-471 Sequence 471, App
c 8	51	100.0	812 14	US-10-010-940-471 Sequence 3, Appli
c 9	51	100.0	876 11	US-09-957-708-3 Sequence 469, App
c 10	51	100.0	2229 9	US-09-759-143-469 Sequence 469, App
c 11	51	100.0	2229 9	US-09-780-669-469 Sequence 469, App
c 12	51	100.0	2229 9	US-09-822-827-469 Sequence 469, App
c 13	51	100.0	2229 10	US-09-895-793-469 Sequence 469, App
c 14	51	100.0	2229 10	US-09-895-814-469 Sequence 469, App
c 15	51	100.0	2229 12	US-10-144-678A-469 Sequence 470, App
c 16	51	100.0	2229 13	US-10-012-896-469 Sequence 469, App
c 17	51	100.0	2229 14	US-10-010-940-469 Sequence 469, App
c 18	51	100.0	2426 9	US-09-759-143-470 Sequence 470, App
c 19	51	100.0	2426 9	US-09-780-669-470 Sequence 470, App
c 20	51	100.0	2426 9	US-09-822-827-470 Sequence 470, App
c 21	51	100.0	2426 10	US-09-895-793-470 Sequence 470, App
c 22	51	100.0	2426 10	US-09-895-814-470 Sequence 470, App
c 23	51	100.0	2426 12	US-10-144-678A-470 Sequence 470, App
c 24	51	100.0	2426 13	US-10-012-896-470 Sequence 470, App
c 25	51	100.0	2426 14	US-10-010-940-470 Sequence 470, App
c 26	51	100.0	2426 14	US-10-205-823-448 Sequence 448, App
c 27	51	100.0	3112 9	US-09-759-143-468 Sequence 468, App
c 28	51	100.0	3112 9	US-09-780-669-468 Sequence 468, App
c 29	51	100.0	3112 9	US-09-822-827-468 Sequence 468, App
c 30	51	100.0	3112 10	US-09-895-793-468 Sequence 468, App
c 31	51	100.0	3112 10	US-09-895-814-468 Sequence 468, App
c 32	51	100.0	3112 12	US-10-144-678A-468 Sequence 468, App
c 33	51	100.0	3112 13	US-10-012-896-468 Sequence 468, App
c 34	51	100.0	3112 14	US-10-010-940-468 Sequence 468, App
c 35	51	100.0	3923 9	US-09-759-143-630 Sequence 630, App
c 36	51	100.0	3923 9	US-09-780-669-630 Sequence 630, App
c 37	51	100.0	3923 9	US-09-822-827-630 Sequence 630, App
c 38	51	100.0	3923 10	US-09-895-793-630 Sequence 630, App
c 39	51	100.0	3923 10	US-09-895-814-630 Sequence 630, App
c 40	51	100.0	3923 12	US-10-144-678A-630 Sequence 630, App
c 41	51	100.0	3923 13	US-10-012-896-630 Sequence 630, App
c 42	51	100.0	3923 13	US-10-012-896-630 Sequence 630, App
c 43	51	100.0	718 9	US-09-759-143-313 Sequence 313, App
c 44	51	100.0	718 9	US-09-780-669-313 Sequence 313, App
c 45	51	100.0	718 9	US-09-822-827-313 Sequence 313, App

ALIGNMENTS

RESULT 1
US-09-759-143-471/c
Sequence 471, Application US/09759143
Patent No. US200202248A1
GENERAL INFORMATION:
APPLICANT: Xu, Jianshun
APPLICANT: Dillon, David C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: JIANG, Yugu
APPLICANT: Henderson, Robert A.
APPLICANT: Kalos, Michael D.
APPLICANT: Fanger, Gary R.
APPLICANT: Retter, Marc W.
APPLICANT: Stoik, John A.
APPLICANT: Day, Craig H.
APPLICANT: Vedrick, Thomas S.
APPLICANT: Carter, Darrick
APPLICANT: Li, Samuel
APPLICANT: Wang, Aijun
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Hepler, William
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
FILE REFERENCE: 210121.427C23
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER

```
; CURRENT APPLICATION NUMBER: US/09/759,143
; CURRENT FILING DATE: 2001-01-12
; NUMBER OF SEQ ID NOS: 934
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 471
; LENGTH: 812
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-759-143-471

Alignment Scores:
Pred. No.: 2.3e-43      Length: 812
Score: 51.00           Matches: 51
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%    Mismatches: 0
Query Match: 100.00%      Indels: 0
DB: 9                  Gaps: 0

US-09-402-713a-2 (1-51) x US-09-759-143-471 (1-812)

OY      1 MetPheLeuHisIleSerSerProPheLysTYrProHisThrGlnGluAlaGlnLysGlu 20
        |||
Db      604 ATGTTTTCACATTTCCACAGCCCTTTAAATATCCACACACAGAGGACAAAGGAA 545

OY      21 AlaGlnArgSerLeuGlyGluMetProGlyArgHisLeuGlySerSerMetSerLeuAla 40
        |||
Db      544 GCACAGAGATCCCTGGAGAAATGCCGCCGCATCTGGTCATGATGAGACCTCGCC 485

OY      41 LeuCysLeuValProLeuValArgGluGlyHis 51
        |||
Db      484 CTGTGCTGTGCTCCGCTTGAGGGAAGACAT 452

RESULT 2
US-09-780-669-471/c
; Sequence 471, Application US/09780669
; Patent No. US20020051977A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yugu
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; APPLICANT: Hurai, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C24
; CURRENT APPLICATION NUMBER: US/09/780,669
; CURRENT FILING DATE: 2001-02-09
; NUMBER OF SEQ ID NOS: 943
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 471
; LENGTH: 812
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-780-669-471

Alignment Scores:
Pred. No.: 2.3e-43      Length: 812
Score: 51.00           Matches: 51
; FILE REFERENCE: 210121.427C24
; CURRENT APPLICATION NUMBER: US/09/780,669
; CURRENT FILING DATE: 2001-02-09
; NUMBER OF SEQ ID NOS: 943
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 471
; LENGTH: 812
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-780-669-471
```

```
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%    Mismatches: 0
Query Match: 100.00%      Indels: 0
DB: 9                  Gaps: 0

US-09-402-713a-2 (1-51) x US-09-780-669-471 (1-812)

OY      1 MetPheLeuHisIleSerSerProPheLysTYrProHisThrGlnGluAlaGlnLysGlu 20
        |||
Db      604 ATGTTTTCACATTTCCACAGCCCTTTAAATATCCACACACAGAGGACAAAGGAA 545

OY      21 AlaGlnArgSerLeuGlyGluMetProGlyArgHisLeuGlySerSerMetSerLeuAla 40
        |||
Db      544 GCACAGAGATCCCTGGAGAAATGCCGCCGCATCTGGTCATGATGAGACCTCGCC 485

OY      41 LeuCysLeuValProLeuValArgGluGlyHis 51
        |||
Db      484 CTGTGCTGTGCTCCGCTTGAGGGAAGACAT 452

RESULT 3
US-09-822-827-471/c
; Sequence 471, Application US/09822827
; Patent No. US20020081808A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yugu
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; APPLICANT: Hurai, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.534C1
; CURRENT APPLICATION NUMBER: US/09/822,827
; CURRENT FILING DATE: 2001-03-28
; NUMBER OF SEQ ID NOS: 982
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 471
; LENGTH: 812
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-822-827-471

Alignment Scores:
Pred. No.: 2.3e-43      Length: 812
Score: 51.00           Matches: 51
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%    Mismatches: 0
Query Match: 100.00%      Indels: 0
DB: 9                  Gaps: 0

US-09-402-713a-2 (1-51) x US-09-822-827-471 (1-812)

OY      1 MetPheLeuHisIleSerSerProPheLysTYrProHisThrGlnGluAlaGlnLysGlu 20
        |||
Db      604 ATGTTTTCACATTTCCACAGCCCTTTAAATATCCACACACAGAGGACAAAGGAA 545

OY      21 AlaGlnArgSerLeuGlyGluMetProGlyArgHisLeuGlySerSerMetSerLeuAla 40
        |||
Db      544 GCACAGAGATCCCTGGAGAAATGCCGCCGCATCTGGTCATGATGAGACCTCGCC 485

OY      41 LeuCysLeuValProLeuValArgGluGlyHis 51
        |||
Db      484 CTGTGCTGTGCTCCGCTTGAGGGAAGACAT 452

RESULT 4
US-09-895-793-471/c
; Sequence 471, Application US/09895793
; Publication No. US20020192763A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yugu
; APPLICANT: Kalos, Michael D.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; APPLICANT: Hurai, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C24
; CURRENT APPLICATION NUMBER: US/09/895,793
; CURRENT FILING DATE: 2001-02-09
; NUMBER OF SEQ ID NOS: 943
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 471
; LENGTH: 812
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-895-793-471
```

```

: APPLICANT: Day, Craig H.
: APPLICANT: Vedvick, Thomas S.
: APPLICANT: Carter, Darick
: APPLICANT: Li, Samuel X.
: APPLICANT: Wang, Aljun
: APPLICANT: Skeiky, Yasir A.W.
: APPLICANT: Hepler, William T.
: APPLICANT: Henderson, Robert A.
: APPLICANT: Hural, John
: APPLICANT: McNeill, Patricia D.
: APPLICANT: Houghton, Raymond L.
: APPLICANT: Vinals de Bassols, Carlota
: APPLICANT: Foy, Teresa
: APPLICANT: Fanger, Gary R.
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
: TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
: FILE REFERENCE: 210121.534C2
: CURRENT APPLICATION NUMBER: US/09/895,793
: CURRENT FILING DATE: 2001-06-29
: NUMBER OF SEQ ID NOS: 982
: SOFTWARE: FASTSEQ for Windows Version 3.0
: SEQ ID NO: 471
: LENGTH: 812
: TYPE: DNA
: ORGANISM: Homo sapiens
US-09-895-793-471

```

```

Alignment Scores:
Pred. No.: 2.3e-43 Length: 812
Score: 51.00 Matches: 51
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: Gaps: 0

```

US-09-402-713A-2 (1-51) x US-09-895-793-471 (1-812)

```

QY 1 MethpLeuHISleSeSerProPhelySTyrProHISThrGInGluAlaGlnLysGlu 20
DB 604 ATGTTTGGCACATTTCCAGCCCTTTAAATATCCACACACAGGAAGCAAAAGGAA 545
QY 21 AlaGlnArGserLeuGluGluMetProGlyArGHisLeuGlySerMetSerLeuAla 40
DB 544 GCACAGAGATCCCGGGGAATGCGCGCCCATCTTGSGTATCATGATGAGCTCGCC 485
QY 41 LeuCysLeuValProLeuValArgGluGlyHis 51
DB 484 CTGTGCTGTGTCGCGCTGTGAGGGAAGACAT 452

```

RESULT 5

```

US-09-895-814-471/C
: Sequence 471, Application US/09895814
: Publication No. US20020193296A1
: GENERAL INFORMATION:
: APPLICANT: Xu, Jiangchun
: APPLICANT: Dillon, Davin C.
: APPLICANT: Mitcham, Jennifer L.
: APPLICANT: Harlocker, Susan L.
: APPLICANT: Jiang, Yugu
: APPLICANT: Kalos, Michael D.
: APPLICANT: Retter, Marc W.
: APPLICANT: Stolk, John A.
: APPLICANT: Day, Craig H.
: APPLICANT: Vedvick, Thomas S.
: APPLICANT: Carter, Darick
: APPLICANT: Li, Samuel X.
: APPLICANT: Wang, Aljun
: APPLICANT: Skeiky, Yasir A.W.
: APPLICANT: Hepler, William T.
: APPLICANT: Henderson, Robert A.
: APPLICANT: Hural, John
: APPLICANT: McNeill, Patricia D.
: APPLICANT: Houghton, Raymond L.

```

```

: APPLICANT: Vinals de Bassols, Carlota
: APPLICANT: Foy, Teresa
: APPLICANT: Fanger, Gary R.
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
: TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
: FILE REFERENCE: 210121.427C26
: CURRENT APPLICATION NUMBER: US/09/895,814
: CURRENT FILING DATE: 2001-06-29
: NUMBER OF SEQ ID NOS: 990
: SOFTWARE: FASTSEQ for Windows Version 3.0
: SEQ ID NO: 471
: LENGTH: 812
: TYPE: DNA
: ORGANISM: Homo sapiens
US-09-895-814-471

```

```

Alignment Scores:
Pred. No.: 2.3e-43 Length: 812
Score: 51.00 Matches: 51
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: Gaps: 0

```

US-09-402-713A-2 (1-51) x US-09-895-814-471 (1-812)

```

QY 1 MethpLeuHISleSeSerProPhelySTyrProHISThrGInGluAlaGlnLysGlu 20
DB 604 ATGTTTGGCACATTTCCAGCCCTTTAAATATCCACACACAGGAAGCAAAAGGAA 545
QY 21 AlaGlnArGserLeuGluGluMetProGlyArGHisLeuGlySerMetSerLeuAla 40
DB 544 GCACAGAGATCCCGGGGAATGCGCGCCCATCTTGSGTATCATGATGAGCTCGCC 485
QY 41 LeuCysLeuValProLeuValArgGluGlyHis 51
DB 484 CTGTGCTGTGTCGCGCTGTGAGGGAAGACAT 452

```

RESULT 6

```

US-10-144-678A-471/C
: Sequence 471, Application US/10144678A
: Publication No. US20030157089A1
: GENERAL INFORMATION:
: APPLICANT: Xu, Jiangchun
: APPLICANT: Dillon, Davin C.
: APPLICANT: Mitcham, Jennifer L.
: APPLICANT: Harlocker, Susan L.
: APPLICANT: Jiang, Yugu
: APPLICANT: Henderson, Robert A.
: APPLICANT: Kalos, Michael D.
: APPLICANT: Fanger, Gary R.
: APPLICANT: Retter, Marc W.
: APPLICANT: Stolk, John A.
: APPLICANT: Day, Craig H.
: APPLICANT: Vedvick, Thomas S.
: APPLICANT: Carter, Darick
: APPLICANT: Li, Samuel X.
: APPLICANT: Wang, Aljun
: APPLICANT: Skeiky, Yasir A.W.
: APPLICANT: Hepler, William T.
: APPLICANT: Hural, John
: APPLICANT: McNeill, Patricia D.
: APPLICANT: Houghton, Raymond L.
: APPLICANT: Vinals y de Bassols, Carlota
: APPLICANT: Foy, Teresa M.
: APPLICANT: Matanabe, Yoshihiro
: APPLICANT: Deng, Ta
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
: TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
: FILE REFERENCE: 210121.427C28
: CURRENT APPLICATION NUMBER: US/10/144,678A
: CURRENT FILING DATE: 2002-08-12
: NUMBER OF SEQ ID NOS: 1033

```

SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 471
; LENGTH: 812
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-144-678A-471

Alignment Scores:

Pred. No.:	2.3e-43	Length:	812
Score:	51.00	Matches:	51
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	12	Gaps:	0

US-09-402-713A-2 (1-51) x US-10-144-678A-471 (1-812)

QY 1 MetPhleuH1s1leSerSerpPhelysTyPrOH1sthrGlnGluA1agInlySglu 20

Db 604 ATGTTTTCACATTTCAGCCCTTTAATATCCACACACAGGAGCAAAAAGGAA 545

QY 21 AlaGlnArgSerLeuGlyGluMetProGlyArgHisLeuGlySerSermetsSerLeuAla 40

Db 544 GCACAGAGATCCCTGGAGAAATGCCCGGCCCATCTTGTCATCGATGAGCCTCGCC 485

QY 41 LeuCysLeuValProLeuValArgGluGlyHis 51

Db 484 CTGTGCTGTGCTCCGCTTGAGGAGGACAT 452

RESULT 7

US-10-012-896-471/c
; Sequence 471, Application US/10012896
; Publication No. US20020183251A1
; GENERAL INFORMATION:

APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Jiang, Yugu
APPLICANT: Kalos, Michael D.
APPLICANT: Retter, Marc W.
APPLICANT: Stolck, John A.
APPLICANT: Day, Craig H.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Darick
APPLICANT: Li, Samuel X.
APPLICANT: Wang, Aijun
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Hepler, William T.
APPLICANT: Henderson, Robert A.
APPLICANT: Hurai, John
APPLICANT: McNeill, Patricia D.
APPLICANT: Houghton, Raymond L.
APPLICANT: Vinals de Bassols, Carloca
APPLICANT: Foy, Teresa
APPLICANT: Fanger, Gary R.
APPLICANT: Mantanabe, Yoshinori
APPLICANT: Meagher, Madeleine Joy
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
FILE REFERENCE: 210121.427C27
CURRENT APPLICATION NUMBER: US/10/012.896
CURRENT FILING DATE: 2001-12-10
NUMBER OF SEQ ID NOS: 1011
SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 471
; LENGTH: 812
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-012-896-471

Alignment Scores: 2.3e-43 Length: 812
Pred. No.: 2.3e-43 Length: 812

Score:	51.00	Matches:	51
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	13	Gaps:	0

US-09-402-713A-2 (1-51) x US-10-012-896-471 (1-812)

QY 1 MetPhleuH1s1leSerSerpPhelysTyPrOH1sthrGlnGluA1agInlySglu 20

Db 604 ATGTTTTCACATTTCAGCCCTTTAATATCCACACACAGGAGCAAAAAGGAA 545

QY 21 AlaGlnArgSerLeuGlyGluMetProGlyArgHisLeuGlySerSermetsSerLeuAla 40

Db 544 GCACAGAGATCCCTGGAGAAATGCCCGGCCCATCTTGTCATCGATGAGCCTCGCC 485

QY 41 LeuCysLeuValProLeuValArgGluGlyHis 51

Db 484 CTGTGCTGTGCTCCGCTTGAGGAGGACAT 452

RESULT 8

US-10-010-940-471/c
; Sequence 471, Application US/10010940
; Publication No. US2003008062A1
; GENERAL INFORMATION:

APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan Louise
APPLICANT: Jiang Yugu
APPLICANT: Reed, Steven G.
APPLICANT: Kalos, Michael
APPLICANT: Fanger, Gary
APPLICANT: Retter, Mark
APPLICANT: Solk, John
APPLICANT: Day, Craig
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
FILE REFERENCE: 210121.427D3
CURRENT APPLICATION NUMBER: US/10/010.940
CURRENT FILING DATE: 2001-12-05
NUMBER OF SEQ ID NOS: 575
SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 471
; LENGTH: 812
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-010-940-471

Alignment Scores:	2.3e-43	Length:	812
Pred. No.:	51.00	Matches:	51
Score:	100.00%	Conservative:	0
Percent Similarity:	100.00%	Mismatches:	0
Best Local Similarity:	100.00%	Indels:	0
Query Match:	100.00%	Gaps:	0
DB:	14		

US-09-402-713A-2 (1-51) x US-10-010-940-471 (1-812)

QY 1 MetPhleuH1s1leSerSerpPhelysTyPrOH1sthrGlnGluA1agInlySglu 20

Db 604 ATGTTTTCACATTTCAGCCCTTTAATATCCACACACAGGAGCAAAAAGGAA 545

QY 21 AlaGlnArgSerLeuGlyGluMetProGlyArgHisLeuGlySerSermetsSerLeuAla 40

Db 544 GCACAGAGATCCCTGGAGAAATGCCCGGCCCATCTTGTCATCGATGAGCCTCGCC 485

QY 41 LeuCysLeuValProLeuValArgGluGlyHis 51

Db 484 CTGTGCTGTGCTCCGCTTGAGGAGGACAT 452

RESULT 9
US-09-957-708-3

```
; Sequence 3, Application US/09957708
; Publication No. US20030031678A1
; GENERAL INFORMATION:
; APPLICANT: Sun, Yonming
; APPLICANT: Recipon, Heve
; APPLICANT: Cafierkey, Robert
; APPLICANT: Ali, Shujath
; TITLE OF INVENTION: Compositions and Methods Relating to Prostate Specific
; TITLE OF INVENTION: Genes
; FILE REFERENCE: DEX-0239
; CURRENT APPLICATION NUMBER: US/09/957,708
; CURRENT FILING DATE: 2001-09-19
; PRIOR APPLICATION NUMBER: 60/233,746
; PRIOR FILING DATE: 2000-09-19
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: Patentn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 876
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-957-708-3

Alignment Scores:
Pred. No.: 2.45e-43 Length: 876
Score: 51.00 Matches: 51
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 11 Gaps: 0

US-09-402-713A-2 (1-51) x US-09-957-708-3 (1-876)

Qy 1 MethelenuHisIleSerProphelysTyProhIsthrngIngluaIaGlnLysGlu 20
Db 243 ATGTTTTCACATTTCCAGCCCTTAAATATCCACACACAGGAAGCAAAAGGAA 302
Qy 21 AlaGlnArgSerLeuGlyGluMetProGlyArgHisLeuGlySerMetSerLeuAla 40
Db 303 GCACAGAGATCCCTGGGAGAAATGCCCGCCCATCTTGGTCATGATGAGCCTCGCC 362
Qy 41 LeuCySLeuValProLeuValArgGluGlyHis 51
Db 363 CTGTGCTGTGTCGCCGCTTGTGAGGAGAGACAT 395

RESULT 10
US-09-759-143-469/c
; Sequence 469, Application US/09759143
; Patent No. US20020022248A1
; GENERAL INFORMATION:
; APPLICANT: Xu, JIANGCHUN
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yugu
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kaios, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolck, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C23
; CURRENT APPLICATION NUMBER: US/09/759,143
; CURRENT FILING DATE: 2001-01-12
; NUMBER OF SEQ ID NOS: 934
; SOFTWARE: FastSeq for Windows Version 3.0
```

```
; SEQ ID NO 469
; LENGTH: 2229
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-759-143-469

Alignment Scores:
Pred. No.: 5.34e-43 Length: 2229
Score: 51.00 Matches: 51
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-09-402-713A-2 (1-51) x US-09-759-143-469 (1-2229)

Qy 1 MethelenuHisIleSerProphelysTyProhIsthrngIngluaIaGlnLysGlu 20
Db 1659 ATGTTTTCACATTTCCAGCCCTTAAATATCCACACACAGGAAGCAAAAGGAA 1600
Qy 21 AlaGlnArgSerLeuGlyGluMetProGlyArgHisLeuGlySerMetSerLeuAla 40
Db 1599 GCACAGAGATCCCTGGGAGAAATGCCCGCCCATCTTGGTCATGATGAGCCTCGCC 1540
Qy 41 LeuCySLeuValProLeuValArgGluGlyHis 51
Db 1539 CTGTGCTGTGTCGCCGCTTGTGAGGAGAGACAT 1507

RESULT 11
US-09-780-669-469/c
; Sequence 469, Application US/09780669
; Patent No. US20020051977A1
; GENERAL INFORMATION:
; APPLICANT: Xu, JIANGCHUN
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yugu
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kaios, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolck, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; APPLICANT: Hurai, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C24
; CURRENT APPLICATION NUMBER: US/09/780,669
; CURRENT FILING DATE: 2001-02-09
; NUMBER OF SEQ ID NOS: 943
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 469
; LENGTH: 2229
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-780-669-469

Alignment Scores:
Pred. No.: 5.34e-43 Length: 2229
Score: 51.00 Matches: 51
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0
```

```
US-09-402-713a-2 (1-51) x US-09-780-669-469 (1-2229)
QY      1 MetPheLeuHisIleSerSerProPheLysTYRProHisThrGlnGluAlaGlnLysGlu 20
      |||||||
Db      1659 ATGTTTTCACATTTCCAGCCCTTTAAATATCCACACACAGGAGGACAAAGGAA 1600
QY      21 AlaGlnArgSerLeuGlyMetProGlyArgHisLeuGlySerSerMetSerLeuAla 40
      |||||||
Db      1599 GCACAGAGATCCCTGGAGAAATGCCCGGCCCATCTTGATCATGATGAGCTCGCC 1540
QY      41 LeuCysLeuValProLeuValArgGlnGlyHis 51
      |||||||
Db      1539 CTGTGCTGTGCTCCGCTTGTGAGGAGAGACAT 1507

RESULT 12
US-09-822-827-469/c
; Sequence 469, Application US/09822827
; Patent No. US20020081680A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.534c1
; CURRENT APPLICATION NUMBER: US/09/822,827
; NUMBER OF SEQ ID NOS: 982
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 469
; LENGTH: 2229
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-822-827-469

Alignment Scores:
Pred. No.:      5,34e-43      Length:      2229
Score:          51.00      Matches:      51
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches: 0
Query Match:    100.00%      Indels:      0
DB:             9      Gaps:      0

US-09-402-713a-2 (1-51) x US-09-822-827-469 (1-2229)
QY      1 MetPheLeuHisIleSerSerProPheLysTYRProHisThrGlnGluAlaGlnLysGlu 20
      |||||||
Db      1659 ATGTTTTCACATTTCCAGCCCTTTAAATATCCACACACAGGAGGACAAAGGAA 1600
QY      21 AlaGlnArgSerLeuGlyMetProGlyArgHisLeuGlySerSerMetSerLeuAla 40
      |||||||
Db      1599 GCACAGAGATCCCTGGAGAAATGCCCGGCCCATCTTGATCATGATGAGCTCGCC 1540
QY      41 LeuCysLeuValProLeuValArgGlnGlyHis 51
      |||||||
Db      1539 CTGTGCTGTGCTCCGCTTGTGAGGAGAGACAT 1507

RESULT 13
US-09-895-793-469/c
; Sequence 469, Application US/09895793
; Publication No. US20020192763A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yugu
; APPLICANT: Kalos, Michael D.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel X.

US-09-402-713a-2 (1-51) x US-09-895-793-469 (1-2229)
QY      1 MetPheLeuHisIleSerSerProPheLysTYRProHisThrGlnGluAlaGlnLysGlu 20
      |||||||
Db      1659 ATGTTTTCACATTTCCAGCCCTTTAAATATCCACACACAGGAGGACAAAGGAA 1600
QY      21 AlaGlnArgSerLeuGlyMetProGlyArgHisLeuGlySerSerMetSerLeuAla 40
      |||||||
Db      1599 GCACAGAGATCCCTGGAGAAATGCCCGGCCCATCTTGATCATGATGAGCTCGCC 1540
QY      41 LeuCysLeuValProLeuValArgGlnGlyHis 51
      |||||||
Db      1539 CTGTGCTGTGCTCCGCTTGTGAGGAGAGACAT 1507

RESULT 14
US-09-895-814-469/c
; Sequence 469, Application US/09895814
; Publication No. US20020193296A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yugu
; APPLICANT: Kalos, Michael D.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aljun
; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Vinals de Bassols, Carlota
; APPLICANT: Foy, Teresa
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
```



```
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C26
; CURRENT APPLICATION NUMBER: US/09/895,814
; CURRENT FILING DATE: 2001-06-29
; NUMBER OF SEQ ID NOS: 990
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 469
; LENGTH: 2229
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-895-814-469

Alignment Scores:
Pred. No.: 5.34e-43      Length: 2229
Score: 51.00           Matches: 51
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%    Mismatches: 0
Query Match: 100.00%      Indels: 0
DB: 10                  Gaps: 0

US-09-402-713a-2 (1-51) x US-09-895-814-469 (1-2229)

QY 1 MetPheLeuHISleSerSerProPhelystyrProHISthrGlnGluAlaGlnLysGlu 20
    |||||||
Db 1659 ATGTTTTCACATTTCACAGCCCTTTAAATATCCACACACAGAGGAAAGCAAAAGGAA 1600

QY 21 AlaGlnArgSerLeuGlyGluMetProGlyArgHISleuGlySerSerMetSerLeuAla 40
    |||||||
Db 1599 GCACAGAGATCCCTGGAGAAATGCCGCGCCGCGCATCTGGTGCATGATGAGCCTCGCC 1540

QY 41 LeuCysLeuValProLeuValArgGluGlyHis 51
    |||||||
Db 1539 CTGTGCTGTGCTCCGCTTGTGAGGAGAGACAT 1507

RESULT 15
US-10-144-678a-469/C
; Sequence 469, Application US/10144678A
; Publication No. US20030157089A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, David C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yugu
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Derrick
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A. W.
; APPLICANT: Hepler, William T.
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Vinals y de Bassols, Carlotia
; APPLICANT: Foy, Teresa M.
; APPLICANT: Melanabe, Yoshihiro
; APPLICANT: Deng, Ta
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C28
; CURRENT APPLICATION NUMBER: US/10/144,678A
; CURRENT FILING DATE: 2002-08-12
; NUMBER OF SEQ ID NOS: 1033
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 469
; LENGTH: 2229
; TYPE: DNA
```

```
; ORGANISM: Homo sapiens
US-10-144-678a-469

Alignment Scores:
Pred. No.: 5.34e-43      Length: 2229
Score: 51.00           Matches: 51
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%    Mismatches: 0
Query Match: 100.00%      Indels: 0
DB: 12                  Gaps: 0

US-09-402-713a-2 (1-51) x US-10-144-678a-469 (1-2229)

QY 1 MetPheLeuHISleSerSerProPhelystyrProHISthrGlnGluAlaGlnLysGlu 20
    |||||||
Db 1659 ATGTTTTCACATTTCACAGCCCTTTAAATATCCACACACAGAGGAAAGCAAAAGGAA 1600

QY 21 AlaGlnArgSerLeuGlyGluMetProGlyArgHISleuGlySerSerMetSerLeuAla 40
    |||||||
Db 1599 GCACAGAGATCCCTGGAGAAATGCCGCGCCGCGCATCTGGTGCATGATGAGCCTCGCC 1540

QY 41 LeuCysLeuValProLeuValArgGluGlyHis 51
    |||||||
Db 1539 CTGTGCTGTGCTCCGCTTGTGAGGAGAGACAT 1507

Search completed: September 26, 2003, 21:44:11
Job time : 280 secs
```

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: September 26, 2003, 19:58:16 ; Search time 2216 Seconds
(without alignments)
559.354 Million cell updates/sec

Title: US-09-402-713A-2
Perfect score: 51
Sequence: 1 MFLHSSPFKYPHTQEAQKE.....HLGSSMALCLVPLVREGH 51

Scoring table:
OLIGO
Xgapop 60.0 , Xgapext 60.0
Ygapop 60.0 , Ygapext 60.0
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 22781392 segs, 1215238056 residues

Word size: 1

Total number of hits satisfying chosen parameters: 45562604

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Command line parameters:

-MODEL-frame+_p2n_model -DEV-xlh
-O/cgn2.1/USPRO.spool/US09402713.rst -unat_26092003_143059_16972/app_query.fasta.1.199
-DB-BST -QFMT-fastap -SUFFIX-oligo -rnt -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS-bits -START=1 -END=1 -MATRIX-oligo -TRANS-human40.cdi -LIST=45
-DOCALLIGN=200 -THR.SCORE=quality -THR.MIN=1 -ALIGN=15 -MODE=LOCAL -OUTFMT=plc
-NORR-ext -HEARST=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09402713.ecgn.1.12810 -cgnat_26092003_143059_16972 -NCPU=6 -ICPU=3
-NO_MMAP -LARGESQUEERY -NEG.SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV.TIMEOUT=120 -WARN.TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7

Database :

1: em_estba:*
2: em_esthum:*
3: em_estlin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hlc:*
9: gb_est1:*
10: gb_est2:*
11: gb_hlc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: em_gss_hum:*
18: em_gss_inv:*
19: em_gss_pln:*
20: em_gss_vrt:*
21: em_gss_fun:*
22: em_gss_mus:*
23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_tod:*
26: em_gss_phg:*
27: em_gss_vrl:*
28: gb_gss1:*

29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	37	72.5	176	10 BF373406	BF373406 IL2-FT015
2	37	72.5	167	9 A1780885	A1780885 EST261764
3	37	72.5	382	10 BG631598	BG631598 CC-estfcl
4	37	72.5	438	29 FR0024676	FR0024676 CC-estfcl
5	37	72.5	494	13 BY641551	BY641551 F.tubrtipe
6	37	72.5	528	9 AW093357	AW093357 EST286537
7	37	72.5	531	12 B1801819	B1801819 H061G05 E
8	37	72.5	572	9 AW624953	AW624953 EST313782
9	37	72.5	741	10 BB634056	BB634056 BB634056
10	37	72.5	754	12 BM410648	BM410648 EST584975
11	37	72.5	132	10 BG527932	BG527932 602556894
12	37	72.5	174	13 BY370977	BY370977 BY370977
13	37	72.5	239	13 BQ368838	BQ368838 PML-GN051
14	37	72.5	243	13 BY370387	BY370387 BY370387
15	37	72.5	266	10 BF887863	BF887863 OV2-TN017
16	37	72.5	273	28 A2113501	A2113501 RPL1-23-4
17	37	72.5	292	28 AQ006096	AQ006096 C1T-HSP-2
18	37	72.5	314	13 BY688754	BY688754 BY688754
19	37	72.5	318	29 B2765908	B2765908 SALK.1354
20	37	72.5	332	14 C80550	C80550 C80550 Mous
21	37	72.5	361	13 BY088994	BY088994 BY088994
22	37	72.5	388	14 CB779343	CB779343 AMGNNUC:S
23	37	72.5	389	10 BF455095	BF455095 UT-M-BE1-
24	37	72.5	401	28 A2238755	A2238755 RPL1-23-8
25	37	72.5	411	29 B2917002	B2917002 CH240.102
26	37	72.5	416	12 BG979998	BG979998 PM3-CNO10
27	37	72.5	418	14 BY694175	BY694175 BY694175
28	37	72.5	421	10 BB786885	BB786885 BB786885
29	37	72.5	422	12 B1319624	B1319624 1e3.f04.y
30	37	72.5	429	14 CA045471	CA045471 wds3f.pko
31	37	72.5	437	14 CA045471	CA045471 ssa1p1c15
32	37	72.5	469	10 BB829415	BB829415 BB829415
33	37	72.5	488	29 AG248548	AG248548 locus_jap
34	37	72.5	497	14 CA564802	CA564802 K0330009-
35	37	72.5	510	10 BB766938	BB766938 BB766938
36	37	72.5	518	9 AA756841	AA756841 vu20b03.f
37	37	72.5	521	10 BB283541	BB283541 BB283541
38	37	72.5	527	28 AQ975708	AQ975708 RPL1-23-3
39	37	72.5	537	9 A1235734	A1235734 EST232296
40	37	72.5	558	14 CB500521	CB500521 ssa1g8503
41	37	72.5	558	28 AQ727566	AQ727566 HS_5456_A
42	37	72.5	569	12 B1342171	B1342171 369865 MA
43	37	72.5	576	10 BE065497	BE065497 RC3-BT031
44	37	72.5	576	13 B0194674	B0194674 UI-R-CN1-
45	37	72.5	577	14 C804939	C804939 C804939 Mous

ALIGNMENTS

RESULT 1
LOCUS BF373406
DEFINITION IL2-FT0159-070800-120-H01 FT0159 Homo sapiens CDNA, mRNA sequence.
ACCESSION BF373406
VERSION BF373406.1 GI:11335431
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE
1 (bases 1 to 167)
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Britones,M.R.,

TITLE	Shotgun sequencing of the human transcriptome with ORF expressed sequence tags					
JOURNAL MEDLINE	Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)					
PUBMED COMMENT	10737800 Contact: Simpson A.J.G. Laboratory of Cancer Genetics Ludwig Institute for Cancer Research Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil Tel: +55-11-2704922 Fax: +55-11-2707001 Email: asimpson@ludwig.org.br This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL. http://www.ludwig.org.br/scripts/gethtml2.pl?tl=IL2&tl2=IL2-Ft0159-070800-120-H01&t3=2000-08-07&t4=1 Seq primer: puc 18 forward High quality sequence stop: 167.					
FEATURES	Location/Qualifiers .167 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /dev_stage="Adult" /clone_idb="FT0159" /note="Organ: prostate,tumor; Vector: puc18; site_1: SmaI; site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."					
BASE COUNT	47 a 38 c 49 g 33 t					
ORIGIN						
Alignment Scores:						
Prod. No.:	1.29e-27		Length:		167	
Score:	37.00		Matches:		37	
Percent Similarity:	100.00%		Conservative:		0	
Best Local Similarity:	100.00%		Mismatch:		0	
Query Match:	72.55%		Indels:		0	
DB:	10		Gaps:		0	
US-09-402-713A-2 (1-51) x BF373406 (1-167)						
OY	15 GINGUALAGTlnlySGUALAGlnArgSerLeuGylunetProGIATgHisLeuGly 34 3 CAGGAACACAAAAAGGAGACACAGAGATCCCTGGAGAAATGCCCGCCGCACATCTTG 62					
bh						
OY	35 SerSerMetSerleuaAlalaLeuCysLeuValProleuValArngGluGlyHis 51 63 TCATCATGTGAGCCTTCGCCCTTCGCTGCTGCTGCTGCTGAGGAGAAGCAAT 113					
Dh						
RESULT 2						
A1780885/c	176 bp mRNA linear EST 18-MAY-2001					
LOCUS	EST261764 tomato susceptible, Cornell Lycopersicon esculentum CDNA					
DEFINITION	clone cUES1302, mRNA sequence.					
ACCESSION	A1780885					
VERSION	A1780885.1 GI:5278926					
KEYWORDS	EST.					
SOURCE	Lycopersicon esculentum (tomato)					
ORGANISM	Lycopersicon esculentum Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; lamiales; Solanales; Solanaceae; Solanum; Lycopersicon, 1 (bases 1 to 176)					
REFERENCE						

AUTHORS
 D Ascenzo, M., He, X., Lyman, J., Matera, A.L., Vision, T., Holt, I.E., Liang, F., Upcon, J., Ronning, C.M., Craven, M.B., Fujii, C.Y., Bowman, C.L., Nieman, W., Fraser, C.M., Venter, D.C., Tanksley, S.D., Giovannoni, J.J. and Martin, G.B.
TITLE
 Generation of ESTs from *Pseudomonas* susceptible tomato
JOURNAL
 Unpublished
COMMENT
 Contact: CUGI
 Clemson University Genomics Institute
 Clemson University
 100 Jordan Hall, Clemson, SC 29634, USA
 Email: <http://www.genome.clemson.edu/orders/index.html>
 5 prime sequence.

FEATURES
 source
 1..176
 /organism="Lycopersicon esculentum"
 /mol_type="mRNA"
 /cultivar="R11-13 (Rio Grande x Money Maker)"
 /db_xref="taxon:4081"
 /clone="CLES1302"
 /tissue_type="leaf"
 /dev_stage="4-week old"
 /lab_host="SOLR"
 /clone_lib="tomato susceptible, Cornell"
 /note="Vector: pBluescript SK(-); Site1: EcoRI, Site2: XhoI; cles - Tomato *Pseudomonas* Susceptible EST Library. Directionally cloned cDNAs inserted into pBluescript SK(-) at 5' end with EcoRI and 3' end with XhoI site"
) at 5' end with EcoRI and 3' end with XhoI site"

BASE COUNT
 74 a 35 c 27.9 40 t

ORIGIN

Alignment Scores:
 Pred. No.: 14.7 Length: 176
 Score: 9.00 Matches: 9
 Percent Similarity: 100.00% Conservative: 0
 Best local Similarity: 100.00% Mismatches: 0
 Query Match: 17.65% Indels: 0
 DB: 9 Gaps: 0

US-09-402-713A-2 (1-51) x A1780885 (1-176)
 Oy 38 SerLeuAlaLeuCyLeuValProLeu 46
 |||||||
 53 TCATTGGCATTGTGTATTGTCACATTA 27

RESULT 3
 BG631598/c 382 bp mRNA linear EST 19-APR-2001
LOCUS
 BG631598/c
DEFINITION
 cc-eflicEL8181d1 tomato flower library from a mixture of developmental stages *Lycopersicon esculentum* cDNA clone
 cc-eflicEL8181d1, mRNA sequence.
ACCESSION
 BG631598
VERSION
 BG631598.1 GI:13683072
KEYWORDS
 EST.

ORGANISM
Lycopersicon esculentum (tomato)
Lycopersicon esculentum
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; lamnids; Solanales; Solanaceae; Solanum; *Lycopersicon*.

REFERENCE
 1 (bases 1 to 382)
 van der Hoeven, R.S. and Tanksley, S.D.
 ESTs from a tomato flower library
 Unpublished
 Contact: Rutgers S. van der Hoeven
 Cornell University
 252 Emerson Hall, Ithaca, NY 14850, USA
 Tel: 607 255 7886
 Fax: 607 255 6683
 Email: rv19@cornell.edu
 3 prime sequence.

FEATURES
 Location/Qualifiers
 1..382
 /organism="Lycopersicon esculentum"
 /mol_type="mRNA"

/cultivar="E6203"
 /db_xref="taxon:4081"
 /clone="cc-escficle8l81d1"
 /tissue_type="developing flower buds and open flowers"
 /dev_stage="4-8 week old plants"
 /lab_host="XtLR"
 /clone_id="Tomato flower library from a mixture of developmental stages"
 /note="Vector: pBK CMV; Site 1: EcoRI; Site 2: XhoI; Flowers and flower buds were collected from greenhouse grown plants and used for library construction (cLEL)."

BASE COUNT 124 a 94 c 56 g 108 t

ORIGIN

Alignment Scores:

Pred. No.: 35 6 Length: 382
 Score: 9.00 Matches: 9
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 17.65% Indels: 0
 DB: 10 Gaps: 0

US-09-402-713a-2 (1-51) x BG631598 (1-382)

OY 38 SerleuAlaLeuCySleuValProleu 46
 DB 106 TCATTCGCACTGTGTTCGCCATTA 80

RESULT 4

FR0024676/c FR0024676 438 bp DNA linear GSS 10-DEC-1997
 LOCUS F.rubripes GSS sequence, clone 127M03aA4, genomic survey sequence.
 DEFINITION AL017520.1 GI:2683888
 ACCESSION
 VERSION
 KEYWORDS GSS: genome survey sequence.
 SOURCE Takifugu rubripes
 ORGANISM Takifugu rubripes

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 Acanthomorpha; Acanthopterygii; Percormorpha; Tetraodontiformes;
 Tetraodontidae; Tetraodontidae; Takifugu.

REFERENCE 1 (bases 1 to 438)
 AUTHORS Elgar,G., Clark,M., Smith,S., Meek,S., Warner,S., Umranta,Y., Williams,G. and Brenner,S.

TITLE Direct Submission
 JOURNAL Submitted (08-DEC-1997) MRC Human Genome Mapping Project Resource Centre Hinxton, Cambridge, CB10 1SB. Email: bhohelp@hmp.mrc.ac.uk
 COMMENT Vector: pBluescript II KS
 PRIMER: KS
 DESCR: One pass dye-terminator sequencing of cosmid cloned genomic sequence.

FEATURES
 source location/Qualifiers

1..438
 /organism="Takifugu rubripes"
 /mol_type="genomic DNA"
 /db_xref="taxon:31033"
 /clone="127M03aA4"
 /clone_id="cosmid 127M03"
 BASE COUNT 119 a 95 c 74 g 149 t 1 others
 ORIGIN

Alignment Scores:

Pred. No.: 41 6 Length: 438
 Score: 9.00 Matches: 9
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 17.65% Indels: 0
 DB: 29 Gaps: 0

US-09-402-713a-2 (1-51) x FR0024676 (1-438)

OY 34 GlySerSerMetSerLeuAlaLeuCyS 42
 DB 175 GGTTCACCATGACGCTTACCACTTGT 149

RESULT 5

BY641551 494 bp mRNA linear EST 15-DEC-2002
 DEFINITION BY641551 RIKEN full-length enriched, visual cortex Mus musculus
 LOCUS cDNA clone K4303435F21 3', mRNA sequence.
 ACCESSION BY641551
 VERSION BY641551.1 GI:26976733
 KEYWORDS EST.

Mus musculus (house mouse)
 SOURCE
 ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 494)
 Okazaki,Y., Furuno,M., Kasukawa,T., Adachi,J., Bono,H., Kondo,S.,
 Nikaido,I., Osato,N., Saito,R., Suzuki,H., Yamana,I., Kiyosawa,H.,
 Yagi,K., Tomaru,Y., Hasegawa,Y., Nogami,A., Schonbach,C.,
 Gojobori,T., Baldarelli,R., Hill,D.P., Bult,C., Hume,D.A.,
 Quackenbush,J., Schriml,L.M., Kanapin,A., Matsuda,H., Batalov,S.,
 Beisel,K.W., Blake,J.A., Bradt,D., Bruscia,V., Chochila,C., Corbani,
 L.E., Cousins,S., Dalla,E., Dragani,T.A., Fletcher,C.F., Forrest,
 A., Frazer,K.S., Gaasterland,T., Gariboldi,M., Gissi,C., Godzik,A.,
 Gough,J., Grimmond,S., Gustincich,S., Hirokawa,N., Jackson,I.J.,
 Jarvis,E.D., Kanai,A., Kawaji,H., Kawasawa,Y., Kedzierski,R.M.,
 King,B.L., Konagaya,A., Kurochkin,I.V., Lee,Y., Lenhard,B., Lyons,
 P.A., Maglott,D.R., Maltais,L., Marchionni,L., McKenzie,L., Miki,
 H., Nagashima,T., Numata,K., Okido,T., Pavan,M.J., Pertea,G.,
 Pesole,G., Petrosky,N., Pillai,R., Pontius,J.U., Qi,D.,
 Ramachandran,S., Ravasi,T., Reed,J.C., Reed,D.J., Reid,J., Ring,
 B.Z., Ringwald,M., Sandelin,A., Schneider,C., Sempke,C.A., Setou,
 M., Shimada,K., Sultana,R., Takenaka,Y., Taylor,M.S., Teasdale,
 R.D., Tomita,M., Verardo,R., Wagner,L., Wallstedt,C., Wang,Y.,
 Watanabe,Y., Wells,C., Wilming,L.G., Wyshew-Boris,A., Yanagisawa,
 M., Yang,I., Yang,L., Yuan,Z., Zavolan,M., Zhu,Y., Zimmer,A.,
 Carninci,P., Hayatsu,N., Hirozane-Kishikawa,T., Kono,H., Nakamura,
 M., Sakazume,N., Sato,K., Shiraki,T., Waki,K., Kawai,J., Alizawa,K.,
 Araiawa,T., Fukuda,S., Hara,A., Hashizume,M., Imotani,K., Ishii,
 Y., Itoh,M., Kagawa,I., Miyazaki,A., Sakai,K., Sasaki,D., Shibata,
 K., Shingawa,A., Yasunishi,A., Yoshino,M., Waterston,R., Lander,
 E.S., Rogers,J., Birney,E. and Hayashizaki,Y.

TITLE Analysis of the mouse transcriptome based on functional annotation
 of 60,770 full-length cDNAs
 JOURNAL Nature 420, 563-573 (2002)
 MEDLINE 22354683
 PUBMED 12466851

COMMENT Contact: Yoshihide Hayashizaki

Laboratory for Genome Exploration Research Group, RIKEN Genomic
 Sciences Center (GSC), Yokohama Institute
 The Institute of Physical and Chemical Research (RIKEN)
 1-7-22 Sugaicho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
 Tel: 81-45-503-9222
 Fax: 81-45-503-9216
 Email: genome-res@sc.riken.go.jp.

URL: http://genome.gsc.riken.go.jp/
 Alizawa,K., Akimura,T., Araiawa,T., Carninci,P., Fukuda,S., Hirozane,
 T., Imotani,K., Ishii,Y., Itoh,M., Kawai,J., Kono,H., Miyazaki,A.,
 Murata,M., Nakamura,M., Nomura,K., Numazaki,R., Ohno,M., Sakai,K.,
 Sakazume,N., Sasaki,D., Sato,K., Shibata,K., Shiraki,T., Tagami,
 M., Waki,K., Watanishi,A., Muramatsu,M. and Hayashizaki,Y. Direct
 Submission

Computational Analysis of Full-length Mouse cDNAs Compared with
 Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
 Normalization and subtraction of cap-trapper-selected cDNAs to
 prepare full-length cDNA libraries for rapid discovery of new
 genes. Genome Res. 10 (10), 1617-1630 (2000)

RIKEN integrated sequence analysis (RISA) system--384-format
 sequencing pipeline with 384 multicapillary sequencer. Genome Res.
 10 (11), 1757-1771 (2000)

Computer-based methods for the mouse full-length cDNA
 encyclopedia: real-time sequence clustering for construction of a

nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
 cDNA library was prepared and sequenced in Mouse Genome
 Encyclopedia Project of Genome Exploration Research Group in Riken
 Genomic Sciences Center and Genome Science Laboratory in RIKEN.
 Division of Experimental Animal Research in Riken contributed to
 prepare mouse tissues.
 Tissues were provided by Michela Fagioli and Takao K. Hensch (
 Laboratory for Neuronal Circuit Development Brain Science Institute
 RIKEN 2-1 Hirotsawa, Mako-shi, Saitama 351-0198 Japan) whose
 assistance we gratefully acknowledge.
 Please visit our web site (<http://genome.gsc.riken.go.jp>) for
 further details.

FEATURES

source

1. 494
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="K430345F21"
 /tissue_type="visual cortex"
 /clone_lib="RIKEN full-length enriched, visual cortex"
 BASE COUNT 147 a 109 c 98 g 139 t 1 others
 ORIGIN

Alignment Scores:

Pred. No.: 47.8 Length: 494
 Score: 9.00 Matches: 9
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 17.65% Indels: 0
 DB: 13 Gaps: 0

US-09-402-713a-2 (1-51) x BY641551 (1-494)

Qy 18 GlnLysGluAlaGlnArgSerLeuGly 26
 Db 350 CAGAAAGAGGCCGACGAGACTTGGCA 376

RESULT 6
 AM093357 528 bp mRNA linear EST 18-MAY-2001
 LOCUS EST286537 tomato mixed elicitor, B71 Lycopersicon esculentum cDNA
 DEFINITION clone cLET24J3, mRNA sequence.
 ACCESSION AM093357.1 GI:6058952
 VERSION EST.
 KEYWORDS Lycopersicon esculentum (tomato)
 SOURCE Lycopersicon esculentum
 ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 asterids; Jamilids; Solanales; Solanaceae; Solanum; Lycopersicon.
 1 (bases 1 to 528)
 D'Ascenzo, M., He, X., Lyman, J., Holt, I. E., Jiang, F., Upton, J.,
 Romling, C. M., Craven, M. B., Fujii, C. Y., Bowman, C. L., Niernman, W.,
 Fraser, C. M., Venter, J. C., Martin, G. B., Tanksley, S. D. and Giovannoni
 J.

REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 COMMENT

unpublished
 Contact: CUGI
 Clemson University Genomics Institute
 Clemson University
 100 Jordan Hall, Clemson, SC 29634, USA
 Email: <http://www.genome.clemson.edu/orders/index.html>
 5 prime sequence.
 Location/Qualifiers
 1. 528

FEATURES

source

/organism="Lycopersicon esculentum"
 /mol_type="mRNA"
 /cultivar="Rio Grande PtoR"
 /db_xref="taxon:4081"
 /clone="cLET24J3"
 /tissue_type="leaf"
 /dev_stage="4-6 week old plants"

/lab_host="XLI-Blue MRF"
 /clone_lib="tomato mixed elicitor, B71"
 /note="Vector: pBluescript SK(-); site 1: EcoRI; site 2:
 XhoI; cLET - Inoculated with a variety of disease response
 elicitors. Plants exposed to 2,6 dichloroisocitric
 acid, BTH, jasmonic acid, ethylene, fenthion, ELX,
 okadaic acid, or systemin prior to tissue harvest. EcoRI
 site was destroyed during cloning."
 BASE COUNT 144 a 88 c 130 g 166 t
 ORIGIN

Alignment Scores:

Pred. No.: 51.5 Length: 528
 Score: 9.00 Matches: 9
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 17.65% Indels: 0
 DB: 9 Gaps: 0

US-09-402-713a-2 (1-51) x AM093357 (1-528)

Qy 38 SerLeuAlaLeuGlySerLeuValProLeu 46
 Db 442 TCATTCGCAATGTGTTCATTCATTA 468

RESULT 7
 BI801819/c 531 bp mRNA linear EST 01-NOV-2001
 LOCUS H061G05 Endosperm library from Oryza sativa (10 days after anthesis
 DEFINITION) Oryza sativa cDNA clone H061G05, mRNA sequence.
 ACCESSION BI801819 GI:16574523
 VERSION EST.
 KEYWORDS Oryza sativa
 SOURCE Oryza sativa
 ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Ehrhartoideae; Oryzaceae; Oryza.
 1 (bases 1 to 531)
 Dong, H. T., Li, D. B., Zhuang, X. F., Dai, C. G., Sun, L. X., Pei, Y. X., Wu
 H. F., Jiang, Y. X., Yu, F. C., Gao, Q. K. and Lou, Y. C.
 A Gene Expression Screen in Oryza sativa

REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 COMMENT

unpublished
 Contact: Dong HT
 Laboratory of Functional Genetics
 Bio-Technology Institute of Zhejiang University
 Kaixuan Road 268#, Hangzhou, Zhejiang, P. R. China
 Tel: 0086-571-86892051
 Fax: 0086-571-86961525
 Email: htdong@zju.edu.cn
 Seq primer: M13 forward primer.
 Location/Qualifiers
 1. 531

FEATURES

source

/organism="Oryza sativa"
 /mol_type="mRNA"
 /db_xref="taxon:4530"
 /clone="H061G05"
 /tissue_type="Endosperm"
 /dev_stage="10 days after anthesis"
 /clone_lib="Endosperm library from Oryza sativa (10 days
 after anthesis)"
 /note="Vector: pSport2"
 BASE COUNT 163 a 116 c 123 g 129 t
 ORIGIN

Alignment Scores:

Pred. No.: 51.9 Length: 531
 Score: 9.00 Matches: 9
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 17.65% Indels: 0
 DB: 12 Gaps: 0


```

BASE COUNT      223 a      45 c      270 g      203 t
ORIGIN
Alignment Scores:
Pred. No.:      75.8      Length:      741
Score:          9.00      Matches:      9
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches: 0
Query Match:    17.65%      Indels:      0
DB:            10      Gaps:      0

US-09-402-713a-2 (1-51) x BB634056 (1-741)
Oy      5 11eSerSerProPhelystyrProHis 13
Db      584 ATATCATCTCCCTTCAATATCCCAT 558

RESULT 10
BM410648      754 bp      mRNA      linear      EST 22-JAN-2002
LOCUS      EST584975 tomato breaker fruit Lycopersicon esculentum cDNA clone
DEFINITION      CLE54K11 5' end, mRNA sequence.
ACCESSION      BM410648
VERSION      BM410648.1 GI:18262278
KEYWORDS      EST.
SOURCE      Lycopersicon esculentum (tomato)
ORGANISM      Lycopersicon esculentum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamids; Solanales; Solanales; Solanum; Lycopersicon.
1 (bases 1 to 754)
Alcala,J., Vredalov,J., White,R., Vision,T., Karamycheva,S.A., Tsai
,J., Bougri,O., Kirkness,E., Uteback,T., Van Aken,S., Romning
,C.M., Fraser,C.M., Martin,G.B., Tanksley,S.D. and Giovannoni,J.
Generation of ESTs from tomato fruit tissue, breaker stage (2002)
Unpublished
Contact: CGCI
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Email: http://www.genome.clemson.edu/orders/index.html
This clone is available through the Clemson University Genomics
Institute
Seq primer: T3.
Location/Qualifiers
1..754
/organism="Lycopersicon esculentum"
/mol_type="mRNA"
/db_xref="taxon:4081"
/clone="CLE54K11"
/tissue_type="Pericarp"
/dev_stage="breaker"
/lab_host="SOLR"
/clone_lib="tomato breaker fruit"
/Note="Vector: pBluescriptSK(-)Mudapt; Site_1: EcoRI;
Site_2: XhoI; supplier: Boyce Thompson Institute;
sequencing: The Institute for Genomic Research. Fruit
were harvested at the breaker stage (first sign of
lycopene accumulation on the blossom end of fruit). Fruit
were cut in half and the seeds and locules were discarded
prior to freezing the pericarp."

BASE COUNT      221 a      135 c      177 g      221 t
ORIGIN
Alignment Scores:
Pred. No.:      77.3      Length:      754
Score:          9.00      Matches:      9
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches: 0
Query Match:    17.65%      Indels:      0
DB:            12      Gaps:      0

```

```

US-09-402-713a-2 (1-51) x BM410648 (1-754)
Oy      38 SerLeuAlaLeuCysLeuValProLeu 46
Db      702 TCATGGCATGTGTAGTCCCATTA 728

RESULT 11
BG527932      132 bp      mRNA      linear      EST 03-APR-2001
LOCUS      60255684F1 NIH_MGC_59 Homo sapiens cDNA clone IMAGE:4685735 5',
DEFINITION      mRNA sequence.
ACCESSION      BG527932
VERSION      BG527932.1 GI:13519469
KEYWORDS      EST.
SOURCE      Homo sapiens (human)
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 132)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgaps-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: CLONTECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.lnl.gov
Plate: LCM1495 row: 1 column: 24
High quality sequence stop: 104.
Location/Qualifiers
1..132
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4685735"
/tissue_type="mucoepidermoid carcinoma"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NIH_MGC_59"
/Note="Organ: Lung; Vector: pDNR-LIB (Clontech); Site_1:
SfiI (ggcgccctcgcc); Site_2: SfiI (ggccatctggcc);
Double-stranded cDNA was prepared from cell line RNA. 5'
and 3' adaptors were used in cloning as follows: 5'
adaptor sequence: 5'-ATTCTAGAGCGCGAGCGCGACATG-dT(30)BN-3'
(where B = A, C, or G and N = A, C, G, or T). Average
insert size 1.65 kb (range 0.9-4.0 kb). 15/15 colonies
contained inserts by PCR. This library was enriched for
full-length clones and was constructed by Clontech
Laboratories (Palo Alto, CA). Note: this is a NIH-MGC
Library."

BASE COUNT      32 a      40 c      31 g      29 t
ORIGIN
Alignment Scores:
Pred. No.:      106      Length:      132
Score:          8.00      Matches:      8
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches: 0
Query Match:    15.69%      Indels:      0
DB:            10      Gaps:      0

US-09-402-713a-2 (1-51) x BG527932 (1-132)
Oy      34 GlySerSerMetSerLeuAlaLeu 41
Db      29 GGSTCTCATGTCTCTGCTCTG 52

RESULT 12

```


BY370977 174 bp mRNA linear EST 12-DEC-2002
 LOCUS BY370977 RIKEN full-length enriched, kidney CCL-142 RAG CDNA Mus
 DEFINITION musculus CDNA clone G430048K16 3', mRNA sequence.
 ACCESSION BY370977
 VERSION BY370977.1 GI:26600465
 KEYWORDS EST.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 174)
 Okazaki,Y., Furuno,M., Kasukawa,T., Adachi,J., Bono,H., Kondo,S.,
 Nakai,I., Otsu,N., Saito,R., Suzuki,H., Yamanaoka,T., Kiyosawa,H.,
 Yagi,K., Tomaru,Y., Hasegawa,Y., Nogami,A., Schonbach,C.,
 Gojobori,T., Baldarelli,R., Hill,D.P., Bul,C., Hume,D.A.,
 Quackenbush,J., Schriml,L.M., Kanapin,A., Matsuda,H., Batalov,S.,
 Belset,K.W., Blake,J.A., Bradt,D., Brusic,V., Chochia,C., Corbani,
 L.E., Cousins,S., Dalla,E., Dragani,T.A., Fletcher,C.F., Forrest,
 A., Frazer,K.S., Gaasterland,T., Gariboldi,M., Gissi,C., Godzik,A.,
 Gough,J., Gilmord,S., Gustincich,S., Hirokawa,N., Jackson,I.J.,
 Jarvis,E.D., Kanai,A., Kawai,H., Kawasawa,Y., Kedzierski,R.M.,
 King,B.L., Konagaya,A., Kurochkin,I.V., Lee,Y., Lenhard,B., Lyons,
 P.A., Maglott,D.R., Maitais,L., Marchionni,L., McKenzie,L., Miki,
 H., Nagashima,T., Numata,K., Okido,T., Pavan,W.J., Perlea,G.,
 Pesole,G., Petrovsky,N., Pillai,R., Pontius,J.U., Qi,D.,
 Ramchandran,S., Ravasi,T., Reed,J.C., Reed,D.J., Reid,J., Ring,
 B.Z., Ringwald,M., Sandelin,A., Schneider,C., Sempile,C.A., Setou,
 M., Shimada,K., Sultana,R., Takenaka,Y., Taylor,M.S., Teasdale,
 R.D., Tomita,M., Verardo,R., Wagner,L., Wahlstedt,C., Wang,Y.,
 Watanabe,Y., Wells,C., Wilming,L.G., Wyshaw-Boris,A., Yanagisawa,
 M., Yang,I., Yang,L., Yuan,Z., Zavolan,M., Zhu,Y., Zimmer,A.,
 Carninci,P., Hayatsu,N., Hirozane-Kishikawa,T., Kono,H., Nakamura,
 M., Sakazume,N., Sato,K., Shiraki,T., Waki,K., Kawai,J., Aizawa,K.,
 Arakawa,T., Fukuda,S., Hara,A., Hashizume,W., Imotani,K., Ishii,
 Y., Itoh,M., Kagawa,I., Miyazaki,A., Sakai,K., Sasaki,D., Shibata,
 K., Shinagawa,A., Yasunishi,A., Yoshino,M., Waterston,R., Lander,
 E.S., Rogers,J., Birney,E. and Hayashizaki,Y.
 Analysis of the mouse transcriptome based on functional annotation
 of 60,770 full-length cDNAs
 Nature 420, 563-573 (2002)
 JOURNAL NATURE
 MEDLINE 22354683
 PUBMED 12466851
 COMMENT
 TITLE
 CONTACT: Yoshihide Hayashizaki
 Laboratory for Genome Exploration Research Group, RIKEN Genomic
 Sciences Center(GSC), Yokohama Institute
 The Institute of Physical and Chemical Research (RIKEN)
 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
 Tel: 81-45-503-9222
 Fax: 81-45-503-9216
 Email: genome-res@sc.riken.go.jp,
 URL: http://genome.gsc.riken.go.jp/
 Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S., Hirozane,
 T., Imotani,K., Ishii,Y., Itoh,M., Kawai,J., Kono,H., Miyazaki,A.,
 Murata,M., Nakamura,M., Nomura,K., Numazaki,R., Ohno,M., Sakai,K.,
 Sakazume,N., Sasaki,D., Sato,K., Shibata,K., Shiraki,T., Tagami,
 M., Waki,K., Watabiki,A., Muramatsu,M. and Hayashizaki,Y. Direct
 Submission
 Computational Analysis of Full-length Mouse cDNAs Compared with
 Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
 Normalization and subtraction of cap-trapper-selected cDNAs to
 prepare full-length cDNA libraries for rapid discovery of new
 genes. Genome Res. 10 (10), 1617-1630 (2000)
 RIKEN integrated sequence analysis (RISA) system--384-format
 sequencing pipeline with 384 multicapillary sequencer. Genome Res.
 10 (11), 1737-1771 (2000)
 Computer-based methods for the mouse full-length cDNA
 encyclopedia: real-time sequence clustering for construction of a
 nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
 Encyclopedia Project of Genome Exploration Research Group in Riken
 Genomic Sciences Center and Genome Science Laboratory in RIKEN.
 Division of Experimental Animal Research in Riken contributed to

prepare mouse tissues.
 Please visit our web site (<http://genome.gsc.riken.go.jp>) for
 further details.
 FEATURES
 source
 Location/Qualifiers
 1..174
 /organism="Mus musculus"
 /mol_type="mRNA"
 /db_xref="taxon:10090"
 /clone="G430048K16"
 /tissue_type="kidney"
 /cell_line="CCL-142 RAG"
 /clone_id="RIKEN full-length enriched, kidney CCL-142 RAG
 CDNA"
 BASE COUNT 51 a 45 c 40 g 38 t
 ORIGIN
 Alignment Scores:
 Pred. No.: 146 Length: 174
 Score: 8.00 Matches: 8
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 15.69% Indels: 0
 DB: 13 Gaps: 0
 US-09-402-713A-2 (1-51) x BY370977 (1-174)
 Oy 29 ProGLYARGHISLEUGlySerSer 36
 Db 97 CCAAGCAGACATCTTGATCTCT 120
 RESULT 13
 BQ368838/C
 LOCUS BQ368838 239 bp mRNA linear EST 21-MAY-2002
 DEFINITION PM1-GN0514-310501-006-H01 GN0514 Homo sapiens CDNA, mRNA sequence.
 ACCESSION BQ368838
 VERSION BQ368838.1 GI:21044352
 KEYWORDS EST.
 SOURCE
 ORGANISM Homo sapiens (human)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 1 (bases 1 to 239)
 Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
 Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
 Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H.,
 Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,
 M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
 Simpson,A.J.
 Shotgun sequencing of the human transcriptome with ORF expressed
 sequence tags
 Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
 JOURNAL 20202663
 MEDLINE 10737800
 PUBMED
 COMMENT
 TITLE
 CONTACT: Simpson A.J.G.
 Laboratory of Cancer Genetics
 Ludwig Institute for Cancer Research
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
 Brazil
 Tel: +55-11-2704922
 Fax: +55-11-2707001
 Email: asimpson@ludwig.org.br
 This sequence was derived from the FAPESP/LICR Human Cancer Genome
 Project. This entry can be seen in the following URL
 (<http://www.ludwig.org.br/scripts/gethtml2.pl?tl=PM1<2=PM1-GN0514-310501-006-h01<3=2001-05-31<4=1>)
 Seq primer: puc 18 forward
 High quality sequence start: 6
 High quality sequence stop: 46.
 FEATURES
 source
 Location/Qualifiers
 1..239
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"

```

/dev_stage="Adult"
/clone_lib="GN0514"
; note="Organ: placenta_normal; Vector: puc18; Site_1: SmaI
; Site_2: SmaI; A mini-library was made by cloning
products derived from ORESTES PCR (U.S. Letters Patent
application No. 196,716 - Ludwig Institute for Cancer
Research) profiles into the pUC 18 vector. Reverse
transcription of tissue mRNA and cDNA amplification were
performed under low stringency conditions."

BASE COUNT      83 a      51 c      61 g      44 t
ORIGIN

Alignment Scores:
Pred. No.:      209      Length:      239
Score:          8.00      Matches:      8
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches: 0
Query Match:      15.69%      Indels:      0
DB:              13      Gaps:      0

US-09-402-713A-2 (1-51) x BQ368838 (1-239)
Oy      38 SerLeuAlaLeuCysLeuValPro 45
Db      150 TCACCTGCGCTTGTGTCTAGTCCA 127

RESULT 14
BY370387      243 bp      mRNA      linear      EST 12-DEC-2002
LOCUS      BY370387      RIKEN full-length enriched, RCB-1283 B16 melanoma cDNA Mus
DEFINITION      BY370387 cDNA clone G43009005 3', mRNA sequence.
ACCESSION      BY370387
VERSION      BY370387.1 GI:26599875
KEYWORDS      EST.
SOURCE      Mus musculus (house mouse)
ORGANISM      Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 243)
Okazaki,Y., Furuno,M., Kasukawa,T., Adachi,T., Bono,H., Kondo,S.,
Nikaido,I., Osato,N., Saito,R., Suzuki,H., Yamanaka,I., Kiyosawa,H.,
Yagi,K., Tomaru,Y., Hasegawa,Y., Nogami,A., Schonbach,C.,
Gojobori,T., Baldarelli,R., Hill,D.P., Bolt,C., Hume,D.A.,
Quackenbush,J., Schriml,L.M., Kanapin,A., Matsuda,H., Batalov,S.,
Beisel,K.W., Blake,J.A., Bradt,D., Brusic,V., Chothia,C., Corbani,
L.E., Cousins,S., Dalla,E., Dragani,T.A., Fletcher,C.F., Forrest,
A., Frazer,K.S., Gaasterland,T., Gariboldi,M., Gissi,C., Godzik,A.,
Gough,J., Grimmond,S., Gustincich,S., Hirokawa,N., Jackson,I.J.,
Jarvis,E.D., Kana,A., Kawaji,H., Kawasawa,Y., Kedzierski,R.M.,
King,B.L., Konagaya,A., Kurochkin,I.V., Lee,Y., Lenhard,B., Lyons,
P.A., Maglott,D.R., Maltais,L., Marchionni,L., McKenzie,L., Mikl,
H., Nagashima,T., Numata,K., Okido,T., Pavan,W.J., Pertea,G.,
Pesole,G., Petrovsky,N., Piliak,R., Pontus,J.U., Qi,D.,
Ramchandran,S., Ravasi,T., Reed,J.C., Reed,D.J., Reid,J., Ring,
B.Z., Ringwald,M., Sandelin,A., Schneider,C., Semple,C.A., Setou,
M., Shimada,K., Sultana,R., Takenaka,Y., Taylor,M.S., Teasdale,
R.D., Tomita,M., Verardo,R., Wagner,L., Wahlstedt,C., Wang,Y.,
Watanabe,Y., Wells,C., Wilming,L.G., Wynshaw-Boris,A., Yanagisawa,
M., Yang,I., Yang,L., Yuan,Z., Zavolan,A., Zhu,Y., Zimmer,A.,
Carinci,P., Hayatsu,N., Hirozane-Kishikawa,T., Kono,H., Nakamura,
M., Sakazume,N., Sato,K., Shiraki,T., Waki,K., Kawai,J., Aizawa,K.,
Aizawa,T., Fukuda,S., Hara,A., Hashizume,W., Imotani,K., Ishii,
Y., Itoh,M., Kagawa,I., Miyazaki,A., Sakai,K., Sasaki,D., Shibata,
K., Shingawa,A., Yasunishi,A., Yoshino,M., Waterston,R., Lander,
E.S., Rogers,J., Birney,E. and Hayashizaki,Y.
Analysis of the mouse transcriptome based on functional annotation
of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
22354683
JOURNAL
MEDLINE
PUBMED
12468851
COMMENT      Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center (GSC), Yokohama Institute

```

```

The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@gs.c.riken.go.jp,
URL: http://genome.gsc.riken.go.jp/
Aizawa,K., Akimura,T., Aizawa,T., Carninci,P., Fukuda,S., Hirozane,
T., Imotani,K., Ishii,Y., Itoh,M., Kawai,J., Kono,H., Miyazaki,A.,
Murata,M., Nakamura,N., Nomura,K., Numazaki,R., Ohno,M., Sakai,K.,
Sakazume,N., Sasaki,D., Sato,K., Shibata,K., Shiraki,T., Tagami,
M., Waki,K., Watanabe,A., Muramatsu,M. and Hayashizaki,Y. Direct
Submission
Computational Analysis of Full-Length Mouse cDNAs Compared with
Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multipillar sequencer. Genome Res.
10 (11), 1757-1771 (2000)
Computer-based methods for the mouse full-length cDNA
encyclopedia: real-time sequence clustering for construction of a
nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in Riken.
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues.
Please visit our web site (http://genome.gsc.riken.go.jp) for
further details.
FEATURES
source      Location/Qualifiers
1. .243
/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/clone="G43009005"
/cell_line="RCB-1283 B16 melanoma"
/clone_lib="RIKEN full-length enriched, RCB-1283 B16
melanoma cDNA"

BASE COUNT      74 a      59 c      48 g      62 t
ORIGIN

Alignment Scores:
Pred. No.:      213      Length:      243
Score:          8.00      Matches:      8
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches: 0
Query Match:      15.69%      Indels:      0
DB:              13      Gaps:      0

US-09-402-713A-2 (1-51) x BY370387 (1-243)
Oy      29 ProGlyArgHisLeuGlySerSer 36
Db      122 CCAGCAGACATCTTGATCTCT 145

RESULT 15
BY370387      266 bp      mRNA      linear      EST 18-JAN-2001
LOCUS      BY370387      RIKEN full-length enriched, RCB-1283 B16
DEFINITION      BY370387 cDNA clone G43009005 3', mRNA sequence.
ACCESSION      BY370387
VERSION      BY370387.1 GI:12279109
KEYWORDS      EST.
SOURCE      Homo sapiens (human)
ORGANISM      Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 266)
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagai,M.A., da Silva,M. Jr., Zago,M.A., Bordin,S., Costa,F.P.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bais,G.S., Simpson,D.H.,
Brunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,
M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and

```

TITLE Simpson,A.J.
Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
JOURNAL Proc Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE 20202663
PUBMED 10737800
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?l1=QV2&t2=QV2-TN0171-
081100-471-c07&t3=2000-11-08&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 49
High quality sequence stop: 266.
Location/Qualifiers

FEATURES

source
1..266
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="TN0171"
/note="Organ: testis_normal; Vector: puc18; Site_1: SmaI;
Site_2: SmaI; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the puc 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."
BASE COUNT 64 a 56 c 59 g 87 t
ORIGIN

Alignment Scores:

Pred. No.:	236	Length:	266
Score:	8.00	Matches:	8
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	15.69%	Indels:	0
DB:	10	Gaps:	0

US-09-402-713a-2 (1-51) x BF887863 (1-266)

QY 2 PhelaH1s1leSerProPhe 9
|||||
Db 191 TTCTTGCAATATCATCACCATT 214

Search completed: September 26, 2003, 21:38:08
Job time : 2221 secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 26, 2003, 21:01:08 ; Search time 6812.49 Seconds
(without alignments)
11241.524 Million cell updates/sec

Title: US-09-402-713A-3

Perfect score: 1872
Sequence: 1 agaagctgcatacagaaaaa.....caataagaatttcaaaaga 1872

Scoring table: OLIGO NUC
Gapop 60.0 , Gapext 60.0

Searched: 2888711 seqs, 20454813386 residues

Word size : 0

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Genbank1.*
1: gb_ba.*
2: gb_hc.*
3: gb_in.*
4: gb_ov.*
5: gb_ov.*
6: gb_pat.*
7: gb_ph.*
8: gb_pl.*
9: gb_pr.*
10: gb_ro.*
11: gb_sts.*
12: gb_sy.*
13: gb_un.*
14: gb_vl.*
15: em_ba.*
16: em_fun.*
17: em_hum.*
18: em_in.*
19: em_mu.*
20: em_om.*
21: em_or.*
22: em_ov.*
23: em_pat.*
24: em_ph.*
25: em_pl.*
26: em_ro.*
27: em_sts.*
28: em_un.*
29: em_vl.*
30: em_htg_hum.*
31: em_htg_inv.*
32: em_htg_other.*
33: em_htg_mus.*
34: em_htg_pln.*
35: em_htg_rtd.*
36: em_htg_mam.*
37: em_htg_vrt.*
38: em_sy.*
39: em_htgo_hum.*
40: em_htgo_mus.*
41: em_htgo_other.*

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1872	100.0	1872	6	BD082483
2	1775	94.8	2037	6	BD082482
3	1367	73.0	3582	6	BD082485
4	1367	73.0	3923	6	AR261166
5	1367	73.0	3923	6	AR278697
6	1367	73.0	3923	6	AX200988
7	1367	73.0	3923	6	AX267716
8	1367	73.0	3923	9	AF103907
9	1185	63.3	5435	9	AF103908
10	1155	61.7	2426	6	AR261038
11	1155	61.7	2426	6	AR278569
12	1155	61.7	2426	6	AX106206
13	1155	61.7	2426	6	AX106689
14	1155	61.7	2426	6	AX140980
15	1155	61.7	2426	6	AX200840
16	1155	61.7	2426	6	AX267496
17	1155	61.7	3112	6	AR261036
18	1155	61.7	3112	6	AR278567
19	1155	61.7	3112	6	AX106204
20	1155	61.7	3112	6	AX106687
21	1155	61.7	3112	6	AX140978
22	1155	61.7	3112	6	AX200838
23	1155	61.7	3112	6	AX267494
24	1034	55.2	2229	6	AR261037
25	1034	55.2	2229	6	AR278568
26	1034	55.2	2229	6	AX106205
27	1034	55.2	2229	6	AX106688
28	1034	55.2	2229	6	AX140979
29	1034	55.2	2229	6	AX200839
30	1034	55.2	2229	6	AX267495
31	972	51.9	128480	9	AL359314
32	820	43.8	820	6	BD082484
33	812	43.4	812	6	AR261039
34	812	43.4	812	6	AR278570
35	812	43.4	812	6	AX106207
36	812	43.4	812	6	AX106690
37	812	43.4	812	6	AX140981
38	812	43.4	812	6	AX200841
39	812	43.4	812	6	AX267497
40	473	25.3	597	6	BD078456
41	330	17.6	359	6	AX018075
42	330	17.6	359	6	BD134961
43	276	14.7	129109	9	AL390239
44	260	13.9	437	6	BD030513
45	257	13.7	718	6	AR237401

ALIGNMENTS

RESULT 1
LOCUS BD082483 1872 bp DNA linear PAT 27-AUG-2002
DEFINITION PCA3, PCA3 genes, and methods of use.
ACCESSION BD082483
VERSION BD082483.1 GI:22628093
KEYWORDS JP 2001522240-A/2.
SOURCE Mastadenovirus
ORGANISM Mastadenovirus
REFERENCE 1 (bases 1 to 1872)
AUTHORS Bussemakers,M.J.G.
TITLE PCA3, PCA3 genes, and methods of use
JOURNAL Patent: JP 2001522240-A 2 13-NOV-2001;
DIAGNOCURE INC

COMMENT	PN	JP	2001522240-A/2
	PD	13-NOV-2001	
	PF	09-APR-1998	JP 1998542194
	PR	10-APR-1997	US 60/041836
	PI	MARION J G	BUSEEMAKERS
	PC	C12N15/00, C12N15/12, C12N5/12, C12N1/21, C07K14/47, C07K16/18, PC C1201/68,	
	PC	G01N33/577, A61K39/395, A01K67/027	
	CC	Strandedness: Double;	
	CC	Topology: Linear;	
FEATURES	FN	key	Location/Qualifiers.
SOURCE			Location/Qualifiers
			1. 1872
			/organism="Mastadenovirus"
			/mol_type="genomic DNA"
			/db_xref="taxon:10509"
BASE COUNT		567 a	389 c 369 g 539 t 8 others
ORIGIN			

Query Match	100.0%;	Score 1872;	DB 6;	Length 1872;
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches 1872; Conservative	0;	Mismatches	0;	Gaps 0;

OY	1	AGAAGCTGGCATCAGAAAAACAGAGGGAGATTGTGTGGCTGCAGCCAGGGAGACAG	60
Db	1	AGAAGCTGGCATCAGAAAAACAGAGGGAGATTGTGTGGCTGCAGCCAGGGAGACAG	60
OY	61	GAAGATCTGCATGTGGGAGGACCTGATGATACAGAGGTGAAATAAGAAAGGCTGCT	120
Db	61	GAAGATCTGCATGTGGGAGGAGACTGATGATACAGAGGTGAAATAAGAAAGGCTGCT	120
OY	121	GACTTTACCATCTGAGGGCCACACATCTGCTGAAATGAGATATAATTACACTACATAGAAC	180
Db	121	GACTTTACCATCTGAGGGCCACACATCTCTGAAATGAGATATAATTACACTACATAGAAC	180
OY	181	AGCAAGATGACAAATTAATGTCTTAAGTAGTGATGTCATGTTTTCACATTTCCAGCCCTTT	240
Db	181	AGCAAGATGACAAATTAATGTCTTAAGTAGTGATGTCATGTTTTCACATTTCCAGCCCTTT	240
OY	241	AAATATCCACACACACAGAGAACACAAAAAGAAAGCACAGATCCCTGGGAGAAAAATGCC	300
Db	241	AAATATCCACACACACAGAGAACACAAAAAGAAAGCACAGATCCCTGGGAGAAAAATGCC	300
OY	301	GGCCGCCATCTTGGGTATCGATGAGCCTCGCCCTGTGCTGTGTCCTGTTGAGGGAA	360
Db	301	GGCCGCCATCTTGGGTATCGATGAGCCTCGCCCTGTGCTGTGTCCTGTTGAGGGAA	360
OY	361	GGACATTGAAAAATGATGATGATGCTTCTTAAAGATGGGACAGAAAAACATCTGTT	420
Db	361	GGACATTGAAAAATGATGATGATGCTTCTTAAAGATGGGACAGAAAAACATCTGTT	420
OY	421	GTGATATTTATTTGGAACGGGATTCACAGATTTGAAATGAAGTCACAAAAGTAGCATTACC	480
Db	421	GTGATATTTATTTGGAACGGGATTCACAGATTTGAAATGAAGTCACAAAAGTAGCATTACC	480
OY	481	AATGAGAGAAAAACAGACGAGAAAAATCTTGATGCTTCACAGACATGCACAAACAAA	540
Db	481	AATGAGAGAAAAACAGACGAGAAAAATCTTGATGCTTCACAGACATGCACAAACAAA	540
OY	541	TGGAATACGTGATGACATGAGGCGCAAGCGTGGGGAGAGATTAACACGGGGCAGAG	600
Db	541	TGGAATACGTGATGACATGAGGCGCAAGCGTGGGGAGAGATTAACACGGGGCAGAG	600
OY	601	GTCAGATTTGGCCCTGCTGCTTAACGTATGCGTTCAATACCAATCATTTCAATATTC	660
Db	601	GTCAGATTTGGCCCTGCTGCTTAACGTATGCGTTCAATACCAATCATTTCAATATTC	660
OY	661	TAACCTCAAAAACAAAGCTGTGTATATTCGATCTCAAGGTTCTCTTGCGCCACA	720
Db	661	TAACCTCAAAAACAAAGCTGTGTATATTCGATCTCAAGGTTCTCTTGCGCCACA	720
OY	721	TTCTCCATATATCCAGCACACTATTTTAAATATTTAGTTCCAGATCTGTACTGTGAC	780
Db	721	TTCTCCATATATCCAGCACACTATTTTAAATATTTAGTTCCAGATCTGTACTGTGAC	780

Dd	721	TTCTCCAAATATCCAGCCACACTATTTTAAATATTAGTTCCAGATCTGTACTGTGAC	780
OY	781	CTTCTACACGTGAGAAATACATTTCTCATTTTGTTCAAAGACCCTTGTTGGCTGCT	840
Dd	781	CTTCTACACGTGAGAAATACATTTCTCATTTTGTTCAAAGACCCTTGTTGGCTGCT	840
OY	841	AATATGTAAGCTGACTGTTTTTCTTAAGAGTGTTCTGGCCAGGGGATCTGTGAACAGCC	900
Dd	841	AATATGTAAGCTGACTGTTTTTCTTAAGAGTGTTCTGGCCAGGGGATCTGTGAACAGCC	900
OY	901	TGGGAAGATCTCAAGATCTTTCGCGGGTTTACTTACTTACACACACATGATCATTTAC	960
Dd	901	TGGGAAGATCTCAAGATCTTTCGCGGGTTTACTTACTTACACACACATGATCATTTAC	960
OY	961	GGAGTGAATTAATCAATCAATCATCTCCAGTGTCTTGGCCATACAGAAATTCATTTTC	1020
Dd	961	GGAGTGAATTAATCAATCAATCATCTCCAGTGTCTTGGCCATACAGAAATTCATTTTC	1020
OY	1021	CCACTTTTGTGCCATTTCTCAAGACCTCAAAATGTCAATTCATTATATTCACAGATTAA	1080
Dd	1021	CCACTTTTGTGCCATTTCTCAAGACCTCAAAATGTCAATTCATTATATTCACAGATTAA	1080
OY	1081	CTTTTTTTTTTAACTGGGAAGAAATTCATGTTACTATGGAGTATGGGAATTAATTAAT	1140
Dd	1081	CTTTTTTTTTTAACTGGGAAGAAATTCATGTTACTATGGAGTATGGGAATTAATTAAT	1140
OY	1141	ATTTTGTTTTCCAGTGCACAAAGATGACTAAGTCCTTTATCCCTCCCTTGTGTGATTTT	1200
Dd	1141	ATTTTGTTTTCCAGTGCACAAAGATGACTAAGTCCTTTATCCCTCCCTTGTGTGATTTT	1200
OY	1201	TTTCCAGTATTAAGTTAAATATGCTTAGCCTTGTAAGCTGTATACAGACAGCCTCT	1260
Dd	1201	TTTCCAGTATTAAGTTAAATATGCTTAGCCTGTGTACTGAGCTGTATACAGACAGCCTCT	1260
OY	1261	CCCCATCCCTCCAGCCTTATCTGTCATACCATCAACCCCTCCCATNYSACCTAAACAA	1320
Dd	1261	CCCCATCCCTCCAGCCTTATCTGTCATACCATCAACCCCTCCCATNYSACCTAAACAA	1320
OY	1321	ATCTAACCTTGAATTCCTTGAACATGTGACAGNCATACATTTTCTCTTGTGCTGAGAAGC	1380
Dd	1321	ATCTAACCTTGAATTCCTTGAACATGTGACAGNCATACATTTTCTCTTGTGCTGAGAAGC	1380
OY	1381	TCTTCTCTTGTCTCTTAANTCTAGATGATGTGAAGTTTGAATTAAGTTGACTATCTTACT	1440
Dd	1381	TCTTCTCTTGTCTCTTAANTCTAGATGATGTGAAGTTTGAATTAAGTTGACTATCTTACT	1440
OY	1441	TCATGCAAGAAGGAGACATATGATGATTCATCATCATATGACAGAGCAAAATCTAAAG	1500
Dd	1441	TCATGCAAGAAGGAGACATATGATGATTCATCATCATATGACAGAGCAAAATCTAAAG	1500
OY	1501	TGTAAATTTGATTATAGAGTTTAGTAAATATATGAAGTGCACAAKCCACAGAGGGAATG	1560
Dd	1501	TGTAAATTTGATTATAGAGTTTAGTAAATATATGAAGTGCACAAKCCACAGAGGGAATG	1560
OY	1561	TTTATAGGGGACGTTTGTAGCCTGGGATGTGAAGMAAAGCCAGGGAACCTCATAGTATC	1620
Dd	1561	TTTATAGGGGACGTTTGTAGCCTGGGATGTGAAGMAAAGCCAGGGAACCTCATAGTATC	1620
OY	1621	TTATATATATATACTTCTCTATCTCTATCTCTATCAAAATATCAACAAACCTTTTACAGAA	1680
Dd	1621	TTATATATATATACTTCTCTATCTCTATCTCTATCAAAATATCAACAAACCTTTTACAGAA	1680
OY	1681	TTTATAGCAGTGCAAATCCCCAAAGGTAACTTTATCCATTTTCATGAGTGGCGCTTTAG	1740
Dd	1681	TTTATAGCAGTGCAAATCCCCAAAGGTAACTTTATCCATTTTCATGAGTGGCGCTTTAG	1740
OY	1741	AATTTTGGCAATCATACTGTGCTACTTATCTCAACTTTGANAATGTGTTTGTCTTGTAGT	1800
Dd	1741	AATTTTGGCAATCATACTGTGCTACTTATCTCAACTTTGANAATGTGTTTGTCTTGTAGT	1800
OY	1801	TAAATGAAGAATAAGGCACTCTTGTGAGCCACTTAGGGTTCACTCTGCGCAATAAAG	1860
Dd	1801	TAAATGAAGAATAAGGCACTCTTGTGAGCCACTTAGGGTTCACTCTGCGCAATAAAG	1860

RESULT 2
BD082482
LOCUS BD082482 2037 bp DNA linear PAT 27-AUG-2002
DEFINITION PC3, PCA3 genes, and methods of use.
ACCESSION BD082482
VERSION BD082482.1 GI:22628092
KEYWORDS JP 2001522240-A/1.
SOURCE Mastadenovirus
ORGANISM Mastadenovirus
VIRUSES; dsDNA viruses, no RNA stage; Adenoviridae.
REFERENCE
AUTHORS Bussemakers, M.J.G.
TITLE PC3, PCA3 genes, and methods of use
JOURNAL Patent: JP 2001522240-A 1 13-NOV-2001;
DIAGNOCURE INC SECRETARY OF THE DEPARTMENT OF HEALTH HUMAN SERVICES
COMMENT
PN JP 2001522240-A/1
PD 13-NOV-2001
PF 09-APR-1998 JP 1998542194
PR 10-APR-1997 US 60/041836
PI MARION J G BUSSEMAKERS
PC C12N15/00,C12N15/12,C12N5/12,C12N1/21,C07K14/47,C07K16/18, PC
C1201/68,
PC G01N33/577,A61K39/395,A01K67/027
CC Strandedness: Double;
CC Topology: Linear;
FH Key Location/Qualifiers
FT CDS 379..531.
1. 2037
Location/Qualifiers
/organism="Mastadenovirus"
/mol_type="genomic DNA"
/db_xref="taxon:10509"
BASE COUNT 622 a 426 c 406 g 575 t 8 others
ORIGIN
Query Match 94.8%; Score 1775; DB 6; Length 2037;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1775; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 98 GGTAGAAATTAAGAAAGCTCTGACTTTACCATCTGAGCCACACATCTCTGAAATGG 157
DB 263 GGTAGAAATTAAGAAAGCTCTGACTTTACCATCTGAGCCACACATCTCTGAAATGG 322
QY 158 AGATAATTACACTACTGAAACAGACAGATGACAAATTAATGCTAGTAGTGATGT 217
DB 323 AGATAATTACACTACTGAAACAGACAGATGACAAATTAATGCTAGTAGTGATGT 382
QY 218 TTTTGCACATTTCCAGCCCTTTAAATATCCACACACAGAGAAACACAAAAGAGAC 277
DB 383 TTTTGCACATTTCCAGCCCTTTAAATATCCACACACAGAGAAACACAAAAGAGAC 442
QY 278 AGAATCCCTGGGAGAAATGCCCCGCCCATCTTGGGTCAATGATGAGCCTCGCCCTGT 337
DB 443 AGAATCCCTGGGAGAAATGCCCCGCCCATCTTGGGTCAATGATGAGCCTCGCCCTGT 502
QY 338 GCTGTGCTCCGCTGTGAGGAGAGACATTTAGAAAATGAATGATGTTCTTTAAAGA 397
DB 503 GCTGTGCTCCGCTGTGAGGAGAGACATTTAGAAAATGAATGATGTTCTTTAAAGA 562
QY 398 TGGGACGAGAAAACAGATCCTGTGTGATATTATTGTAACGGGATTACAGATTTGAAT 457
DB 563 TGGGACGAGAAAACAGATCCTGTGTGATATTATTGTAACGGGATTACAGATTTGAAT 622
QY 458 GAATGCACAAGTAGCATTTACCAATGAGAGAGAAAACAGAGAAAATCTTGATGGCTT 517
DB 623 GAATGCACAAGTAGCATTTACCAATGAGAGAGAAAACAGAGAAAATCTTGATGGCTT 682

QY 518 CACAAGATGCAACAACAATAATGAAATGACTGTGATGACATGAGGACGACCAAGCTGGG 577
DB 683 CACAAGATGCAACAACAATAATGAAATGACTGTGATGACATGAGGACGACCAAGCTGGG 742
QY 578 AGAGATTAACCAAGGGGAGAGGGTCAAGATTTG6CCCTGCTGCTAACTGTGCTTC 637
DB 743 AGAGATTAACCAAGGGGAGAGGGTCAAGATTTG6CCCTGCTGCTAACTGTGCTTC 802
QY 638 ATAACCAATATCTTCAATTTCTTAACCTCAACCAAGAGCTGTTGTAATATGATGTC 697
DB 803 ATAACCAATATCTTCAATTTCTTAACCTCAACCAAGAGCTGTTGTAATATGATGTC 862
QY 698 TACGTTCTCTTG6GGCCCAACATCTTCCATATATCCAGCACACTATTTTAAATATT 757
DB 863 TACGTTCTCTTG6GGCCCAACATCTTCCATATATCCAGCACACTATTTTAAATATT 922
QY 758 AGTTCCAGATCTGTACTGTGACCTTTCTACAGCTGATGAATATACATTTACTATTTGTTTC 817
DB 923 AGTTCCAGATCTGTACTGTGACCTTTCTACAGCTGATGAATATACATTTACTATTTGTTTC 982
QY 818 AAAGACCTTGTGTTGCTGCTTAATATGATGACTGACTGTTTCTTAAGAGTGTCTG 877
DB 983 AAAGACCTTGTGTTGCTGCTTAATATGATGACTGACTGTTTCTTAAGAGTGTCTG 1042
QY 878 GCCCAGGGGATCTGTGAACAGGCTGGAGACATCTCAAGATCTTCCAGGGTTATACCTTA 937
DB 1043 GCCCAGGGGATCTGTGAACAGGCTGGAGACATCTCAAGATCTTCCAGGGTTATACCTTA 1102
QY 938 CTAGCACACAGATGATCATTTAAGAGATGAATATCTAATCAACATCATCTCTAGTGTCT 997
DB 1103 CTAGCACACAGATGATCATTTAAGAGATGAATATCTAATCAACATCATCTCTAGTGTCT 1162
QY 998 TTGGCCATACATGAATATTTATTTCCACATTTTGTGCCCCATCTCAAGACCTCAAAAATGTC 1057
DB 1163 TTGGCCATACATGAATATTTATTTCCACATTTTGTGCCCCATCTCAAGACCTCAAAAATGTC 1222
QY 1058 TTCCATTAATATCAAGATTAACCTTTTATTTTAACTGAGAGATTAATGATGATACATG 1117
DB 1223 TTCCATTAATATCAAGATTAACCTTTTATTTTAACTGAGAGATTAATGATGATACATG 1282
QY 1118 CAGCTAGGGAATTAATTAATATTTTGTTCAGTGAACAGATGATGATGATGATGATGATG 1177
DB 1283 CAGCTAGGGAATTAATTAATATTTTGTTCAGTGAACAGATGATGATGATGATGATGATG 1342
QY 1178 TCCCTCCCTTGTGTTGATTTTTCAGATTAATAGTTAAATGCTTACCTGTACTG 1237
DB 1343 TCCCTCCCTTGTGTTGATTTTTCAGATTAATAGTTAAATGCTTACCTGTACTG 1402
QY 1238 AGGCTGTATACAGCACAGCTCTCCCATCTCCAGCTTATCTGTATCATCAGCATCAAC 1297
DB 1403 AGGCTGTATACAGCACAGCTCTCTCCCATCTCCCATCTCCAGCTTATCTGTATCATCAGCATCAAC 1462
QY 1298 CCTTCCATATTAACCAATCTAATCTTGAATTTCTTGAACATGTCAGGATGATGATGATG 1357
DB 1463 CCTTCCATATTAACCAATCTAATCTTGAATTTCTTGAACATGTCAGGATGATGATGATG 1522
QY 1358 ATTTTCCCTGCTGGAAGCTCTTCTGCTTCTTAATGATGATGATGATGATGATGATG 1417
DB 1523 ATTTTCCCTGCTGGAAGCTCTTCTGCTTCTTAATGATGATGATGATGATGATGATG 1582
QY 1418 TTGAATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1477
DB 1583 TTGAATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1642
QY 1478 CATGACAGCAATTAATAAGTGTAAATTTGATTTATAGAGTTTATGATTAATATATGAA 1537
DB 1643 CATGACAGCAATTAATAAGTGTAAATTTGATTTATAGAGTTTATGATTAATATATGAA 1702
QY 1538 ATGCAAGKCCACAGAGGAGATGTTATGAGGACAGCTTGAAGCCGAGGATGAGAAAMA 1597
DB 1703 ATGCAAGKCCACAGAGGAGATGTTATGAGGACAGCTTGAAGCCGAGGATGAGAAAMA 1762
QY 1598 AAGCAGGAACTTCATAGTATCTTAATATATATATATATATATATATATATATATATAT 1657

Db	1763	AAGGAGGGAACCTCATGTATCTATATTAATATATCTTCACTTCTCTATCTATACAA	18222
QY	1658	TATCCACACAGCTTTTCACAGAAATTCATGCAAGTGCAAATVCCCAAGSTAACCTTATCC	17171
Db	1823	TATCCAAACACCTTTTCACAGAAATTCATGCAAGTGCAAATVCCCAAGSTAACCTTATCC	18822
QY	1728	ATTTCATGCTAGTGGCGGCTTTAGATTTTGGCAAAATCATCTAGTGCATTTATTCACACT	17777
Db	1883	ATTTCATGCTAGTGGCGGCTTTAGATTTTGGCAAAATCATCTAGTGCATTTATTCACACT	19422
QY	1778	TCGATGTGTGTGTTCCTTGTAGTTAATTTGAAAGAAATAGGGCACTCTGTGAGCCACTT	18377
Db	1943	TCGATGTGTGTGTTCCTTGTAGTTAATTTGAAAGAAATAGGGCACTCTGTGAGCCACTT	20022
QY	1838	AGGGTTCACCTCGGCATTAAGAATTATTCACAAGA	1872
Db	2003	AGGGTTCACCTCGGCATTAAGAATTATTCACAAGA	2037
RESULT 3			
LOCUS	BD082485	3582 bp	DNA
DEFINITION	PCA3, PCA3 genes, and methods of use.	linear	PAT 27-AUG-2002
ACCESSION	BD082485		
VERSION	BD082485.1		
KEYWORDS	JP 2001522240-A/4.		
SOURCE	Mastadenovirus		
ORGANISM	Mastadenovirus		
REFERENCE	1 (bases 1 to 3582)		
AUTHORS	Busemackers,M.J.G.		
TITLE	PCA3, PCA3 genes, and methods of use		
JOURNAL	Patent: JP 2001522240-A 4 13-NOV-2001;		
COMMENT	DIAGNOCURE INC		
	PN JP 2001522240-A/4		
	PD 13-NOV-2001		
	PF 09-APR-1998 JP 1998542194		
	PR 10-APR-1997 US 60/041836		
	PI MARION J G BUSEMACKERS		
	PC C12N15/00,C12N15/12,C12N5/12,C12N1/21,C07K14/47,C07K16/18, PC		
	C12O1/68,		
	PC G01N33/577,A61K39/395,A01K67/027		
	CC Strandedness: Double;		
	CC Topology: Linear;		
	EH Key		
	FT CDS		
FEATURES			
source	1..3582		
	/organism="Mastadenovirus"		
	/mol_type="genomic DNA"		
	/db_xref="taxon:10509"		
BASE COUNT	1052 a 787 c 680 g 1063 t		
ORIGIN			
Query Match	73.0%: Score 1367; DB 6; Length 3582;		
Best Local Similarity	99.5%: Pred. No. 0;		
Matches 1767; Conservative	0; Mismatches 8; Indels 0; Gaps 0;		
QY	98	GGTGAGAAATAGAAAGGCTGCTGACTTTACACTGTAGGCGCACACATCTGCTGAAATGG	157
Db	285	GGTGAGAAATAGAAAGGCTGCTGACTTTACACTGTAGGCGCACACATCTGCTGAAATGG	344
QY	158	AGATAATTAACATCTACATAGAAACGCAAGATGACATATATATCTCTAAGTAGTGACATGT	217
Db	345	AGATAATTAACATCTACATAGAAACGCAAGATGACATATATATCTCTAAGTAGTGACATGT	404
QY	218	TTTTCGACATTTCCAGCCCTTTTAAATATCCACACACACAGGAAGCAAAAGGAACAC	277
Db	405	TTTTCGACATTTCCAGCCCTTTTAAATATCCACACACACAGGAAGCAAAAGGAACAC	464
QY	278	AGAGATCCCTGGGAGAAATGCCGCGCCCATCTTGGGTCATCGATAGGCTCGCCCTGT	337

Db	465	AGAGATCCCTGGGAGAAATGCCCGGCCCATCTGGGTCATGCATGAGCCCTGGCCCTGT	524
QY	338	GCTGTGCTCCGCTGTGAGGGAGACATTAGAAAAATGAAATGATGTCTCTTAAAGCA	397
Db	525	GCTGTGCTCCGCTGTGAGGGAGACATTAGAAAAATGAAATGATGTCTCTTAAAGCA	584
QY	398	TGGGAGGAAAAACATCCTGTGTGGATATTTATTTGAGGGATTTACAGATTTGAAT	457
Db	565	TGGGAGGAAAAACATCCTGTGTGGATATTTATTTGAGGGATTTACAGATTTGAAT	644
QY	458	GAAGTCACAAAGTAGACATTACCAATGAGAGAAAAACAGACGAAAAATCTTGATGCTT	517
Db	645	GAAGTCACAAAGTAGACATTACCAATGAGAGAAAAACAGACGAAAAATCTTGATGCTT	704
QY	518	CACAAGACATGCAACAAACAAATGGAATACGTGTATGATACATGAGGAGCCAAAGCTGGGG	577
Db	705	CACAAGACATGCAACAAACAAATGGAATACGTGTATGATGATGAGGAGCCAAAGCTGGGG	764
QY	578	AGGAGATTAACACAGGGGGAGAGGGTCAGAGATTTCTGGCCCTGTGCTTAAACTGTGCTTC	637
Db	765	AGGAGATTAACACAGGGGGAGAGGGTCAGAGATTTCTGGCCCTGTGCTTAAACTGTGCTTC	824
QY	638	ATAACCAATCATTTTCATTTTCTTAACCCCTCAAAACAAAGCTGTGTAAATATCTGATCTC	697
Db	825	ATAACCAATCATTTTCATTTTCTTAACCCCTCAAAACAAAGCTGTGTAAATATCTGATCTC	884
QY	698	TACGGTTCCTTCTGGGCCCAACATTTCTCCATATATCCAGCCACACCTCATTTTATATTT	757
Db	885	TACGGTTCCTTCTGGGCCCAACATTTCTCCATATATCCAGCCACACCTCATTTTATATTT	944
QY	758	AGTTCACAGATCTGACTGTGACCTTTCTACCTGTAGAAATPAACATTAATCTCATTTTGTTC	817
Db	945	AGTTCACAGATCTGACTGTGACCTTTCTACCTGTAGAAATPAACATTAATCTCATTTTGTTC	1004
QY	818	AAAGACCCCTGTGTGTGCTGCCTAATATGATGACGTGTTTCTTAAGGAGTGTCTG	877
Db	1005	AAAGACCCCTGTGTGTGCTGCCTAATATGATGACGTGTTTCTTAAGGAGTGTCTG	1064
QY	878	GCCCCGGGAGATCTGTGAACAGGCTGGGAGACATCAAGATCTTTCACGGGTTATATCTTA	937
Db	1065	GCCCCGGGAGATCTGTGAACAGGCTGGGAGACATCAAGATCTTTCACGGGTTATATCTTA	1124
QY	938	CTAGACACACAGCATGATCATTTACGAGATGAAATATCTAATCAACATCATCTCTCACTGTCT	997
Db	1125	CTAGACACACAGCATGATCATTTACGAGATGAAATATCTAATCAACATCATCTCTCACTGTCT	1184
QY	998	TTGGCCATACAGAAATTCATTTCACATTTGTGCCATCTTGTCCAAAGACCTCAAAATGCA	1057
Db	1185	TTGGCCATACAGAAATTCATTTCACATTTGTGCCATCTTGTCCAAAGACCTCAAAATGCA	1244
QY	1058	TTCCATTAAATACAGAGATTAACTTTTTTTTTTAACTGAGAGAAATCAATGTTACATG	1117
Db	1245	TTCCATTAAATACAGAGATTAACTTTTTTTTTTAACTGAGAGAAATCAATGTTACATG	1304
QY	1118	CAGCATAGGGAATTAATTAACATATTTGTTTCCAGGCAAAAGATGCTAAGTCCCTTA	1177
Db	1305	CAGCATAGGGAATTAATTAACATATTTGTTTCCAGGCAAAAGATGCTAAGTCCCTTA	1364
QY	1178	TCCCTCCCTTGTGTTGATTTTTTTTTTCCAGTATAAAGTTAAAGTCTTAAGCCTGTACTG	1237
Db	1365	TCCCTCCCTTGTGTTGATTTTTTTTTTCCAGTATAAAGTTAAAGTCTTAAGCCTGTACTG	1424
QY	1238	AGGCTGTATTAAGACACAGCCTCTCCCATCTCCCTCAGCCTTATCTGTACATACCATCAAC	1297
Db	1425	AGGCTGTATTAAGACACAGCCTCTCCCATCTCCCTCAGCCTTATCTGTACATACCATCAAC	1484
QY	1298	CCCTCCCATNTSACCTTAACAAATCTAACTGTAAATCCCTTGAACATGTCAAGCCTATAC	1357
Db	1485	CCCTCCCATNTSACCTTAACAAATCTAACTGTAAATCCCTTGAACATGTCAAGCCTATAC	1544
QY	1358	ATTATTCTCTTGCCTGAGAAAGCTCTCTCTCTCTTAANTCTAGAATGATGTPAACTT	1417
Db	1545	ATTATTCTCTTGCCTGAGAAAGCTCTCTCTCTCTCTTAANTCTAGAATGATGTPAACTT	1604

OY	1418	TTGAAATAAGTGCATATCTTACTCTCATGCAAGAAGGACACATATAGATTTCATATCA	1477
Db	1605	TTTGATATAAGTTGATATCTTACTCTCATGCAAGAAGGACACATATGATTTCATATCA	1664
OY	1478	CATGAGACAGCAATTAATAAGTGAATTTGATTATAGAGTTTAGATAATATATGAA	1537
Db	1665	CATGAGACAGCAATTAATAAGTGAATTTGATTATAGAGTTTAGATAATATATGAA	1724
OY	1538	ATGCAAGACCACAGAGGGAATGTTTATGSGGACGTTTGTAAGCCTGGATGTGAAGMA	1597
Db	1725	ATGCAAGAGCCACAGAGGGAATGTTTATGSGGACGTTTGTAAGCCTGGATGTGAAGCA	1784
OY	1598	AAGCAGAGGAACCATATGATATCTTATATATATATACCTATTTGTCATCTCATACAA	1657
Db	1785	AAGCAGAGGAACCATATGATATCTTATATATATATACCTATTTGTCATCTCATACAA	1844
OY	1658	TATCCAAACAACTTTTCACAGAAATTCATGACAGTGCCAATCCCAAGGTATACCTTATCC	1717
Db	1845	TATCCAAACAACTTTTCACAGAAATTCATGACAGTGCCAATCCCAAGGTATACCTTATCC	1904
OY	1718	ATTTCATGGTGATGAGCGCTTTAGAAATTTTGGCAATCATACTGGTCACTTATCTCACTT	1777
Db	1905	ATTTCATGGTGATGAGCGCTTTAGAAATTTTGGCAATCATACTGGTCACTTATCTCACTT	1964
OY	1778	TGAGATGCTGTTGCTCTGTAGTAATTTGAAGAATAATGGGCACTCTGTGAGCACTTT	1837
Db	1965	TGAGATGCTGTTGCTCTGTAGTAATTTGAAGAATAATGGGCACTCTGTGAGCACTTT	2024
OY	1838	AGGCTTCACTCCTGGCAATTAAGAATTTTACAAGA	1872
Db	2025	AGGCTTCACTCCTGGCAATTAAGAATTTTACAAGA	2059

RESULT	4
AR261166	
LOCUS	
DEFINITION	AR261166 3923 bp DNA linear PAT 29-JAN-2003
ACCESSION	Sequence 690 from patent US 6321716.
VERSION	AR261166
KEYWORDS	AR261166.1 GI :28071929
SOURCE	.
ORGANISM	. Unknown .
REFERENCE	. Unknown .
AUTHORS	Unclassified.
TITLE	1 (bases 1 to 3923)
JOURNAL	Mashiki,Z. and Harada,J. Negative pressure control apparatus for engine mounted in vehicle Patent: US 6321716-A 690 Z7-NOV-2001.
FEATURES	Location/Qualifiers 1..3923 ./organism="unknown"
BASE COUNT	1157 a 840 c 740 g 1186 t
ORIGIN	

	Query Match	73.0%	Score 1367;	DB 6;	Length 3923;
	Best Local Similarity	99.5%	Pred. No. 0's	Mismatches 8;	Indels 0;
	Matches 167;	Conservative	0;	Indels 8;	Gaps 0;
OY	98	GGTGAGAAATTAAGAAAGGCTGCTCAGCTTACCATCTGAGGCGACACATCTGCTGAAATGG	157		
Db	285	GGTGAGAAATTAAGAAAGGCTGCTGACTTACCATCTGAGGCGACACATCTGCTGAAATGG	344		
OY	158	AGATTAATTACATCACTTGAAGAACGCAAGATGACAAATTAATGTCTTAAGTGTGATCATGT	217		
Db	345	AGATTAATTACATCACTTGAAGAACGCAAGATGACAAATTAATGTCTTAAGTGTGATCATGT	404		
OY	218	TTTTGCACATTTCCAGCCCTTTTAAATPTCCACACACACAGAGAACACAAAAGGAGTAC	277		
Db	405	TTTTGCACATTTCCAGCCCTTTTAAATPTCCACACACACAGAGAACACAAAAGGAGTAC	464		
OY	278	AGAGATCCCTGGAGAAATGCGCGCGCGCATCTTGGGTCTCATGATGAGCTCGGCCCTGT	337		
Db	465	AGAGATCCCTGGAGAAATGCGCGCGCGCATCTTGGGTCTCATGATGAGCTCGGCCCTGT	524		

QY	338	GCCTGTCGCCCTGTGTGAGGGAGACATTTACAAAATGATTTGATGTCTTCTCTTAAAGCA	397
Db	525	GCCTTGTCGCCCTGTGTGAGGGAGACATTTACAAAATGATTTGATGTCTTCTCTTAAAGCA	584
QY	398	TGGGAGGAAAAACAGATCCTGTGTGGATTAATTTATTTGAAGGGGANTTACAGATTTGAAAT	457
Db	565	TGGGAGGAAAAACAGATCCTGTGTGGATTAATTTATTTGAAGGGGANTTACAGATTTGAAAT	644
QY	458	GAAGTACAGAAAGTGAGCATTTACCAATGAGAGGAAAAACAGACGAGAAAATCTTGATGGCTT	517
Db	645	GAAGTACAGAAAGTGAGCATTTACCAATGAGAGGAAAAACAGACGAGAAAATCTTGATGGCTT	704
QY	518	CACAAGACATGCAACAAACAAAATGGAATACGTGTATGATCAATGAGGCAACCAAGCTGGGG	577
Db	705	CACAAGACATGCAACAAACAAAATGGAATACGTGTATGATCAATGAGGCAACCAAGCTGGGG	764
QY	578	AGGAGATTAACACGGGGGAGAGGGTCAGAGATCTTGCCCTGCTGCTTAACTGTCGGCTTC	637
Db	765	AGGAGATTAACACGGGGGAGAGGGTCAGAGATCTTGCCCTGCTGCTTAACTGTCGGCTTC	824
QY	638	ATAACCAATCATTTTCATATTTTCTTAACCTCAAAACAAAGCTGTTGTAAATPCTGATCTC	697
Db	825	ATAACCAATCATTTTCATATTTTCTTAACCTCAAAACAAAGCTGTTGTAAATPCTGATCTC	884
QY	698	TACGGTTCCTTTGGGGCCCAACATTTCTCATATPACGACGACACATCTTTTAAATATTT	757
Db	885	TACGGTTCCTTTGGGGCCCAACATTTCTCATATPACGACGACACATCTTTTAAATATTT	944
QY	758	AGTTCCCAAGATCTGTACTGTGACCTTCTTCACTGTAGATAATACATTTACTCATTTTGTTC	817
Db	945	AGTTCCCAAGATCTGTACTGTGACCTTCTTCACTGTAGATAATACATTTACTCATTTTGTTC	1000
QY	818	AAAGACCCCTGCTGTGTGCGCTTAATPAGTACTGTACGTCTTTTCCCTAGAGGTGCTTCG	877
Db	1005	AAAGACCCCTGCTGTGTGCGCTTAATPAGTACTGTACGTCTTTTCCCTAGAGGTGCTTCG	1060
QY	878	GCCCGAGGGGATCTGTGAACAGGCTGGGAGACATCTCAAGANTCTTCCAGGCTTATACCTTA	937
Db	1065	GCCCGAGGGGATCTGTGAACAGGCTGGGAGACATCTCAAGANTCTTCCAGGCTTATACCTTA	1122
QY	938	CTAGACACACAGATGATCATTTACGAGGTAATTTATCTAATCAACATCATCTCAGTGTCT	997
Db	1125	CTAGACACACAGATGATCATTTACGAGGTAATTTATCTAATCAACATCATCTCAGTGTCT	1180
QY	998	TTGCCCATACGTAATTTCAATTTCCCACTTTTGCCCATCTTCAAGCACTCAAAATGTCA	1050
Db	1185	TTGCCCATACGTAATTTCAATTTCCCACTTTTGCCCATCTTCAAGCACTCAAAATGTCA	1240
QY	1058	TTCCATTAATATCACAGATTAACCTTTTTTTTAACTGGAAGAAATTCATGTTCATG	1110
Db	1245	TTCCATTAATATCACAGATTAACCTTTTTTTTAACTGGAAGAAATTCATGTTCATG	1300
QY	1118	CAGCATAGGGAATTTAATACATTTTGTCTTCCAGTGCAGAAAGAGTACTAGTCTCTTA	1170
Db	1305	CAGCATAGGGAATTTAATACATTTTGTCTTCCAGTGCAGAAAGAGTACTAGTCTCTTA	1360
QY	1178	TCCCTCCCTTGTGTGATTTTTTTTCCAGTAAAGTAAAGTAAAGTGGCTGTGACTG	1230
Db	1365	TCCCTCCCTTGTGTGATTTTTTTTCCAGTAAAGTAAAGTAAAGTGGCTGTGACTG	1420
QY	1238	AGGCTGTATACGACACAGCTCTCCCCATCCCTCCAGCTTATCTGTATACACATCAAC	1290
Db	1425	AGGCTGTATACGACACAGCTCTCCCCATCCCTCCAGCTTATCTGTATACACATCAAC	1480
QY	1298	CCCTCCCATNTSACCTAAACAAATCTACTGTGATTTCTTGAACATCTCAGGNCATAC	1350
Db	1485	CCCTCCCATNTSACCTAAACAAATCTACTGTGATTTCTTGAACATCTCAGGNCATAC	1540
QY	1358	ATTATTTCTCTGTGCTGAGAGCTCTCTGTCTCTTAAATCTAGATGATGTAAAGTT	1410
Db	1545	ATTATTTCTCTGTGCTGAGAGCTCTCTGTCTCTTAAATCTAGATGATGTAAAGTT	1600

QY 1418 TTGAATAGTGTACTTACTTACTTCATGCAAGAGGACATATGAGATTATCATCA 1477
Db 1605 TTAAATTAAGTTGACTATCTTACTTCTCATGCAAGAGGACATATGAGATTATCA 1664
QY 1478 CATGAGACAGCAATCTATAAGTGTATATTTAGTTATAGATTATATATGAA 1537
Db 1665 CATGAGACAGCAATCTATAAGTGTATATTTAGTTATAGATTATATATGAA 1724
QY 1538 ATGCAAGAKCCACAGAGGGAATGTTATGCGGACGTTTGAAGCCTGGAGTGA 1597
Db 1725 ATGCAAGAGCCACAGAGGGAATGTTATGCGGACGTTTGAAGCCTGGAGTGA 1784
QY 1598 AAGCGAGGGAACCTCTAGATCTTATATATATCTTCTATCTATCTATCA 1657
Db 1785 AAGCGAGGGAACCTCTAGATCTTATATATATCTTCTATCTATCTATCA 1844
QY 1658 TATCAACAAGCTTTTACAGATTCATGAGTGAATCCCAAGAGTAACTTATCC 1717
Db 1845 TATCAACAAGCTTTTACAGATTCATGAGTGAATCCCAAGAGTAACTTATCC 1904
QY 1718 ATTTCATGTGAGTGGCTTTTGAATTTGGCAATCATCTGCTACTTATCTCA 1777
Db 1905 ATTTCATGTGAGTGGCTTTTGAATTTGGCAATCATCTGCTACTTATCTCA 1964
QY 1778 TGAATGTGTTTCTCTGTAGTTAATGAAAGAAATAGGCACTGTGAGCCACTT 1837
Db 1965 TGAATGTGTTTCTCTGTAGTTAATGAAAGAAATAGGCACTGTGAGCCACTT 2024
QY 1838 AGGTTCACTCTCTGCAATTAAGATTTTACAAAGA 1872
Db 2025 AGGTTCACTCTCTGCAATTAAGATTTTACAAAGA 2059

RESULT 5
LOCUS AR278697 3923 bp DNA linear PAT 10-Apr-2003
DEFINITION Sequence 690 from patent US 6512094.
ACCESSION AR278697
VERSION AR278697.1 GI:29712943
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 3923)
AUTHORS Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y., Kalos,M.D., Fanger,G.R., Rietter,M.W., Stolk,J.A., Day,C.H., Vedvyck,T.S., Carter,D., Li,S.X., Wang,A., Skeiky,Y.A.W., Hedler,W.T. and Henderson,R.A.
TITLE Compositions and methods for the therapy and diagnosis of prostate cancer
JOURNAL Patent: US 6512094-A 690 28-JAN-2003;
FEATURES
source Location/Qualifiers
BASE COUNT 1157 a 840 c 740 g 1186 t
ORIGIN

Query Match 73.0%; Score 1367; DB 6; Length 3923;
Best Local Similarity 99.5%; Pred. No. 0;
Matches 1767; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 278 AGAGATCCCTGGAGAAATCCCGGCCCATCTTGGGTATGATGAGCCTGCCCTGT 337
Db 465 AGAGATCCCTGGAGAAATCCCGGCCCATCTTGGGTATGATGAGCCTGCCCTGT 524
QY 338 GCGTGGCCCGCTTGGAGGAGAGGACATTAGAAAATGAATGTATGCTCTTAAAGGA 397
Db 525 GCGTGGCCCGCTTGGAGGAGAGGACATTAGAAAATGAATGTATGCTCTTAAAGGA 584
QY 398 TGGGCAAGAAACAGATCCTGTTGTGATATTTATTTGAACGGGATTACAGATTTGA 457
Db 585 TGGGCAAGAAACAGATCCTGTTGTGATATTTATTTGAACGGGATTACAGATTTGA 644
QY 458 GAAGTCAAAAGTGAGCATTTACAAATGAGAGAAACAGACGAGAAATTTATGCTT 517
Db 645 GAAGTCAAAAGTGAGCATTTACAAATGAGAGAAACAGACGAGAAATTTATGCTT 704
QY 518 CACAAGCATGCAACAACAAGTAATGGAATCTGTGATGACATGAGGAGCAAGCTGGG 577
Db 705 CACAAGCATGCAACAACAAGTAATGGAATCTGTGATGACATGAGGAGCAAGCTGGG 764
QY 578 AGAGATTAACACAGGGGACAGAGGATCAGATTTGGCCCTGCTTAAACTGTGCTTC 637
Db 765 AGAGATTAACACAGGGGACAGAGGATCAGATTTGGCCCTGCTTAAACTGTGCTTC 824
QY 638 ATTAACCAATCATTTATTTTAAACCTCAAAACAAAGCTGTGATATCTGATCTC 697
Db 825 ATTAACCAATCATTTATTTTAAACCTCAAAACAAAGCTGTGATATCTGATCTC 884
QY 698 TAGGTTCCCTTGGGGCCCAACATTCCTCCATATTCAGCCACACATTTTAAATTT 757
Db 885 TAGGTTCCCTTGGGGCCCAACATTCCTCCATATTCAGCCACACATTTTAAATTT 944
QY 758 AGTTCCAGATCTGTACTGTGACCTTCTACACTGATGATAATACATTTACTTTGCTT 817
Db 945 AGTTCCAGATCTGTACTGTGACCTTCTACACTGATGATAATACATTTACTTTGCTT 1004
QY 818 AAGACCCCTTCTGTTGCTGCTTAATATGTAGTACTGTTTCTTAAAGAGTGTCTG 877
Db 1005 AAGACCCCTTCTGTTGCTGCTTAATATGTAGTACTGTTTCTTAAAGAGTGTCTG 1064
QY 878 GCCCAGAGGATCTGTGAACAGGCTGGGAAGCATCTCAAGATCTTCCAGGGTATCTTA 937
Db 1065 GCCCAGAGGATCTGTGAACAGGCTGGGAAGCATCTCAAGATCTTCCAGGGTATCTTA 1124
QY 938 CTAGCACACAGCATGATCATTTAGGAGTGAATATCTAATCAACATCATCTCAGTCT 997
Db 1125 CTAGCACACAGCATGATCATTTAGGAGTGAATATCTAATCAACATCATCTCAGTCT 1184
QY 998 TTGCCCATCTGAAATTCATTTTCCCACTTTTGGCCCATTCACAAGCTCAAAAATGCA 1057
Db 1185 TTGCCCATCTGAAATTCATTTTCCCACTTTTGGCCCATTCACAAGCTCAAAAATGCA 1244
QY 1058 TTCCATTAATATCACAGATTAATCTTTTAACTGGAAGATTTCAATGTTACATG 1117
Db 1245 TTCCATTAATATCACAGATTAATCTTTTAACTGGAAGATTTCAATGTTACATG 1304
QY 1118 CAGCTATGGGAATTAATTAATTAATTTGTTTCCAGTCAAGATGACTAAGTCTTTA 1177
Db 1305 CAGCTATGGGAATTAATTAATTAATTTGTTTCCAGTCAAGATGACTAAGTCTTTA 1364
QY 1178 TTCCCTCCCTTGTGATTTTTCACAGTAAAGTTAAATGCTTAGCCTGTGACG 1237
Db 1365 TTCCCTCCCTTGTGATTTTTCACAGTAAAGTTAAATGCTTAGCCTGTGACG 1424
QY 1238 AGGCTATATACAGACAGCCTCCCATCCCTCCAGCTTATCTGATCAACATCAAC 1297
Db 1425 AGGCTATATACAGACAGCCTCCCATCCCTCCAGCTTATCTGATCAACATCAAC 1484
QY 1298 CCCTCCCATNYSACCTTAAACAAATCTAACTGTGTAATCTTGAACATCTCAGNCATAC 1357
Db 1485 CCCTCCCATNYSACCTTAAACAAATCTAACTGTGTAATCTTGAACATCTCAGNCATAC 1544
QY 1358 ATTRTTCTTGTGCTGAGAGAGCTTCTTGTGCTTAAATCTAAGATGATGAAGTT 1417

Db 1545 ATATTCCTCTGCTGAGAGAGCTCTCTCTCTTAATCTAGATGATGAAGTT 1604
Oy 1418 TTGAAATAGTGAATCTTACTTCATGCAAAAGAGACATATGATTCATCA 1477
Db 1605 TTGAATAGTGAATCTTACTTCATGCAAAAGAGACATATGATTCATCA 1664
Oy 1478 CATGAGACAGCAATTAAGTGTAAATTTGATTAATAGAGTTAGATTAATATGA 1537
Db 1665 CATGAGACAGCAATTAAGTGTAAATTTGATTAATAGAGTTAGATTAATATGA 1724
Oy 1538 ATGCAAGACCCACAGAGGAAATGTTATGGGCAAGTTGTAAGCTGGATGTGAAG 1597
Db 1725 ATGCAAGAGCCACAGAGGAAATGTTATGGGCAAGTTGTAAGCTGGATGTGAAG 1784
Oy 1598 AAGCAGGAAACCTATAGTATCTATATATATATATCTATCTATCTATCA 1657
Db 1785 AAGCAGGAAACCTATAGTATCTATATATATATATCTATCTATCTATCA 1844
Oy 1658 TATCCAAACAGCTTTTCACAGAAATTCATGCAATCCCAAGGTAACCTTATCC 1717
Db 1845 TATCCAAACAGCTTTTCACAGAAATTCATGCAATCCCAAGGTAACCTTATCC 1904
Oy 1718 ATTTCAATGAGTATGAGCTTTAGAAATTTGGCAATCTACTGCTATCTCACTT 1777
Db 1905 ATTTCAATGAGTATGAGCTTTAGAAATTTGGCAATCTACTGCTATCTCACTT 1964
Oy 1778 TGAGATGTTGTCCTTGTATGTTAATGAAGAATGGGACCTGTGAGGCACATT 1837
Db 1965 TGAGATGTTGTCCTTGTATGTTAATGAAGAATGGGACCTGTGAGGCACATT 2024
Oy 1838 AGGCTCACTCTGCGCAATAAAGATTTTACAAAG 1872
Db 2025 AGGCTCACTCTGCGCAATAAAGATTTTACAAAG 2059

RESULT 6
AX200988 3923 bp DNA linear PAT 29-AUG-2001
LOCUS Sequence 618 from Patent W00151633.
DEFINITION AX200988
ACCESSION AX200988
VERSION AX200988.1 GI:15390814
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE
AUTHORS Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y.,
Reed,S.G., Kalos,M.D., Fanger,G.R., Day,C.H., Retter,M.W.,
Stolk,J.A., Skeiky,Y.A., Wang,A. and Mesgher,M.J.
TITLE Compositions and methods for the therapy and diagnosis of prostate
cancer
JOURNAL Patent: WO 0151633-A 618 19-JUL-2001;
CORIXA CORPORATION (US)
FEATURES
source 1..3923
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
BASE COUNT 1157 a 840 c 740 g 1186 t
ORIGIN

Query Match 73.0%; Score 1367; DB 6; Length 3923;
Best Local Similarity 99.5%; Pred. No. 0;
Matches 1767; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Oy 98 GGTGAATTAAGAAAGCTGCTGACTTACATCTGAGCCACACATCTGCTGAATGG 157
Db 285 GGTGAATTAAGAAAGCTGCTGACTTACATCTGAGCCACACATCTGCTGAATGG 344
Oy 158 AGATTAATTAACATCACTGAAACAGCAAGATGACAATTAATGTTAAGTACATGT 217

Db 345 AGATTAATTAACATCACTGAAACAGCAAGATGACAATTAATGTTAAGTACATGT 404
Oy 218 TTTTGACATTTCCAGCCCCCTTTAATTTCCACACACAGAGAACCAAAAGAGCAC 277
Db 405 TTTTGACATTTCCAGCCCCCTTTAATTTCCACACACAGAGAACCAAAAGAGCAC 464
Oy 278 AGAGATCCCTGGGAGAAATGCCCCGCCCATCTTGGGTCATGATAGACCTCGCCCTGT 337
Db 465 AGAGATCCCTGGGAGAAATGCCCCGCCCATCTTGGGTCATGATAGACCTCGCCCTGT 524
Oy 338 GCTTGCTCCCTGCTGTGAGGAGACATTTGAAATGATATGATGTCTTAAAGGA 397
Db 525 GCTTGCTCCCTGCTGTGAGGAGACATTTGAAATGATATGATGTCTTAAAGGA 584
Oy 398 TGGGAGGAAACAGATCTGTGGATTTATTTAATTAAGGGATTCAGATTTGAAT 457
Db 585 TGGGAGGAAACAGATCTGTGGATTTATTTAATTAAGGGATTTAAGATTTGAAT 644
Oy 458 GAACTCACAAAGTACATTTACCAATGAGAGAAACAGAGAAATCTTGATGCTT 517
Db 645 GAACTCACAAAGTACATTTACCAATGAGAGAAACAGAGAAATCTTGATGCTT 704
Oy 518 CACAAGATGCAACAAACAAATGGAATCTGTGATGATGATGAGGACCAAGCTGGGG 577
Db 705 CACAAGATGCAACAAACAAATGGAATCTGTGATGATGATGAGGACCAAGCTGGGG 764
Oy 578 AGGAGATTAACACAGGGGAGAGGGTCAGAGATTTGGCCCTGCTGCTAACTGTGCTTC 637
Db 765 AGGAGATTAACACAGGGGAGAGGGTCAGAGATTTGGCCCTGCTGCTAACTGTGCTTC 824
Oy 638 ATTAACCAATCATTTATTTCTAACCCTCAAAACAAAGCTGTTGTAATATGATCTC 697
Db 825 ATTAACCAATCATTTATTTCTAACCCTCAAAACAAAGCTGTTGTAATATGATCTC 884
Oy 698 TACGTTCTCTCTGGGCCCAACATCTTCATATATCCAGCCACACTGATTTTAATATT 757
Db 885 TACGTTCTCTCTGGGCCCAACATCTTCATATATCCAGCCACACTGATTTTAATATT 944
Oy 758 AGTTCCAGATCTGACTGATGACCTTTTACACTAGAAATACATTTCTGATTTGCTTC 817
Db 945 AGTTCCAGATCTGACTGATGACCTTTTACACTAGAAATACATTTCTGATTTGCTTC 1004
Oy 818 AAAGACCTTGTGCTGCTGCTATATATGATGATGATGATGATGATGATGATGATG 877
Db 1005 AAAGACCTTGTGCTGCTGCTATATATGATGATGATGATGATGATGATGATGATG 1064
Oy 878 GCCCAGGGGATCTGGAACAGGCTGGGAAGCATCTCAAGATCTTCCAGGGTTATACCTTA 937
Db 1065 GCCCAGGGGATCTGGAACAGGCTGGGAAGCATCTCAAGATCTTCCAGGGTTATACCTTA 1124
Oy 938 CTAGCACACAGATGATGATTTACGAGAGAAATATCTAATCAACATCATCTCAGTGCT 997
Db 1125 CTAGCACACAGATGATGATTTACGAGAGAAATATCTAATCAACATCATCTCAGTGCT 1184
Oy 998 TTGCCATATGAAATTTCCATTTCCACTTTTGGCCATCTTCCAGAGCTCAAAATGTCA 1057
Db 1185 TTGCCATATGAAATTTCCATTTCCACTTTTGGCCATCTTCCAGAGCTCAAAATGTCA 1244
Oy 1058 TTCCATTAATATCACAGATTAATTTTATTAATCTGGAAGATTCATGTTACATG 1117
Db 1245 TTCCATTAATATCACAGATTAATTTTATTAATCTGGAAGATTCATGTTACATG 1304
Oy 1118 CAGCTATGGAATTAATTAATATTTTTCAGAGTAAAGTAAATCTTACGCTGTACTG 1177
Db 1305 CAGCTATGGAATTAATTAATATTTTTCAGAGTAAAGTAAATCTTACGCTGTACTG 1364
Oy 1178 TCCCTCCCTTGTGATTTTTCAGATTAATTAATCTTACGCTGTACTG 1237
Db 1365 TCCCTCCCTTGTGATTTTTCAGATTAATTAATCTTACGCTGTACTG 1424
Oy 1238 AGGCTATATACAGACAGCTCTCCCATCTCCAGCTTATCTGTCATCAATCAAC 1297
Db 1425 AGGCTATATACAGACAGCTCTCCCATCTCCAGCTTATCTGTCATCAATCAAC 1484

QY 1298 CCCTCCATNYSACCTAAACAAATCTAACCTGTAACTTCCTTGAACATGTCAGGNCATAC 1357
 DB 1485 CCTCCCATACACACCTAAACAAATCTAACCTGTAACTTCCTTGAACATGTCAGGNCATAC 1544
 QY 1358 ATTRTTCCTTCTGCTGAGAGAGCTCTTCCCTGTCTCTTAANTCTAGATATGTAAGTT 1417
 DB 1545 ATTTATTCCTTCTGCTGAGAGAGCTCTTCCCTGTCTCTTAANTCTAGATATGTAAGTT 1604
 QY 1418 TTGAATTAAGTGAATCTTACTTCTTCAATGCAAGAGGACACATATGATGATCATCA 1477
 DB 1605 TTGAATTAAGTGAATCTTACTTCTTCAATGCAAGAGGACACATATGATGATCATCA 1664
 QY 1478 CATGACACAGCAAAATCTAAAGTGTATTTAGATTAGATTAGATTAATATATGAA 1537
 DB 1665 CATGACACAGCAAAATCTAAAGTGTATTTAGATTAGATTAGATTAATATATGAA 1724
 QY 1538 ATGCAAGACCAAGAGGGAATGTTATGAGGACGCTTTTGAAGCCGAGATGTAAGAA 1597
 DB 1725 ATGCAAGACCAAGAGGGAATGTTATGAGGACGCTTTTGAAGCCGAGATGTAAGAA 1784
 QY 1598 AAGCAGAGGACCTCTAGATCTTATATATATATCTTCAATTCCTATCTATACAA 1657
 DB 1785 AAGCAGAGGACCTCTAGATCTTATATATATATCTTCAATTCCTATCTATACAA 1844
 QY 1658 TATCAACAAGCTTTTACAGAAATGACATGCAATCCCAAGAGTAACCTTATCC 1717
 DB 1845 TATCAACAAGCTTTTACAGAAATGACATGCAATCCCAAGAGTAACCTTATCC 1904
 QY 1718 ATTTCAATGAGATGGCTTTAGAAATTTGGCAAAATCATCTGCTACTATCTCACTT 1777
 DB 1905 ATTTCAATGAGATGGCTTTAGAAATTTGGCAAAATCATCTGCTACTATCTCACTT 1964
 QY 1778 TGAGATGTGTGCTTCTTGTAGTTAAATGCAAAATAGGACCTGTTGAGCCACTT 1837
 DB 1965 TGAGATGTGTGCTTCTTGTAGTTAAATGCAAAATAGGACCTGTTGAGCCACTT 2024
 QY 1838 AGGCTCAGCTCCCTGCAATTAAGATTTTCAAGA 1872
 DB 2025 AGGCTCAGCTCCCTGCAATTAAGATTTTCAAGA 2059

RESULT 7
 AX267716 3923 bp DNA linear PART 26-OCT-2001
 LOCUS AX267716 Sequence 690 from Patent WO0173032.
 DEFINITION AX267716
 ACCESSION AX267716.1 GI:16516388
 VERSION
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 REFERENCE 1
 Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y.,
 Kalos,M.D., Fanger,G.R., Retter,M.W., Stolk,J.A., Day,C.H.,
 Vedrick,T.S., Carter,D., Li,S.X., Wang,A., Skeiky,Y.A., Hepler,W.T.
 and Henderson,R.A.
 Compositions and methods for the therapy and diagnosis of prostate
 cancer
 Patent: WO 0173032-A 690 04-OCT-2001;
 JOURNAL CORIXA CORPORATION (US)
 FEATURES
 source Location/Qualifiers
 1..3923
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"
 BASE COUNT 1157 a 840 c 740 g 1186 t
 ORIGIN
 Query Match 73.0%; Score 1367; DB 6; Length 3923;
 Best Local Similarity 99.5%; Pired. No. 0;
 Matches 1767; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 98 GGTGAGAAATTAAGAAAGGCTGTGACTTTACATCTGAGGCCACACATCTGTGAATGG 157
 DB 285 GGTGAGAAATTAAGAAAGGCTGTGACTTTACATCTGAGGCCACACATCTGTGAATGG 344
 QY 158 AGATTAATTAACATCTAGTAAGAACACAGATGACATATATATGTTCTTAAGTATGATGT 217
 DB 345 AGATTAATTAACATCTAGTAAGAACACAGATGACATATATATGTTCTTAAGTATGATGT 404
 QY 218 TTTTGCACATTCCTCAGGCCCTTTAAATATCCACACACAGGAAGCAAAAGGAAGCAC 277
 DB 405 TTTTGCACATTCCTCAGGCCCTTTAAATATCCACACACAGGAAGCAAAAGGAAGCAC 464
 QY 278 AGAGATCCCTGGAGAAATGCCCCGCCATCTTGGGTATCATGATGAGCCTCGCCCTGT 337
 DB 465 AGAGATCCCTGGAGAAATGCCCCGCCATCTTGGGTATCATGATGAGCCTCGCCCTGT 524
 QY 338 GCTTGTCCTCCCTGTTGAGGGAAGGACATTAAGAAATGAATATGTTCTTAAAGGA 397
 DB 525 GCTTGTCCTCCCTGTTGAGGGAAGGACATTAAGAAATGAATATGTTCTTAAAGGA 584
 QY 398 TGGGCAAGAAACAGATCCCTGTTGAGATTTTAAATGAAACGGATTAAGATTTGAAT 457
 DB 585 TGGGCAAGAAACAGATCCCTGTTGAGATTTTAAATGAAACGGATTAAGATTTGAAT 644
 QY 458 GAAATCAACAAGTGAACATTCATGAGAGAAACAGACGAAATCTGATGCTT 517
 DB 645 GAAATCAACAAGTGAACATTCATGAGAGAAACAGACGAAATCTGATGCTT 704
 QY 518 CAAACACATGCAACAACAATGGAATATCTGTATGATGATGAGCAGCAAGCTGGGG 577
 DB 705 CAAACACATGCAACAACAATGGAATATCTGTATGATGATGAGCAGCAAGCTGGGG 764
 QY 578 AGAGATTAACCAAGGGGAGAGGGTCAAGATTCCTGAGCCCTGCTTAACTGTGCTTC 637
 DB 765 AGAGATTAACCAAGGGGAGAGGGTCAAGATTCCTGAGCCCTGCTTAACTGTGCTTC 824
 QY 638 ATTAACCAATCATTTATATTTTAAACCTCAAAACAAGCTTGTATATCTGATCTC 697
 DB 825 ATTAACCAATCATTTATATTTTAAACCTCAAAACAAGCTTGTATATCTGATCTC 884
 QY 698 TACGTTCTCTGGGCCCCAACATTCCTCAATATACAGGACACATCTTAAATAT 757
 DB 885 TACGTTCTCTGGGCCCCAACATTCCTCAATATACAGGACACATCTTAAATAT 944
 QY 758 AGTTCCAGATCTGTACTGTGACCTTTCTACACTGTAGAATAACATTTACTTGTTC 817
 DB 945 AGTTCCAGATCTGTACTGTGACCTTTCTACACTGTAGAATAACATTTACTTGTTC 1004
 QY 818 AAGACCCCTTCGTTGCTGCTGCTTAATATGATGATGCTGTTTCTTAAGAGCTTCG 877
 DB 1005 AAGACCCCTTCGTTGCTGCTGCTTAATATGATGATGCTGTTTCTTAAGAGCTTCG 1064
 QY 878 GCCCAGGGATCTGTAAACAGGCTGGAGCATCTCAAGATCTTCCAGGGTATACCTTA 937
 DB 1065 GCCCAGGGATCTGTAAACAGGCTGGAGCATCTCAAGATCTTCCAGGGTATACCTTA 1124
 QY 938 CTAGCACACAGCATGATCTTACGAGTGAATTAATCAACATCATCTCAGTGTCT 997
 DB 1125 CTAGCACACAGCATGATCTTACGAGTGAATTAATCAACATCATCTCAGTGTCT 1184
 QY 998 TTGCCCATCTGAAATTCATTTCCCATCTTGTGCCCCATTCACACACCTCAAAAGTGA 1057
 DB 1185 TTGCCCATCTGAAATTCATTTCCCATCTTGTGCCCCATTCACACACCTCAAAAGTGA 1244
 QY 1058 TTCCATTATATACAGATTAATCTTTTAACTGGAAGAAATTCATGATGATCATG 1117
 DB 1245 TTCCATTATATACAGATTAATCTTTTAACTGGAAGAAATTCATGATGATCATG 1304
 QY 1118 CAGCTATGGGAATTAATTAATATATTTGTTTTCAGTGCAGGAAGATGACTAAGCTCTTA 1177
 DB 1305 CAGCTATGGGAATTAATTAATATATTTGTTTTCAGTGCAGGAAGATGACTAAGCTCTTA 1364


```
Db 1005 AAGAGCCCTTCGTGCTGCTCCCTAATATGTAAGTGAAGTCTGTTTTCCTAAGAGAGTGTCTG 1064
QY 878 GCCAGAGGGATCTGTGAACAGGCTGGAGACATCTCAAGATCTTCCAGGGTTATCTTA 937
Db 1065 GCCAGAGGGATCTGTGAACAGGCTGGAGACATCTCAAGATCTTCCAGGGTTATCTTA 1124
QY 938 CTAGACACAGCATGATCATTTAGGAGTGAATTAATCAATCAATCATCTCCAGTGTCT 997
Db 1125 CTAGACACAGCATGATCATTTAGGAGTGAATTAATCAATCAATCATCTCCAGTGTCT 1184
QY 998 TTGCCCATCTGAATTCATTTCCCATCTTTGGCCCATCTCAAGACCCCAAAATGTCA 1057
Db 1185 TTGCCCATCTGAATTCATTTCCCATCTTTGGCCCATCTCAAGACCCCAAAATGTCA 1244
QY 1058 TTCCATTAATATACAGATTAACTTTTAACTTGAAGAAATTCATGTATACATG 1117
Db 1245 TTCCATTAATATACAGATTAACTTTTAACTTGAAGAAATTCATGTATACATG 1304
QY 1118 CAGCTATGGGAATTTATATCATATTTTGTTCAGTGCAGAGATGACTAAGTCTTTA 1177
Db 1305 CAGCTATGGGAATTTATATCATATTTTGTTCAGTGCAGAGATGACTAAGTCTTTA 1364
QY 1178 TTCCCTCCCTTTGTTGATTTTTCAGTATAAAGTTAAATAGCTTAGCCTTGATCTG 1237
Db 1365 TTCCCTCCCTTTGTTGATTTTTCAGTATAAAGTTAAATAGCTTAGCCTTGATCTG 1424
QY 1238 AGGCTGTATACAGACAGCCTCTCCCATCCCTCAGCCTTATCTGTATCACCATCAAC 1297
Db 1425 AGGCTGTATACAGACAGCCTCTCCCATCCCTCAGCCTTATCTGTATCACCATCAAC 1484
QY 1298 CCTCCCATTTTACCTTAACAAATCAATCTTGAATCTCTTGAACATGTCAGNCATAC 1357
Db 1485 CCTCCCATTTTACCTTAACAAATCAATCTTGAATCTCTTGAACATGTCAGNCATAC 1544
QY 1358 ATTTTCCTTCTGCTGAGAGAGCTCTCCTGTCTCTTAATCTAGATGATTAAGTT 1417
Db 1545 ATTTTCCTTCTGCTGAGAGAGCTCTCCTGTCTCTTAATCTAGATGATTAAGTT 1604
QY 1418 TTGAATTAAGTGAATCTTACTTATCTGCAAGAGGACATATGAGATTCATCA 1477
Db 1605 TTGAATTAAGTGAATCTTACTTATCTGCAAGAGGACATATGAGATTCATCA 1664
QY 1478 CATGAGACAGCAATCTAATAGTATTTAGATTAAGATTAATATATATGAA 1537
Db 1665 CATGAGACAGCAATCTAATAGTATTTAGATTAAGATTAATATATATGAA 1724
QY 1538 ATGCAAGACACAGAGGAGATGTTATGAGGACGCTTTGTAAGCCTGGAGTGAAGMA 1597
Db 1725 ATGCAAGACACAGAGGAGATGTTATGAGGACGCTTTGTAAGCCTGGAGTGAAGMA 1784
QY 1598 AAGGACGAGAACCTCATATGATCTATATATATATATCTTCAATCTATCTATCAAA 1657
Db 1785 AAGGACGAGAACCTCATATGATCTATATATATATATCTTCAATCTATCTATCAAA 1844
QY 1658 TATCCAAAGAGCTTTCACAGATTCATGAGTGAATCCCAAGGTAACCTTTATCC 1717
Db 1845 TATCCAAAGAGCTTTCACAGATTCATGAGTGAATCCCAAGGTAACCTTTATCC 1904
QY 1718 ATTTCAATGATGAGTGGCTTTAGAAATTTGGCAATCATCTGATCACTATCTCAACT 1777
Db 1905 ATTTCAATGATGAGTGGCTTTAGAAATTTGGCAATCATCTGATCACTATCTCAACT 1964
QY 1778 TGAGATGTGTGTGCTTGTAGTAAATGAAGAAATAGGACCTGTGTGAGCCACTTT 1837
Db 1965 TGAGATGTGTGTGCTTGTAGTAAATGAAGAAATAGGACCTGTGTGAGCCACTTT 2024
QY 1838 AGGCTCACTCTCGGCAATTAAGAATTTTCAAGA 1872
Db 2025 AGGCTCACTCTCGGCAATTAAGAATTTTCAAGA 2059
```

RESULT 9
AF103908

```
LOCUS AF103908 5435 bp DNA linear PRI 14-AUG-2000
DEFINITION Homo sapiens non-coding RNA DD3 gene, exons 2, 3, and 4.
ACCESSION AF103908
VERSION AF103908.1 GI:6165974
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
REFERENCE
AUTHORS Bussemakers,M.J., van Bokhoven,A., Verhaegh,G.W., Smit,F.P.,
Karlhaus,H.F., Schalken,J.A., Debruyne,F.M.J., Ru.N. and Isaacs,W.B.
TITLE Bussemakers,M.J., van Bokhoven,A., Verhaegh,G.W., Smit,F.P.,
Karlhaus,H.F., Schalken,J.A., Debruyne,F.M.J., Ru.N. and Isaacs,W.B.
D03: a new prostate-specific gene, highly overexpressed in prostate
cancer
JOURNAL Cancer Res. 59 (23), 5975-5979 (1999)
MEDLINE 20072260
PUBMED 10606244
REFERENCE 2 (bases 1 to 5435)
AUTHORS Bussemakers,M.J.G., Van Bokhoven,A., Verhaegh,G.W., Smit,F.P.,
Karlhaus,H.F.M., Schalken,J.A., Debruyne,F.M.J., Ru.N. and
Isaacs,W.B.
TITLE Direct Submission
JOURNAL Submitted (28-OCT-1998) Urology Research Laboratory, University
Hospital Nijmegen, P.O. Box 9101, Nijmegen 6500 HB, Netherlands
FEATURES
source
1..5435
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="9"
/map="9q21-q22"
1..78
/rpt_family="AluY"
/rpt_type="dispersed
533..697
/note="alternative exon present in 5% of cDNA clones"
number=2
1035..1294
/rpt_family="Alu"
/rpt_type="dispersed
join(1571..1753,1981..5435)
/product="non-coding RNA DD3"
/note="transcript III"
join(1571..1753,1981..3579)
/product="non-coding RNA DD3"
/note="transcript (major) II"
join(1571..1753,1981..2517)
/product="non-coding RNA DD3"
/note="transcript I"
1571..1753
/number=3
1981..5435
/number=4
2495..2499
/note="transcript I"
2517
/note="transcript I"
3553..3558
/note="transcript (major) II"
3579
/note="transcript (major) II"
5268..5423
/note="LINE"
/rpt_family="L1"
/rpt_type="dispersed
5435
/note="transcript III"
BASE COUNT 1546 a 1188 c 1036 g 1654 t 11 others
ORIGIN
Query Match 63.3%; Score 1185; DB 9; Length 5435;
Best Local Similarity 99.5%; Pred. No. 0;
Matches 1585; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
```


QY	280	AGATGCCCTGGGAGAAATGCCCGGGCCATCTGGGGATCGATGATGAGCTCGCCCTGGC	339
Db	1979	AGATTCCTCGGGAGAAATGCCCGGGCCATCTGGGGATCGATGATGAGCTCGCCCTGGC	2038
QY	340	CTGCTCCCGCTGTGTGAGGAGGAGGACATTAGAAAAATGAAATGATGTCTTCCCTTAAAGATG	399
Db	2039	CTGGTCCCGCTGTGTGAGGAGGAGGACATTAGAAAAATGAAATGATGTCTTCCCTTAAAGATG	2098
QY	400	GGCAGGAAAAACAGATCCTGTTGTGGAATTTATTGAAACGGGATTACAGATTTGAAATGA	459
Db	2099	GGCAGGAAAAACAGATCCTGTTGTGGAATTTATTGAAACGGGATTACAGATTTGAAATGA	2158
QY	460	AGTACACAAAGGACATTACCAATGAGAGGAAAAACAGACGGAAATCTTGATGGCTTCA	519
Db	2159	AGTACACAAAGGACATTACCAATGAGAGGAAAAACAGACGGAAATCTTGATGGCTTCA	2218
QY	520	CAAGACATGCAACAACAAATGGAATACGTGATGACATGAGCAGCAGCAAGCTGGGAG	579
Db	2219	CAAGACATGCAACAACAAATGGAATACGTGATGACATGAGCAGCAGCAAGCTGGGAG	2278
QY	580	GAGATTAACACAGGGGGCAGAGGGTATGAGATTTGTGGCCTGCTGCTTAAACTGTGGCTCAT	639
Db	2279	GAGATTAACACAGGGGGCAGAGGGTATGAGATTTGTGGCCTGCTGCTTAAACTGTGGCTCAT	2338
QY	640	AACCAAAATCATTTTATATTTTCTAACCCTCAACAAACAAAGCTGTGTAAATATGATCTCTA	699
Db	2339	AACCAAAATCATTTTATATTTTCTAACCCTCAACAAACAAAGCTGTGTAAATATGATCTCTA	2398
QY	700	CGGTTCCTTGTGGGCCACACATTCCTCATATATATCCAGCCACATCATTTTAAATATTAAG	759
Db	2399	CGGTTCCTTGTGGGCCACACATTCCTCATATATATCCAGCCACACATCATTTTAAATATTAAG	2458
QY	760	TTTCCAGATCTGTACTGTGACCTTTCACACTGTAGATATACATTACTCATTTTGTGTCAA	819
Db	2459	TTTCCAGATCTGTACTGTGACCTTTCACACTGTAGATATACATTACTCATTTTGTGTCAA	2518
QY	820	AGACCCTTTCGTGTGCTGCTTAATATGATGACTGCTGTTTTTCCCTAAGAGAGTGTTCGGC	879
Db	2519	AGACCCTTTCGTGTGCTGCTTAATATGATGACTGCTGTTTTTCCCTAAGAGAGTGTTCGGC	2578
QY	880	CCAGGGGATCTGTGTAACAGGCTGGGAGGACATCTCAAGATCTGTCGAGGGTATATCTACT	939
Db	2579	CCAGGGGATCTGTGTAACAGGCTGGGAGGACATCTCAAGATCTGTCGAGGGTATATCTACT	2638
QY	940	AGCAGACAGCATGTATCTTAACGAGAGTAAATATCTAATCAACATCATCTCAGTGTCTT	999
Db	2639	AGCAGACAGCATGTATCTTAACGAGAGTAAATATCTAATCAACATCATCTCAGTGTCTT	2698
QY	1000	GCCCATACGTAAATTCATTTCCACTTTTGTGCCATTCCTCAAGACCTCAAAATGTCTAT	1059
Db	2699	GCCCATACGTAAATTCATTTCCACTTTTGTGCCATTCCTCAAGACCTCAAAATGTCTAT	2758
QY	1060	CCATTAAATATACAGGATTAACCTTTTTTTTAACTCGAAGGAAATTCAGTTTACATGCA	1119
Db	2759	CCATTAAATATACAGGATTAACCTTTTTTTTAACTCGAAGGAAATTCAGTTTACATGCA	2818
QY	1120	GCTATGGGAATTAATTAACATATTTTGTGTTTCCAGTGCAAGATGACTAAATGCTTTATC	1179
Db	2819	GCTATGGGAATTAATTAACATATTTTGTGTTTCCAGTGCAAGATGACTAAATGCTTTATC	2878
QY	1180	CCCTCCCTTGTGTGATTTTTTTTCCAGTAAAGTTAAATGCTGAGCCCTGTGACGTAG	1239
Db	2879	CCCTCCCTTGTGTGATTTTTTTTCCAGTAAAGTTAAATGCTGAGCCCTGTGACGTAG	2938
QY	1240	GCTGTATACACAGACAGCCTCTCCCATCCCTCAAGCCTTATCTGTCAATCACATCAACCC	1299
Db	2939	GCTGTATACACAGACAGCCTCTCCCATCCCTCAAGCCTTATCTGTCAATCACATCAACCC	2998
QY	1300	CTCCCATATTAACCTAAACAAATCTAATCTGTAATCTCTTGAACATGTACAGNCAATACAT	1359
Db	2999	CTCCCATATTAACCTAAACAAATCTAATCTGTAATCTCTTGAACATGTACAGNCAATACAT	3058

OY	1360	TTTTCCCTTCGCCGAGAAAGCTCTCCCTGTCTCTCTTAATCTTAAGATGAAGTAAAGTTT	1419
Db	3059	TATTCCTTCTTCCTCGAGAGCTCTTCCCTGTCTCTTAATCTTAAGATGAAGTAAAGTTT	3118
OY	1420	GAATTAAGTTGACTATCTTACTTTCATTCGCAAGAGGAGACATATAGATTCATCATCA	1479
Db	3119	GAATTAAGTTGACTATCTTACTTTCATTCGCAAGAGGAGACATATAGATTCATCATCA	3178
OY	1480	TGAACACGCAATTACTATAAAGTGTATTTGATTATTAAGAGTTTGAATTAATATGAAT	1539
Db	3179	TGAGACAGCAAAATCTAAAGTGTATTTGATTATTAAGAGTTTGAATTAATATGAAT	3238
OY	1540	GCAAGKACACAGAGGGGAATGTTATATGGGCGACGTTTGTAAGCCTGGGATGTGAAGMAA	1599
Db	3239	GCAAGAGCCACAGAGGGGAATGTTATATGGGCGACGTTTGTAAGCCTGGGATGTGAAGMAA	3298
OY	1600	GGCAGGGAACCTCATAGTATCTTATATATATATTAATTCGATATTCATCTCATCAATA	1659
Db	3299	GGCAGGGAACCTCATAGTATCTTATATATATATATTAATTCGATATTCATCTCATCAATA	3358
OY	1660	TCCAACAAAGCTTTTACAGAAATTCATGCAATGCCAAATCCCAGAGTAACCTTTATCCAT	1719
Db	3359	TCCAACAAAGCTTTTACAGAAATTCATGCAATGCCAAATCCCAGAGTAACCTTTATCCAT	3418
OY	1720	TTCAATGGGATGGGCTTTAGAAATTTGGCAAAATCATACGTCGACCTATATCTCAACTTG	1779
Db	3419	TTCAATGGGATGGGCTTTAGAAATTTGGCAAAATCATACGTCGACCTATATCTCAACTTG	3478
OY	1780	AGATGTGTGTGCTCTTGTAGTTAATTTGAAGAAATAGGCGCACTCTGTGAGCCACTTTAG	1839
Db	3479	AGATGTGTGTGCTCTTGTAGTTAATTTGAAGAAATAGGCGCACTCTGTGTGAGCCACTTTAG	3538
OY	1840	GGTTCACCTCTCGGCAATTAAGAAATTTTACAAAGA	1872
Db	3539	GGTTCACCTCTCGGCAATTAAGAAATTTTACAAAGA	3571
RESULT 10			
LOCUS	AR261038/c		
DEFINITION	Sequence 470 from patent US 6321716.	2426 bp	DNA
ACCESSION	AR261038		Linear
VERSION	AR261038.1	GI:28071801	
KEYWORDS	Unknown.		
SOURCE	Unknown.		
ORGANISM	Unclassified.		
REFERENCE	1 (bases 1 to 2426)		
AUTHORS	Mashiki,Z. and Harada,J.		
TITLE	Negative pressure control apparatus for engine mounted in vehicle		
JOURNAL	Patent: US 6321716-A 470 27-NOV-2001;		
FEATURES	Location/Qualifiers		
source	1..2426		
BASE COUNT	717 a 476 c 548 g 685 t	/organism="unknown"	
ORIGIN			
Query Match	61.7%;	Score 1155;	DB 6; Length 2426;
Best Local Similarity	100.0%;	Pred. NO. 0;	
Matches 1155;	Conservative 0;	Mismatches 0;	Indels 0; Gaps 0;
OY	97	AGGTGAGAAATAAGAAAGGTGCTGACTTTTACATCTGTAGGCCACACATCTGCTGAATG	156
Db	1770	AGGTGAGAAATAAGAAAGGTGCTGACTTTTACATCTGTAGGCCACACATCTGCTGAATG	1711
OY	157	GAGATTAATTAACATCTACTAGAAACAGCAAGATGACAATATATATGTCTAAGTAGACATG	216
Db	1710	GAGATTAATTAACATCTACTAGAAACAGCAAGATGACAATATATGTCTAAGTAGACATG	1651
OY	217	TTTTTGCAATTTCCAGGCCCTTTAAATATCCACACACACAGGAAGCAAAAGAGACGA	276
Db	1650	TTTTTGCAATTTCCAGGCCCTTTAAATATCCACACACACAGGAAGCAAAAGAGACGA	1591

QY	277	CAGAGATCCCTGGGGAAGATGCCGGGCCCATCTTGGGTGATCGATGAGCCTGGCCCTG	336
Db	1550	CAGAGATCCCTGGGGAAGATGCCGGGCCCATCTTGGGTGATCGATGAGCCTGGCCCTG	1531
QY	337	TGCCGTGCTCCGCTGTGAGGGAAGGACATTAGAAAATGAATTGATGTGTCCTTAAAG	396
Db	1530	TGCCGTGCTCCGCTGTGAGGGAAGGACATTAGAAAATGAATTGATGTGTCCTTAAAG	1471
QY	397	ATGGGACGAAAAACAGATCCTGTGTGGATATTTATTTTGAACGGGATTACAGATTTGAAA	456
Db	1470	ATGGGACGAAAAACAGATCCTGTGTGGATATTTATTTTGAACGGGATTACAGATTTGAAA	1411
QY	457	TGAAGTCACAAAGTAGACATTACCAATGAGGGAACAGACAGCAAAAATCTTGATGGCT	516
Db	1410	TGAAGTCACAAAGTAGACATTACCAATGAGGGAACAGACAGCAAAAATCTTGATGGCT	1351
QY	517	TCACAGACATGCAACAAACAAAATGCAATCTGTGATGACATGAGGACGCAACCTGG	576
Db	1350	TCACAGACATGCAACAAACAAAATGCAATCTGTGATGACATGAGGACGCAACCTGG	1291
QY	577	GAGGAGATTAACCAAGGGGACAGAGGTCAGATTCTGGCCCTGTGCCCTAACTGTGCGTT	636
Db	1290	GAGGAGATTAACCAAGGGGACAGAGGTCAGATTCTGGCCCTGTGCCCTAACTGTGCGTT	1231
QY	637	CATAACCAAAATCATTTTCATTTCTTCAACCCCTCAAAACAAAGCTGTGTAATCTGATCT	696
Db	1230	CATAACCAAAATCATTTTCATTTCTTCAACCCCTCAAAACAAAGCTGTGTAATCTGATCT	1171
QY	697	CTAGGATTCCTTGTGGGGCCCAACATCTCCATATATCCAGGCACACTATTTTAAATTT	756
Db	1170	CTAGGATTCCTTGTGGGGCCCAACATCTCCATATATCCAGGCACACTATTTTAAATTT	1111
QY	757	TAGTTCCAGATCTGTACTGTGACCTTCTACACTGTAGAAATTAACATTACTCATTTTGT	816
Db	1110	TAGTTCCAGATCTGTACTGTGACCTTCTACACTGTAGAAATTAACATTACTCATTTTGT	1051
QY	817	CAAGAGACCCCTCGTGTCTGCTGCCCTAATATGTAGCTGACTGTTTTTCCTAAGAGCTTCT	876
Db	1050	CAAGAGACCCCTCGTGTCTGCTGCCCTAATATGTAGCTGACTGTTTTTCCTAAGAGCTTCT	991
QY	877	GGCCAGAGGGATCTGTGAACAGGCTGGGAGACATCTCAAGATCTTCCAGGGTTATACTT	936
Db	990	GGCCAGAGGGATCTGTGAACAGGCTGGGAGACATCTCAAGATCTTCCAGGGTTATACTT	931
QY	937	ACTAGCACACAGCATGATCATTTAAGGATGTAATTATCTCAATCAACATCATCTCAGTGTG	996
Db	930	ACTAGCACACAGCATGATCATTTAAGGATGTAATTATCTCAATCAACATCATCTCAGTGTG	871
QY	997	TTTGCCCATCTGAATTCATTTTCCCACTTTTGTGCCCAATTCACAGCTCAAAAATGTC	1056
Db	870	TTTGCCCATCTGAATTCATTTTCCCACTTTTGTGCCCAATTCACAGCTCAAAAATGTC	811
QY	1057	ATTCATTAATATACAGATTAACCTTTTTTTTAAACCTGGAAGAAATCTCAATGTTACAT	1116
Db	810	ATTCATTAATATACAGATTAACCTTTTTTTTAAACCTGGAAGAAATCTCAATGTTACAT	751
QY	1117	GCAGCTATGGAAATTAATTAACATATTTGTTTCCAGTGCAGAAAGATGACTAAAGCTT	1176
Db	750	GCAGCTATGGAAATTAATTAACATATTTGTTTCCAGTGCAGAAAGATGACTAAAGCTT	691
QY	1177	ATCCCTCCCTTTGTGTGATTTTTTTTCCAGATATAAAGTTAAATGCTTTAGCCTGTACT	1236
Db	690	ATCCCTCCCTTTGTGTGATTTTTTTTCCAGATATAAAGTTAAATGCTTTAGCCTGTACT	631
QY	1237	GAGGCTGTATACAGC 1251	
Db	630	GAGGCTGTATACAGC 616	

ACCESSION	AR278569
VERSION	AR278569.1
KEYWORDS	GI:29712815
SOURCE	.
ORGANISM	Unknown.
REFERENCE	Unclassified.
AUTHORS	1 (bases 1 to 2426) Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y., Kalos,M.D., Fanger,G.R., Retter,M.W., Stolk,J.A., Day,C.H., Vedivick,T.S., Carter,D., Li,S.X., Wang,A., Skelky,Y.A.W., Hepler,W.T. and Henderson,R.A. Compositions and methods for the therapy and diagnosis of prostate cancer Patent: US 6512094-A 470 28-JAN-2003; Location/Qualifiers 1..2426 source
JOURNAL	
FEATURES	
BASE COUNT	717 a 476 c 548 g 685 t
ORIGIN	/organism="unknown"
Query Match	61.7%; Score 1155; DB 6; Length 2426;
Best Local Similarity	100.0%; Pred. No. 0;
Matches 1155; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
OY	97 AGGTGAGAAATAAGAAAGCTGCTGACTTTCACATCTGAGCCACACATCTGCTGAATG 156
Dd	
OY	1770 AGGTGAGAAAATAGAAAGCTGCTGACTTTACCATCTGAGGCCACACATCTGCTGAATG 1711
OY	157 GAGTAAATTAACATCACTAGAACAAGCAAGATGACAAATPATATGCTAAGTAGACATG 216
Dd	
OY	1710 GAGTAAATTAACATCACTAGAACAAGCAAGATGACAAATPATATGCTAAGTAGACATG 1651
OY	217 TTTTTGCACATTTCCAGCCCCCTTAAAAATTCACACACACAGAAAGCACAAAGAGAAC 276
Dd	
OY	1650 TTTTTGCACATTTCCAGCCCCCTTAAAAATTCACACACACAGAAAGCACAAAGAGAAC 1591
OY	277 CAGAGATCCTGGGAGAAATCCCGGCCCATCTTGSGTCATGATGAGCCTCGCCCTG 336
Dd	
OY	1590 CAGAGATCCTGGGAGAAATCCCGGCCCATCTTGSGTCATGATGAGCCTCGCCCTG 1531
OY	337 TGCCGTGCTCCCGCTTGAGGGAAGAGCATTAAGAAATGATGTCATGCTCTTAAAG 396
Dd	
OY	1530 TGCCGTGCTCCCGCTTGAGGGAAGAGCATTAAGAAATGATGTCATGCTCTTAAAG 1471
OY	397 ATGGGCAAGAAACAGATCCTGTTGTGATATTATTGAACGGGATTACAGATTGAA 456
Dd	
OY	1470 ATGGGCAAGAAACAGATCCTGTTGTGATATTATTGAACGGGATTACAGATTGAA 1411
OY	457 TGAAGTCACAAAGTGAGCATTTACCAGTAGAGAGAAACAGACGAGAAATCTTGATGCT 516
Dd	
OY	1410 TGAAGTCACAAAGTGAGCATTTACCAGTAGAGAGAAACAGACGAGAAATCTTGATGCT 1351
OY	517 TCACACAGCATGCAACAACAAATGCAATCTGTGATGACATGAGCAGCCAAGCTGGG 576
Dd	
OY	1350 TCACACAGCATGCAACAACAAATGCAATCTGTGATGACATGAGCAGCCAAGCTGGG 1291
OY	577 GAGGAGATAACACAGGGGACAGAGGTCAGATTTCTGGGCCCTGCGCTAAACCTGGGCTT 636
Dd	
OY	1290 GAGGAGATAACACAGGGGACAGAGGTCAGATTTCTGGGCCCTGCGCTAAACCTGGGCTT 1231
OY	637 CATACACCAATCATTTTCATATTTCTTAAACCCCTCAAACCAAAAGCTGTGTAATATCTGATCT 696
Dd	
OY	1230 CATACACCAATCATTTTCATATTTCTTAAACCCCTCAAACCAAAAGCTGTGTAATATCTGATCT 1171
OY	697 CTACGGTTCCTTCTGGGGCCCAACATTCTCCATATATCCAGCCACACATCATTTTAAATTT 756
Dd	
OY	1170 CTACGGTTCCTTCTGGGGCCCAACATTCTCCATATATCCAGCCACACATCATTTTAAATTT 1111
OY	757 TAGTTCCAGATCTGTACTGTGACCTTTCTACATGTAAGAAATTAACATTAACATTTGTT 816
Dd	
OY	1110 TAGTTCCAGATCTGTACTGTGACCTTTCTACATGTAAGAAATTAACATTAACATTTGTT 1051
OY	817 CAAGACCCCTTCGTTGCTCCTCAATATGATGATGACTGTTTTCTTAAAGATGTTCT 876

Db 1050 CAAAGACCCTGCTGTCTGCTGCTAATATGATGCTGACGTGTTTCCATAGAGTGTCT 991
Qy 877 GGCACAGGGGATCTGTGAACAGCGTGGAGCATCTCAAGATCTTCCAGGTTATCTT 936
Db 990 GGCACAGGGGATCTGTGAACAGCGTGGAGCATCTCAAGATCTTCCAGGTTATCTT 931
Qy 937 ACTACACACAGCATGATCATATACGAGTGAATATATCAATCAATCATCTCAGTGC 996
Db 930 ACTACACACAGCATGATCATATACGAGTGAATATATCAATCAATCATCTCAGTGC 871
Qy 997 TTGGCCATCTAGAAATTCATTTCCACTTTTGTGCCATTCCTCAAGACCTCAAAATGTC 1056
Db 870 TTGGCCATCTAGAAATTCATTTCCACTTTTGTGCCATTCCTCAAGACCTCAAAATGTC 811
Qy 1057 ATTCATTAATATCAGAGATTAACCTTTTTCACCTGGAAGATTCATGTTACT 1116
Db 810 ATTCATTAATATCAGAGATTAACCTTTTTCACCTGGAAGATTCATGTTACT 751
Qy 1117 GCAGCTATGGGAATTAATACATATTTGTTTCCAGTGAAGATGACTAGTCTT 1176
Db 750 GCAGCTATGGGAATTAATACATATTTGTTTCCAGTGAAGATGACTAGTCTT 691
Qy 1177 ATCCCTCCCTTTGTTGATTTTTCAGTATAAAGTTAAATGCTTAGCCTGTACT 1236
Db 690 ATCCCTCCCTTTGTTGATTTTTCAGTATAAAGTTAAATGCTTAGCCTGTACT 631
Qy 1237 GAGGCTGTATACAGC 1251
Db 630 GAGGCTGTATACAGC 616

RESULT 12
AX106206/c 2426 bp DNA linear PAT 30-APR-2001
LOCUS AX106206 Sequence 344 from Patent WO0125273.
DEFINITION AX106206
ACCESSION AX106206
VERSION AX106206.1 GI:13921895
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1
AUTHORS Skelky, Y. A., Xu, J., Cheever, M. A. and Reed, S. G.
TITLE Compositions and methods for wtl specific immunotherapy
JOURNAL Patent: WO 0125273-A 344 12-APR-2001;
CORIXA CORPORATION (US)
FEATURES
source 1. 2426
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
BASE COUNT 717 a 476 c 548 g 685 t
ORIGIN

Query Match 61.7%; Score 1155; DB 6; Length 2426;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1155; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 97 AGGTGAGAAATTAAGAAAGCTGCTGACTTTTACCATCTGAGGCCACACATCTGTAATG 156
Db 1770 AGGTGAGAAATTAAGAAAGCTGCTGACTTTTACCATCTGAGGCCACACATCTGTAATG 1711
Qy 157 GAGATTAATTAACATCTACTAGAAACAGCAAGATGACAAATTAATGTTAAGTGTAGCATG 216
Db 1710 GAGATTAATTAACATCTACTAGAAACAGCAAGATGACAAATTAATGTTAAGTGTAGCATG 1651
Qy 217 TTTTGGCAATTTCCAGCCCTTTTAAATATCCACACACAGAGAACACAAAGAAGCA 276
Db 1650 TTTTGGCAATTTCCAGCCCTTTTAAATATCCACACACAGAGAACACAAAGAAGCA 1591
Qy 277 CAGAGATCCCTGGGAGAAATGCCCGGCCCATCTTGGGTCAATGATGAGCCTGCCTG 336

Db 1590 CAGAGATCCCTGGGAGAAATGCCCGGCCCATCTTGGGTCAATGATGAGCCTGCCTG 1531
Qy 337 TCCCTGGTCCGCTTGTGAGGAGACATTAAGAAATGATGATGTTCTCTTAAAG 396
Db 1530 TCCCTGGTCCGCTTGTGAGGAGACATTAAGAAATGATGATGTTCTCTTAAAG 1471
Qy 397 ATGGGAGGAAACAGATCTCTGTGGATTTATTTGAAGGGATTAACATTTGAA 456
Db 1470 ATGGGAGGAAACAGATCTCTGTGGATTTATTTGAAGGGATTAACATTTGAA 1411
Qy 457 TGAAGTCAAAAGTAGAGATTTACATGAGAGAAACAGACAGAGAAATCTTGATGCT 516
Db 1410 TGAAGTCAAAAGTAGAGATTTACATGAGAGAAACAGACAGAGAAATCTTGATGCT 1351
Qy 517 TCACAGACATCAACAAACAAATGGAATGATGATGATGATGAGGACCAAGCTGG 576
Db 1350 TCACAGACATCAACAAACAAATGGAATGATGATGATGATGAGGACCAAGCTGG 1291
Qy 577 GAGGAGATTAACAGGGGAGAGGGTCAAGATTTGCGCCCTGCTCAACGTGCGTT 636
Db 1290 GAGGAGATTAACAGGGGAGAGGGTCAAGATTTGCGCCCTGCTCAACGTGCGTT 1231
Qy 637 CATTAACCAATCATTTTCAATTTTCAACCCCTCAAAACAAAGCTGTTGAATATGATCT 696
Db 1230 CATTAACCAATCATTTTCAATTTTCAACCCCTCAAAACAAAGCTGTTGAATATGATCT 1171
Qy 697 CTAGGTTCTCTGTGGCCCAACATTTCTCATATATCCAGCCACACTATTTTAAT 756
Db 1170 CTAGGTTCTCTGTGGCCCAACATTTCTCATATATCCAGCCACACTATTTTAAT 1111
Qy 757 TAGTCCAGATCTGTACTGTGACCTTTCTACAGTGTAGATTAATATCTCATTTTGT 816
Db 1110 TAGTCCAGATCTGTACTGTGACCTTTCTACAGTGTAGATTAATATCTCATTTTGT 1051
Qy 817 CAAAGACCCCTTGCTGTGCTGCTAATATGATGATGATGATGATGATGATGATGAT 876
Db 1050 CAAAGACCCCTTGCTGTGCTGCTAATATGATGATGATGATGATGATGATGATGAT 991

Qy 877 GGCACAGGGGATCTGTGAACAGCGTGGAGCATCTCAAGATCTTCCAGGTTATCTT 936
Db 990 GGCACAGGGGATCTGTGAACAGCGTGGAGCATCTCAAGATCTTCCAGGTTATCTT 931
Qy 937 ACTACACACAGCATGATCATATACGAGTGAATATATCAATCAATCATCTCAGTGC 996
Db 930 ACTACACACAGCATGATCATATACGAGTGAATATATCAATCAATCATCTCAGTGC 871
Qy 997 TTGGCCATCTAGAAATTCATTTCCACTTTTGTGCCATTCCTCAAGACCTCAAAATGTC 1056
Db 870 TTGGCCATCTAGAAATTCATTTCCACTTTTGTGCCATTCCTCAAGACCTCAAAATGTC 811
Qy 1057 ATTCATTAATATCAGAGATTAACCTTTTTCACCTGGAAGATTCATGTTACT 1116
Db 810 ATTCATTAATATCAGAGATTAACCTTTTTCACCTGGAAGATTCATGTTACT 751

Qy 1117 GCAGCTATGGGAATTAATTAATATTTGTTTCCAGTGAAGATGACTAGTCTT 1176
Db 750 GCAGCTATGGGAATTAATTAATATTTGTTTCCAGTGAAGATGACTAGTCTT 691
Qy 1177 ATCCCTCCCTTTGTTGATTTTTCAGTATAAAGTTAAATGCTTAGCCTGTACT 1236
Db 690 ATCCCTCCCTTTGTTGATTTTTCAGTATAAAGTTAAATGCTTAGCCTGTACT 631
Qy 1237 GAGGCTGTATACAGC 1251
Db 630 GAGGCTGTATACAGC 616

RESULT 13
AX106689/c 2426 bp DNA linear PAT 30-APR-2001
LOCUS AX106689 Sequence 470 from Patent WO0125272.
DEFINITION AX106689

```

VERSION      AXI06689.1  GI:13922354
KEYWORDS
SOURCE       Homo sapiens (human)
ORGANISM     Homo sapiens
REFERENCE    1
AUTHORS      Xu,J., Skelky,Y.A., Reed,S.G. and Cheever,M.A.
TITLE        Compositions and methods for therapy and diagnosis of prostate
              cancer
JOURNAL      Patent: WO 0125272-A 470 12-APR-2001;
              CORIXA CORPORATION (US)
FEATURES
  source      Location/Qualifiers
              1..2426
              /organism="Homo sapiens"
              /mol_type="genomic DNA"
              /db_xref="taxon:9606"
BASE COUNT   717 a 476 c 548 g 685 t
ORIGIN
Query Match 61.7%; Score 1155; DB 6; Length 2426;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1155; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 97 AGGTGAGAAATAGAAAGGCTGCTGACTTTACATCTGAGGCCACACATCTGCTGAATG 156
DB 1770 AGGTGAGAAATAGAAAGGCTGCTGACTTTACATCTGAGGCCACACATCTGCTGAATG 1711

QY 157 GAGATATTAACATCACTAGAACAGACAGATGACATTAATGTCTAATAGTACATG 216
DB 1710 GAGATATTAACATCACTAGAACAGACAGATGACATTAATGTCTAATAGTACATG 1651

QY 217 TTTTTCACATTTCCAGCCCTTTAAATATCCACACACAGAGAACACAAAAGAGACA 276
DB 1650 TTTTTCACATTTCCAGCCCTTTAAATATCCACACACAGAGAACACAAAAGAGACA 1591

QY 277 CAAGAGATCCCTGGGAGAAATGCCCGCCCATCTTGGGTCATCGATGAGCCCTGCCCTG 336
DB 1590 CAAGAGATCCCTGGGAGAAATGCCCGCCCATCTTGGGTCATCGATGAGCCCTGCCCTG 1511

QY 337 TGCCTGGTCCCGCTTGTGAGGAGAGACATTAGAAATGAATGATGTCTTCTTAAGG 396
DB 1530 TGCCTGGTCCCGCTTGTGAGGAGAGACATTAGAAATGAATGATGTCTTCTTAAGG 1471

QY 397 ATGGGAGAGAAAACAGATCCTGTGTGATATTTATTTGAACGGGATTTACAGATTTGAAA 456
DB 1470 ATGGGAGAGAAAACAGATCCTGTGTGATATTTATTTGAACGGGATTTACAGATTTGAAA 1411

QY 457 TGAAGTCACAAATGAGCATTTACCATGAGAGAAAAACAGAGAAAATCTTGATGGCT 516
DB 1410 TGAAGTCACAAATGAGCATTTACCATGAGAGAAAAACAGAGAAAATCTTGATGGCT 1351

QY 517 TCACAAGACATCCACAACAAACAAATGAAATGATCTGTGATGACATGAGGACCCAAAGCTGGG 576
DB 1350 TCACAAGACATCCACAACAAACAAATGAAATGATCTGTGATGACATGAGGACCCAAAGCTGGG 1291

QY 577 GAGGAGATTAACAACAGGAGGAGGAGGATTCGTGGCCCTGCTGCCCTAAACTGTGGCT 636
DB 1290 GAGGAGATTAACAACAGGAGGAGGAGGATTCGTGGCCCTGCTGCCCTAAACTGTGGCT 1231

QY 637 CATTAACCAATATCTTTCAATATTTCTAACCTCAAAACAAAGCTGTGTAATATCTGATCT 686
DB 1230 CATTAACCAATATCTTTCAATATTTCTAACCTCAAAACAAAGCTGTGTAATATCTGATCT 1171

QY 697 CTACGGTCTCTTGGGCCCAACATCTCTCATATATCCACGACACATCTTTTAATAT 756
DB 1170 CTACGGTCTCTTGGGCCCAACATCTCTCATATATCCACGACACATCTTTTAATAT 1111

QY 757 TAGTTCCAGATCTGTACTGTGACCTTTTACACTGTAGATAACATTAATCAATCTTTTGT 816
DB 1110 TAGTTCCAGATCTGTACTGTGACCTTTTACACTGTAGATAACATTAATCAATCTTTTGT 1051

QY 817 CAAAGACCTCTGCTGTGCTGCTAATATGTAGCTGACTGTTTCTTAAGGAGTGTCT 876

```

```

|||||
DB 1050 CAAAGACCTCTGCTGTGCTGCTAATATGTAGCTGACTGTTTCTTAAGGAGTGTCT 991
QY 877 GGGCCAGGGGATCTGTACACAGGCTGGGAAGCATCTCAAGATCTTCCAGGGTATCTT 936
DB 990 GGGCCAGGGGATCTGTACACAGGCTGGGAAGCATCTCAAGATCTTCCAGGGTATCTT 931
QY 937 ACTAGCACACAGCATGATCATTTAGGAGTGAATATATCAACATCATCTCAGTGC 996
DB 930 ACTAGCACACAGCATGATCATTTAGGAGTGAATATATCAACATCATCTCAGTGC 871
QY 997 TTTGCCATCTGAAATTTCAATTTCCACTTTTGCCCATCTCCAAACCTCAAAATGTC 1056
DB 870 TTTGCCATCTGAAATTTCAATTTCCACTTTTGCCCATCTCCAAACCTCAAAATGTC 811
QY 1057 ATTCATTAATATACAGATTAATCTTTTATTTTAACTGGAAGATTCATATGTTACAT 1116
DB 810 ATTCATTAATATACAGATTAATCTTTTATTTTAACTGGAAGATTCATATGTTACAT 751
QY 1117 GCAGCTATGGAAATTAATTAATATTTTTCAGTGCAGTCAAAAGATGACTAAGTCTTT 1176
DB 750 GCAGCTATGGAAATTAATTAATATTTTTCAGTGCAGTCAAAAGATGACTAAGTCTTT 691
QY 1177 ATCCCTCCCTTTGTGATTTTTCAGTATAAAGTTAAATGCTTAGCCTTGACT 1236
DB 690 ATCCCTCCCTTTGTGATTTTTCAGTATAAAGTTAAATGCTTAGCCTTGACT 631
QY 1237 GAGGCTGATACAGC 1251
DB 630 GAGGCTGATACAGC 616

RESULT 14
AXI140980/c 2426 bp DNA linear PAT 31-MAY-2001
DEFINITION Sequence 470 from Patent W00134802.
ACCESSION AXI140980
VERSION AXI140980.1 GI:14281077
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y.,
          Reed,S.G., Kalos,M.D., Retter,M.W., Stolk,J.A., Day,C.B.,
          Skelky,Y.A. and Wang,A.
TITLE Compositions and methods for the therapy and diagnosis of prostate
        cancer
JOURNAL Patent: WO 0134802-A 470 17-MAY-2001;
        CORIXA CORPORATION (US)
FEATURES
  source      Location/Qualifiers
              1..2426
              /organism="Homo sapiens"
              /mol_type="genomic DNA"
              /db_xref="taxon:9606"
BASE COUNT   717 a 476 c 548 g 685 t
ORIGIN
Query Match 61.7%; Score 1155; DB 6; Length 2426;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1155; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 97 AGGTGAGAAATAGAAAGGCTGCTGACTTTACATCTGAGGCCACACATCTGCTGAATG 156
DB 1770 AGGTGAGAAATAGAAAGGCTGCTGACTTTACATCTGAGGCCACACATCTGCTGAATG 1711

QY 157 GAGATATTAACATCACTAGAACAGACAGATGACATTAATGTCTAATAGTACATG 216
DB 1710 GAGATATTAACATCACTAGAACAGACAGATGACATTAATGTCTAATAGTACATG 1651

QY 217 TTTTTCACATTTCCAGCCCTTTAAATATCCACACACAGAGAACACAAAAGAGACA 276

```

Db 1650 TTTTGGACATTTCCAGCCCTTTAAATATCCACACACAGAGAACAACAAAGAAAGCA 1591
QY 277 CAGAAATCCCTGGGGAANAATGCCCGCCCATCTTGGGTATTCATAGACCTCCGCCCTG 336
Db 1590 CAGAAATCCCTGGGGAANAATGCCCGCCCATCTTGGGTATTCATAGACCTCCGCCCTG 1531
QY 337 TGCCTGGTCCCTGTGGAGGAGACATTTAGAAAATGAATGATGTTCTCTTAAAG 396
Db 1530 TGCCTGGTCCCTGTGGAGGAGACATTTAGAAAATGAATGATGTTCTCTTAAAG 1471
QY 397 ATGGCAGAGAAAACAGATCTGTGGATTTTATTTGACGGGATTAACAGATTGAAA 456
Db 1470 ATGGCAGAGAAAACAGATCTGTGGATTTTATTTGACGGGATTTACAGATTGAAA 1411
QY 457 TGAAGTCAAAAGTAGACATTCACATAGAGAAAACAGAGAAAATCTGTAGTGGT 516
Db 1410 TGAAGTCAAAAGTAGACATTCACATAGAGAAAACAGAGAAAATCTGTAGTGGT 1351
QY 517 TCACAAGACATGCACAACAAATGAATACCTGTGATGACATGAGGACAGCCAGCTGG 576
Db 1350 TCACAAGACATGCACAACAAATGAATACCTGTGATGACATGAGGACAGCCAGCTGG 1291
QY 577 GAGGATTAACACAGGAGGAGAGGTCAGGATTTGGCCCTGCTGCTTAACCTGTGCTT 636
Db 1290 GAGGATTAACACAGGAGGAGAGGTCAGGATTTGGCCCTGCTGCTTAACCTGTGCTT 1231
QY 637 CATTAACCAATCATTTATTTCTAACCTCAAAAGAGCTGTGTAATTCGATCT 696
Db 1230 CATTAACCAATCATTTATTTCTAACCTCAAAAGAGCTGTGTAATTCGATCT 1171
QY 697 CTACGGTTCCTTCTGGGCCCCAATTCCTATATATATATATATATATATATATAT 756
Db 1170 CTACGGTTCCTTCTGGGCCCCAATTCCTATATATATATATATATATATATATAT 1111
QY 757 TAGTTCACAGATCTGTACTGTGACCTTTCTACACTGTAGATTAACATTTCTATT 816
Db 1110 TAGTTCACAGATCTGTACTGTGACCTTTCTACACTGTAGATTAACATTTCTATT 1051
QY 817 CAAGACCTTGTGTGTGCTGCTAATATGTAGCTGACGTTTCTTAAAGAGTGTCT 876
Db 1050 CAAGACCTTGTGTGTGCTGCTAATATGTAGCTGACGTTTCTTAAAGAGTGTCT 991
QY 877 GGGCCAGGGGATCTGTGAACAGGCTGGGAAGCATCTCAAGATCTTTCAGGGTTATAT 936
Db 990 GGGCCAGGGGATCTGTGAACAGGCTGGGAAGCATCTCAAGATCTTTCAGGGTTATAT 931
QY 937 ACTAGCACACAGATGATATTACGAGTGAATTTATCTAATCAACATCTCTCACTGT 996
Db 930 ACTAGCACACAGATGATATTACGAGTGAATTTATCTAATCAACATCTCTCACTGT 871
QY 997 TTTGGCCATACGAATTCATTTCCACTTTTGTGCCCCATTCGAAGACCTCAAAATGTC 1056
Db 870 TTTGGCCATACGAATTCATTTCCACTTTTGTGCCCCATTCGAAGACCTCAAAATGTC 811
QY 1057 ATTTCAATTAATATCAACAGGATTAACCTTTTAACTTGAAGGAAATCAATGTTACAT 1116
Db 810 ATTTCAATTAATATCAACAGGATTAACCTTTTAACTTGAAGGAAATCAATGTTACAT 751
QY 1117 GCAGCTATGGGAATTAATTAACATTTTGTTCAGAGCAAGATGACTAAGCTCTT 1176
Db 750 GCAGCTATGGGAATTAATTAACATTTTGTTCAGAGCAAGATGACTAAGCTCTT 691
QY 1177 ATCCCTCCCTTGTGTTGATTTTTCAGATTAATAAGTAAAGCTTAAAGCTTACT 1236
Db 690 ATCCCTCCCTTGTGTTGATTTTTCAGATTAATAAGTAAAGCTTAAAGCTTACT 631
QY 1237 GAGGCTGTATACAGC 1251
Db 630 GAGGCTGTATACAGC 616

RESULT 15
AX200840/c

LOCUS AX200840 2426 bp DNA linear PAT 29-AUG-2001
DEFINITION Sequence 470 from Patent WO0151633.
ACCESSION AX200840
VERSION AX200840.1 GI:15390743
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1 Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y.,
Reed,S.G., Kalos,M.D., Fanger,G.R., Day,C.H., Rietter,M.W.,
Stolk,J.A., Skelly,Y.A., Wang,A. and Meagher,M.J.
Compositions and methods for the therapy and diagnosis of prostate
cancer
Patent: WO 0151633-A 470 19-JUL-2001;
CORLIXA CORPORATION (US)
FEATURES
Location/Qualifiers
1..2426
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
BASE COUNT 717 a 476 c 348 g 685 t
ORIGIN
Query Match 61.7%; Score 1155; DB 6; Length 2426;
Best Local Similarity 100.0%; Pred No. 0;
Matches 1155; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 97 AGGTGGAATTAAGAAAGGCTGCTGACCTTACCATCTGAGGCCACACATCTGCTGAATG 156
Db 1770 AGGTGGAATTAAGAAAGGCTGCTGACCTTACCATCTGAGGCCACACATCTGCTGAATG 1711
QY 157 GAGATTAATTAATCTCTGTAAGAAACAGAGATGACAAATTAATGTGTAGTAGTGACATG 216
Db 1710 GAGATTAATTAATCTCTGTAAGAAACAGAGATGACAAATTAATGTGTAGTAGTGACATG 1651
QY 217 TTTTGCACATTTCCAGCCCTTTAATATATCAACACACAGAGAAACAAAAAGAAAGCA 276
Db 1650 TTTTGCACATTTCCAGCCCTTTAATATATCAACACACAGAGAAACAAAAAGAAAGCA 1591
QY 277 CAGAGATCCCTGGGAGAAATGCCGGCCCATCTTGGGTATGATGAGCTGCGCCCTG 336
Db 1590 CAGAGATCCCTGGGAGAAATGCCGGCCCATCTTGGGTATGATGAGCTGCGCCCTG 1531
QY 337 TGCCTGGTCCCTGTGTGAGGAGAGACATTTAGAAAATGAATGATGTCTCTTAAAG 396
Db 1530 TGCCTGGTCCCTGTGTGAGGAGAGACATTTAGAAAATGAATGATGTCTCTTAAAG 1471
QY 397 ATGGGAGAGAAAACAGATCTGTGTGATATTTTGAACGGGATTAACAGATTGAAA 456
Db 1470 ATGGGAGAGAAAACAGATCTGTGTGATATTTTGAACGGGATTAACAGATTGAAA 1411
QY 457 TGAAGTCAAAAGTGAAGCATTTACCAATGAGAGAAAAACAGAGAAAATCTTGAATGCT 516
Db 1410 TGAAGTCAAAAGTGAAGCATTTACCAATGAGAGAAAAACAGAGAAAATCTTGAATGCT 1351
QY 517 TCACAAGACATGCACAACAAATGAATACCTGTGATGACATGAGGACAGCCAGCTGG 576
Db 1350 TCACAAGACATGCACAACAAATGAATACCTGTGATGACATGAGGACAGCCAGCTGG 1291
QY 577 GAGGATTAACACAGGAGGAGAGGTCAGGATTTGGCCCTGCTGCTTAACCTGTGCTT 636
Db 1290 GAGGATTAACACAGGAGGAGAGGTCAGGATTTGGCCCTGCTGCTTAACCTGTGCTT 1231
QY 637 CATTAACCAATCATTTATTTCTAACCTCAAAAGAGCTGTGTAATTCGATCT 696
Db 1230 CATTAACCAATCATTTATTTCTAACCTCAAAAGAGCTGTGTAATTCGATCT 1171
QY 697 CTACGGTTCCTTCTGGGCCCCAATTCCTATATATATATATATATATATATATAT 756
Db 1170 CTACGGTTCCTTCTGGGCCCCAATTCCTATATATATATATATATATATATATAT 1111

OY 757 TAGTCCAGATCTGTAAGTGTGACCTTTCTACACTGTAGAAATACATTACTCATTTGTT 816
|||
Db 1110 TAGTCCAGATCTGTAAGTGTGACCTTTCTACACTGTAGAAATACATTACTCATTTGTT 1051
OY 817 CAAAGACCCCTGCGTGTGCTGCTAATATATGAGCTGTTTCCCTAAGAGTGTCT 876
|||
Db 1050 CAAAGACCCCTGCGTGTGCTGCTAATATATGAGCTGTTTCCCTAAGAGTGTCT 991
OY 877 GGGCCAGGGGATCTGTGAACAGGCTGGGAGACATCTCAAGATCTTCCAGGGTTATACTT 936
|||
Db 990 GGGCCAGGGGATCTGTGAACAGGCTGGGAGACATCTCAAGATCTTCCAGGGTTATACTT 931
OY 937 ACTAGCACACAGCATGATCATTAACGAGTGAATATCTAATCAACATCATCTCAGTGTCT 996
|||
Db 930 ACTAGCACACAGCATGATCATTAACGAGTGAATATCTAATCAACATCATCTCAGTGTCT 871
OY 997 TTGCCCATACTGAAATTCATTCTCCCACTTTGTGCCATCTCAAGACCTCAAAATGTC 1056
|||
Db 870 TTGCCCATACTGAAATTCATTCTCCCACTTTGTGCCATCTCAAGACCTCAAAATGTC 811
OY 1057 ATTCCATTAAATATCAGAGATTAACCTTTTAACTGGAAGAAATTCATGTACAT 1116
|||
Db 810 ATTCCATTAAATATCAGAGATTAACCTTTTAACTGGAAGAAATTCATGTACAT 751
OY 1117 GCAGCTATGGGAATTTATACATATTTGTTTCCAGTGCAGAAAGATGACTAAGTCTT 1176
|||
Db 750 GCAGCTATGGGAATTTATACATATTTGTTTCCAGTGCAGAAAGATGACTAAGTCTT 691
OY 1177 ATCCCTCCCTTTGTGATTTTTCAGTATTAAGTAAATGCTTAGCCTGTACT 1236
|||
Db 690 ATCCCTCCCTTTGTGATTTTTCAGTATTAAGTAAATGCTTAGCCTGTACT 631
OY 1237 GAGGCTGTATACAGC 1251
|||
Db 630 GAGGCTGTATACAGC 616

Search completed: September 27, 2003, 06:44:59
Job time : 6816.49 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 26, 2003, 20:07:52 : Search time 490.581 Seconds
(without alignments)
10300.748 Million cell updates/sec

Title: US-09-402-713a-3
1872
Perfect score: 1 agaaagctgcagatcagaaaaa.....cattaagaattcacaaga 1872
Sequence:

Scoring table: OLIGO_NUC
Gapex 60.0 , Gapext 60.0

Searched: 2552756 seqs, 1349719017 residues

Word size : 0

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : N.Geneseq_19Jun03.*

```
1: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1980.DAT:*
2: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT:*
3: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1982.DAT:*
4: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1983.DAT:*
5: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1984.DAT:*
6: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1985.DAT:*
7: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1986.DAT:*
8: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1987.DAT:*
9: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1988.DAT:*
10: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1989.DAT:*
11: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1990.DAT:*
12: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1991.DAT:*
13: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1992.DAT:*
14: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1993.DAT:*
15: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1994.DAT:*
16: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1995.DAT:*
17: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1996.DAT:*
18: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1997.DAT:*
19: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1998.DAT:*
20: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1999.DAT:*
21: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA2000.DAT:*
22: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT:*
23: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT:*
24: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT:*
25: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA2003.DAT:*
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1872	100.0	1872	19	AAV62428
2	1775	94.8	2037	19	AAV62427
3	1367	73.0	3582	19	AAV62430
4	1367	73.0	3923	22	AA564026
5	1367	73.0	3923	22	AAH93861
6	1367	73.0	3923	24	ABK92196
7	1367	73.0	3923	24	ABL95397
8	1367	73.0	3923	25	ACA59834

C	9	1155	61.7	2426	21	AA06689	Human immunogenic
C	10	1155	61.7	2426	22	AA563898	Human prostate CDN
C	11	1155	61.7	2426	22	AAH93805	Human prostate-spe
C	12	1155	61.7	2426	22	AAH85119	Human prostate-spe
C	13	1155	61.7	2426	22	AAH02870	Prostate tumour an
C	14	1155	61.7	2426	22	AAH69448	Human p710P Invent
C	15	1155	61.7	2426	24	ABL95269	Human p710P CDNA s
C	16	1155	61.7	2426	25	ACA59706	Prostate cancer th
C	17	1155	61.7	3112	21	AA06687	Human immunogenic
C	18	1155	61.7	3112	22	AA563896	Human prostate CDN
C	19	1155	61.7	3112	22	AAH93803	Human prostate-spe
C	20	1155	61.7	3112	22	AAH85117	Human prostate-spe
C	21	1155	61.7	3112	22	AAH02868	Prostate tumour an
C	22	1155	61.7	3112	22	AAH69446	Human p710P Invent
C	23	1155	61.7	3112	24	ABL95267	Human p710P CDNA s
C	24	1155	61.7	3112	25	ACA59704	Prostate cancer th
C	25	1034	55.2	2229	21	AA06688	Human immunogenic
C	26	1034	55.2	2229	22	AA563897	Human prostate CDN
C	27	1034	55.2	2229	22	AAH93804	Human prostate-spe
C	28	1034	55.2	2229	22	AAH85118	Human prostate-spe
C	29	1034	55.2	2229	22	AAH02869	Prostate tumour an
C	30	1034	55.2	2229	22	AAH69447	Human p710P Invent
C	31	1034	55.2	2229	24	ABL95268	Human p710P CDNA s
C	32	1034	55.2	2229	25	ACA59705	Prostate cancer th
C	33	835	44.6	876	24	AAD38815	Human PSNA CDNA, p
C	34	820	43.8	820	19	AAV62429	Prostate cancer an
C	35	812	43.4	812	21	AA06690	Human immunogenic
C	36	812	43.4	812	22	AA563899	Human prostate CDN
C	37	812	43.4	812	22	AAH93806	Human prostate-spe
C	38	812	43.4	812	22	AAH85120	Human prostate-spe
C	39	812	43.4	812	22	AAH02871	Prostate tumour an
C	40	812	43.4	812	22	AAH69449	Human p710P Invent
C	41	812	43.4	812	24	ABL95270	Human p710P CDNA s
C	42	812	43.4	812	25	ACA59707	Prostate cancer th
C	43	475	25.4	658	23	ABV42450	Human prostate exp
C	44	475	25.4	671	23	ABV41330	Human prostate exp
C	45	473	25.3	597	20	AAH37486	Human secreted pro

ALIGNMENTS

RESULT 1	
ID	AAV62428 standard; CDNA, 1872 BP.
AAV62428:	
AC	AAV62428:
AC	30-DEC-1998 (first entry)
DE	Prostate cancer antigen (PCA3) CDNA splice variant 2.
DE	Prostate cancer antigen CDNA splice variant 2; PCA3; prostatic cancer;
KW	PC; ds.
KW	
OS	Homo sapiens.
XX	
PN	W09845420-A1.
XX	
PD	15-OCT-1998.
XX	
PF	09-APR-1998; 98WO-CA00346.
XX	
PR	10-APR-1997; 97US-0041836.
XX	
PA	(DIAG-) DIAGNOCURE INC.
XX	
PI	Bussemakers MUG;
XX	
DR	WPI; 1998-568347/48.
XX	
PT	New nucleic acid encoding prostate cancer antigen 3 - for diagnosis,
PT	prevention and treatment of prostatic cancer

XX Claim 4; Pages 76-77; 11pp; English.
 XX The present sequence represents the prostate cancer antigen (PCA3)
 CC cDNA splice variant 2 sequence comprising of exons 1, 3, 4a and
 CC 4b of the PCA3 gene. The PCA3 cDNA splice variant 2 sequence,
 CC isolated from a human primary prostate tumour tissue cDNA library,
 CC was found in approximately 65% of the cDNA clones isolated. The
 CC invention claims for PCA3 cDNA variants and the proteins they encode.
 CC The invention also claims for antibodies against PCA3 protein. The
 CC antibodies are claimed to be useful for detecting PCA3 protein in
 CC immunosay tests, for diagnosing, assessing and prognosis of
 CC prostate cancer (PC). Antibodies, optionally coupled to a cytotoxin
 CC or radioisotope, and nucleic acids antisense to PCA3 cDNA are claimed
 CC to be useful for treating PC, while determining elevated levels of
 CC PCA3 (as RNA or protein) is useful for detecting a predisposition
 CC to development of PC, e.g. in prenatal tests. Detecting PCA3 protein
 CC allows differentiation between malignant and benign prostate disease.
 CC and the level of PCA3 expression allows correlation with the grade of
 CC tumour. PCA3 protein and its fragments are also claimed to be useful
 CC in vaccines for preventing PC; in drug screens for identifying
 CC specific (ant)agonists (potentially useful therapeutically) and for
 CC studying protein-DNA interactions.
 XX
 XX Sequence 1872 BP; 567 A; 389 C; 369 G; 539 T; 8 other;
 SQ
 Query Match 100.0%; Score 1872; DB 19; Length 1872;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1872; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGAAGCTGGCATGAGAAAAACAGAGGGAGATTGTGTGCTGACGCCGAGAGACCAG 60
 Db 1 AGAAGCTGGCATGAGAAAAACAGAGGGAGATTGTGTGCTGACGCCGAGAGACCAG 60
 QY 61 GAAGATCTGCATGCTGGGAAAGACCTGATGATACAGAGGTGAGAAATTAAGAGGCTCT 120
 Db 61 GAAGATCTGCATGCTGGGAAAGACCTGATGATACAGAGGTGAGAAATTAAGAGGCTCT 120
 QY 121 GATTTTACCATCTGAGAGCCACATCTGCTGGAATGAGATTAATTAACATCACTAAGAAC 180
 Db 121 GATTTTACCATCTGAGAGCCACATCTGCTGGAATGAGATTAATTAACATCACTAAGAAC 180
 QY 181 AGCAAGATGACATATATATGTCTAAGTAGAGATGTTTGTGACATTTCCAGCCCTTT 240
 Db 181 AGCAAGATGACATATATATGTCTAAGTAGAGATGTTTGTGACATTTCCAGCCCTTT 240
 QY 241 AATATTCACACACACAGAGAAAGCAAAAGAGACACAGATCCCTGGGAGAAATGCC 300
 Db 241 AATATTCACACACACAGAGAAAGCAAAAGAGACACAGATCCCTGGGAGAAATGCC 300
 QY 301 GGGCGGCATCTTGGGTCATCGATGAGCCCTGCCCTGTGCTGCCGCTTGTGAGAGAA 360
 Db 301 GGGCGGCATCTTGGGTCATCGATGAGCCCTGCCCTGTGCTGCCGCTTGTGAGAGAA 360
 QY 361 GGCATTTAGAAAATGATATGATGTCTCTTAAAGATGGGAGAAACAGATCCGTT 420
 Db 361 GGCATTTAGAAAATGATATGATGTCTCTTAAAGATGGGAGAAACAGATCCGTT 420
 QY 421 GTGGATATTTATTTGAACGGGATTACAGATTTGAAATGAAAGTCACAAAGTACATTACC 480
 Db 421 GTGGATATTTATTTGAACGGGATTACAGATTTGAAATGAAAGTCACAAAGTACATTACC 480
 QY 481 AATGAGAGGAAAAACAGACGAAATCTTGATGGCTTACACAGACATGCAACAAACAAA 540
 Db 481 AATGAGAGGAAAAACAGACGAAATCTTGATGGCTTACACAGACATGCAACAAACAAA 540
 QY 541 TGGAAATCTGTGATGATGAGAGGACCAAGCTGGGGAGAGATTAACACAGGGGAGAGG 600
 Db 541 TGGAAATCTGTGATGATGAGAGGACCAAGCTGGGGAGAGATTAACACAGGGGAGAGG 600
 QY 601 GTGAGATTTCTGGCCCTGCTGCTAAAGTGTGCTTCAATCAACAAATCATTTATTTTC 660
 Db 601 GTGAGATTTCTGGCCCTGCTGCTAAAGTGTGCTTCAATCAACAAATCATTTATTTTC 660

QY 661 TAAACCTCAAAACAAAGCTGTGTATATCTGATCTGACGGTTCCTTGGGCCCAACA 720
 Db 661 TAAACCTCAAAACAAAGCTGTGTATATCTGATCTGACGGTTCCTTGGGCCCAACA 720
 QY 721 TTCTCCATATATCCAGGACACATCTTTAATATTTAGTCCAGATCTGTACTGAGAC 780
 Db 721 TTCTCCATATATCCAGGACACATCTTTAATATTTAGTCCAGATCTGTACTGAGAC 780
 QY 781 CTTTCTACATGTAGAAATTAACATTTTGTGTTCAAGACCTTCGTTGCTGCTCCT 840
 Db 781 CTTTCTACATGTAGAAATTAACATTTTGTGTTCAAGACCTTCGTTGCTGCTCCT 840
 QY 841 AATATGACTGACTGTTTTCCTAAGAGCTTTCTGGCCAGGGATCTGTGAACAGGC 900
 Db 841 AATATGACTGACTGTTTTCCTAAGAGCTTTCTGGCCAGGGATCTGTGAACAGGC 900
 QY 901 TGGGAAGCATCTCAAAAGTCTTCCAGGTTATCTTACTAGACACACAGATGATCAATTTC 960
 Db 901 TGGGAAGCATCTCAAAAGTCTTCCAGGTTATCTTACTAGACACACAGATGATCAATTTC 960
 QY 961 GGAGTGAATTTATCTAATCAACATCAATCTGATGCTGTTGCCATCACTGAATTCATTTC 1020
 Db 961 GGAGTGAATTTATCTAATCAACATCAATCTGATGCTGTTGCCATCACTGAATTCATTTC 1020
 QY 1021 CCACTTTTGTGCCATTTCTCAGACCTCAAAATGTCATTCATTAATACAGATTA 1080
 Db 1021 CCACTTTTGTGCCATTTCTCAGACCTCAAAATGTCATTCATTAATACAGATTA 1080
 QY 1081 CTTTCTTTTAACTGGAAGATTCATGATGATGATGATGATGATGATGATGATGATGAT 1140
 Db 1081 CTTTCTTTTAACTGGAAGATTCATGATGATGATGATGATGATGATGATGATGATGAT 1140
 QY 1141 ATTTTGTTCAGTGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1200
 Db 1141 ATTTTGTTCAGTGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1200
 QY 1201 TTTCCAGTAAATGATTAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1260
 Db 1201 TTTCCAGTAAATGATTAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1260
 QY 1261 CCCCATCCCTCCAGCCTTATCTGATCAATCAACATCAACATCAACATCAACATCAACAT 1320
 Db 1261 CCCCATCCCTCCAGCCTTATCTGATCAATCAACATCAACATCAACATCAACATCAACAT 1320
 QY 1321 ATCTAATCTGATTAATCTTGAACATGTCAGGATCAATCTTCTGCTGCTGAGAGGC 1380
 Db 1321 ATCTAATCTGATTAATCTTGAACATGTCAGGATCAATCTTCTGCTGCTGAGAGGC 1380
 QY 1381 TCTTCTCTGCTTCTAATCTAATGATGATGATGATGATGATGATGATGATGATGATGAT 1440
 Db 1381 TCTTCTCTGCTTCTAATCTAATGATGATGATGATGATGATGATGATGATGATGATGAT 1440
 QY 1441 TCATGCAAGAAAGGACACATATGATGATGATGATGATGATGATGATGATGATGATGAT 1500
 Db 1441 TCATGCAAGAAAGGACACATATGATGATGATGATGATGATGATGATGATGATGATGAT 1500
 QY 1501 TGTAAATTTGATTAAGAGTTTGAATTAATATGAAATGCAAGACCAAGAGGGAATG 1560
 Db 1501 TGTAAATTTGATTAAGAGTTTGAATTAATATGAAATGCAAGACCAAGAGGGAATG 1560
 QY 1561 TTTATGGGACGCTTTGTAAGCCTGGAGATGTAAGAAAGGAGGAGACCTCATATATAC 1620
 Db 1561 TTTATGGGACGCTTTGTAAGCCTGGAGATGTAAGAAAGGAGGAGACCTCATATATAC 1620
 QY 1621 TTTATTAATTAATCTTATCTTCTAATCTGATGATGATGATGATGATGATGATGATGAT 1680
 Db 1621 TTTATTAATTAATCTTATCTTCTAATCTGATGATGATGATGATGATGATGATGATGAT 1680
 QY 1681 TTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1740
 Db 1681 TTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1740


```
OY 1058 TTCCATTAAATACACAGGATTAACCTTTTTTTTAACTGGAGAAATTCATGTTACATG 1117
Db 1223 TTCCATTAAATATCACAGGATTAACCTTTTTTTTAACTGGAGAAATTCATGTTACATG 1282
OY 1118 CAGCTATGGAATTTAAATTAATATTTTGTTCAGTGCAGAAAGATGACTAAGTCCTTTA 1177
Db 1283 CAGCTATGGAATTTAAATTAATATTTTGTTCAGTGCAGAAAGATGACTAAGTCCTTTA 1342
OY 1178 TCCCTCCCTTTGTTGATGATTTTTTTTCCAGTATTAAGTTAAATGCTTAGCCCTGTA 1237
Db 1343 TCCCTCCCTTTGTTGATGATTTTTTTTCCAGTATTAAGTTAAATGCTTAGCCCTGTA 1402
OY 1238 AGGCTGTATACAGACAGCCCTCCGCCATCCCTCCAGCCCTTATCTGATCACCATCAAC 1297
Db 1403 AGGCTGTATACAGACAGCCCTCCGCCATCCCTCCAGCCCTTATCTGATCACCATCAAC 1462
OY 1298 CCGTCCCATNYSACCTTAACAAAATCTAATCTGTAATCTCTGAACTGTCAGGNCATAC 1357
Db 1463 CCGTCCCATNYSACCTTAACAAAATCTAATCTGTAATCTCTGAACTGTCAGGNCATAC 1522
OY 1358 ATTTTCTCTCTGCTGAGAAAGCTCTTCTGCTCTTAACTGAGATGATGAAGTT 1417
Db 1523 ATTTTCTCTCTGCTGAGAAAGCTCTTCTGCTCTTAACTGAGATGATGAAGTT 1582
OY 1418 TTGAATTAAGTGAATCTACTTCTATGCAAGAGGACACATNTGAGATTCATCA 1477
Db 1583 TTGAATTAAGTGAATCTACTTCTATGCAAGAGGACACATNTGAGATTCATCA 1642
OY 1478 CATGAGACACCAATATAAGTGAATTTGATTAAGAGTTAGATTAATATGA 1537
Db 1643 CATGAGACACCAATATAAGTGAATTTGATTAAGAGTTAGATTAATATGA 1702
OY 1538 ATGCAAGAKCCACAGAGGGAATGTTATGCGGACGTTTGAAGCTGGAGTGAAGMA 1597
Db 1703 ATGCAAGAKCCACAGAGGGAATGTTATGCGGACGTTTGAAGCTGGAGTGAAGMA 1762
OY 1598 AAGGACGAGAACCTCATATGATCTTATATATATATCTTCAATCTCTATCTATCA 1657
Db 1763 AAGGACGAGAACCTCATATGATCTTATATATATATCTTCAATCTCTATCTATCA 1822
OY 1658 TATCCAAACAAGCTTTTACAGAAATTCATGCAAGTCAATCCCAAGAGTAACCTTTATCC 1717
Db 1823 TATCCAAACAAGCTTTTACAGAAATTCATGCAAGTCAATCCCAAGAGTAACCTTTATCC 1882
OY 1718 ATTTCATGCGAATGCGCTTTAAGATTTTGGCAATCATCTGCTCACTTATCTCAACTT 1777
Db 1883 ATTTCATGCGAATGCGCTTTAAGATTTTGGCAATCATCTGCTCACTTATCTCAACTT 1942
OY 1778 TGAGATGTGTTTGTCTGCTGATTAATTAAGAAATAGGGCACTCTTGAGCCCACTTT 1837
Db 1943 TGAGATGTGTTTGTCTGCTGATTAATTAAGAAATAGGGCACTCTTGAGCCCACTTT 2002
OY 1838 AGGGTTCACCTCTGCGCAATTAAGAAATTTACAAAGA 1872
Db 2003 AGGGTTCACCTCTGCGCAATTAAGAAATTTACAAAGA 2037

RESULT 3
AAV62430 standard; cDNA: 3582 BP.
XX AAV62430:
AC
XX
DT 30-DEC-1998 (first entry)
XX
DE Prostate cancer antigen (PCA3) wild-type cDNA.
XX
KM Prostate cancer antigen cDNA. PCA3; prostatic cancer;
XX PC; ds.
XX Homo sapiens.
XX OS
XX FH Location/Qualifiers
```

```
FT CDS 401..556
FT /*tag= a
FT /product= "PCA3 protein"
FT polyA_signal 983..987
FT polyA_signal /*tag= b
FT polyA_signal 2041..2046
FT polyA_signal /*tag= c
FT polyA_signal 2597..2602
FT polyA_signal /*tag= d
FT polyA_signal 3494..3496
FT /*tag= e
XX
XX MO9845420-A1.
XX
XX 15-OCT-1998.
XX
XX 09-APR-1998; 98MO-CA00346.
XX
XX 10-APR-1997; 97US-0041836.
XX
XX (DIAG-) DIAGNOCURE INC.
XX
XX Bussemakers MJG;
XX
XX WPI: 1998-568347/48.
XX
XX P-PSDB; AAW79738.
XX
XX New nucleic acid encoding prostate cancer antigen 3 - for diagnosis,
XX prevention and treatment of prostatic cancer
XX
XX Claim 3; Fig 5B-5F; 11pp; English.
XX
XX The present sequence represents the prostate cancer antigen (PCA3)
XX wild-type cDNA sequence comprising of exons 1, 2, 3, 4a-4d of the
XX PCA3 gene. The invention claims for PCA3 cDNA variants and the
XX proteins they encode. The invention also claims for antibodies
XX against PCA3 protein. The antibodies are claimed to be useful for
XX detecting PCA3 protein in immunoassay tests, for diagnosing, assessing
XX and prognosing of prostatic cancer (PC). Antibodies, optionally
XX coupled to a cytotoxin or radioisotope, and nucleic acids antisense
XX to PCA3 cDNA are claimed to be useful for treating PC, while determining
XX elevated levels of PCA3 (as RNA or protein) is useful for detecting a
XX predisposition to development of PC, e.g. in prenatal tests. Detecting
XX PCA3 protein allows differentiation between malignant and benign
XX prostatic disease, and the level of PCA3 expression allows correlation
XX with the grade of tumour. PCA3 protein and its fragments are also
XX claimed to be useful in vaccines for preventing PC; in drug screens
XX for identifying specific (ant)agonists (potentially useful
XX therapeutically) and for studying protein-DNA interactions.
XX
XX Sequence 3582 BP; 1052 A; 788 C; 679 G; 1063 T; 0 other;
XX
XX Query Match 73.0%; Score 1367; DB 19; Length 3582;
XX Best Local Similarity 99.5%; Pred. No. 0;
XX Matches 1767; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
OY 98 GGTGAGAAATTAAGAAAGCTGCTGACTTTACATCTGAGGCCACACATCTGCGTAATGG 157
Db 285 GGTGAGAAATTAAGAAAGCTGCTGACTTTACATCTGAGGCCACACATCTGCGTAATGG 344
OY 158 AGATAATTAACATCATAGTAAAGAGCAAGTGCATATTAATGTCATAGAGAGCATGT 217
Db 345 AGATAATTAACATCATAGTAAAGAGCAAGTGCATATTAATGTCATAGAGAGCATGT 404
OY 218 TTTTGCACATTTCCAGCCCTTTAAATATTCACACACAGAGCAAGCAAAAAGAGACAC 277
Db 405 TTTTGCACATTTCCAGCCCTTTAAATATTCACACACAGAGCAAGCAAAAAGAGACAC 464
OY 278 AGAGATCCCTGGGAGAAATGCGCGCCGCATCTTGCGTCATGATGAGCCTGCGCCTGT 337
Db 465 AGAGATCCCTGGGAGAAATGCGCGCCGCATCTTGCGTCATGATGAGCCTGCGCCTGT 524
OY 338 GCCTGTCCCGCTTGAGAGGAAGGACATTAAGAAATGAATGATGTGCTTAAAGCA 397
```



```
|||||
Db 525 GCGTGTCCGCTGTGAGGAGACATAGAAATGATGATGTTCTTAAAGA 584
Oy 398 TGGCGAGAAAACAGATCTGTTGATATTTATTTGACGGATTAACAGATTGAAT 457
Db 585 TGGCGAGAAAACAGATCTGTTGATATTTATTTGACGGATTAACAGATTGAAT 644
Oy 458 GAATGCACAAAGTGAGCTTACCAATGAGAGAAAACGAGAGAAATCTGATGGTT 517
Db 645 GAAGTCACAAAAGTGAGCTTACCAATGAGAGAAAACGAGAGAAATCTGATGGCTT 704
Oy 518 CACAAGACATCAACAAAATGAGATAGTATGATGATGAGAGCAGCCAGCTGGGG 577
Db 705 CACAAGACATCAACAAAATGAGATAGTATGATGATGAGAGCAGCCAGCTGGGG 764
Oy 578 AGAGATTAACACAGGGGAGAGGGTCAGAGATTGCGCCCTGCTGCTTAACCTGTCGTT 637
Db 765 AGGAGATTAACACAGGGGAGAGGGTCAGAGATTGCGCCCTGCTGCTTAACCTGTCGTT 824
Oy 638 ATAAACAAATGATTTCAATTTCTTAACCTCAAAAACAAAGCTGTTGATATCTGATCTC 697
Db 825 ATAAACAAATGATTTCAATTTCTTAACCTCAAAAACAAAGCTGTTGATATCTGATCTC 884
Oy 698 TACGGTTCCTTCTGGGGCCCAACATTTCTCATATATCCAGCCACTCTTTTATATTT 757
Db 885 TAGGGTTCCTTCTGGGGCCCAACATTTCTCATATATCCAGCCACTCTTTTATATTT 944
Oy 758 AGTTCCAGATCTGATCTGATCTTCTTACAGCTAGAAATTAACATTAATCTGATCTG 817
Db 945 AGTTCCAGATCTGATCTGATCTTCTTACAGCTAGAAATTAACATTAATCTGATCTG 1004
Oy 818 AAAGACCTTGTGCTGCTGCTTAATATGATGATGATGATGATGATGATGATGATG 877
Db 1005 AAAGACCTTGTGCTGCTGCTTAATATGATGATGATGATGATGATGATGATGATG 1064
Oy 878 GCCCAGGGGATCTGTAACAGGCTGGGAGAGATCTCAAGATCTTCCAGGGTATACTTA 937
Db 1065 GCCCAGGGGATCTGTAACAGGCTGGGAGAGATCTCAAGATCTTCCAGGGTATACTTA 1124
Oy 938 CTAGCACACAGATGATCTTACGAGGATTAATCTTAATCAACATCACTCTGATCTG 997
Db 1125 CTAGCACACAGATGATCTTACGAGGATTAATCTTAATCAACATCACTCTGATCTG 1184
Oy 998 TTGGCCATATGAAATTCATTTCCACTTTTGCCCACTTCCCAAGACCTCAAAATGCTCA 1057
Db 1185 TTGGCCATATGAAATTCATTTCCACTTTTGCCCACTTCCCAAGACCTCAAAATGCTCA 1244
Oy 1058 TTCCATTAATATCAACAGATTAATCTTTTAACTGGAAGATTAATGATGATGATG 1117
Db 1245 TTCCATTAATATCAACAGATTAATCTTTTAACTGGAAGATTAATGATGATGATG 1304
Oy 1118 CAGCATATGGAATTAATTAACATATTTGTTTCCAGTGAACAGATGATGATGATG 1177
Db 1305 CAGCATATGGAATTAATTAACATATTTGTTTCCAGTGAACAGATGATGATGATG 1364
Oy 1178 TCCCTCCCTTGTGTTGATTTTTCAGATATAAGTAAATGCTGATGATGATG 1237
Db 1365 TCCCTCCCTTGTGTTGATTTTTCAGATATAAGTAAATGCTGATGATGATG 1424
Oy 1238 AGGCTGTATACAGACAGCTCTCCCATCCCTCAGCTTATCTGATCAGATCAGTCAAC 1297
Db 1425 AGGCTGTATACAGACAGCTCTCCCATCCCTCAGCTTATCTGATCAGATCAGTCAAC 1484
Oy 1298 CCGTCCCATATNSACCTAAACAAATCTTAATCTTGAATGATGATGATGATG 1357
Db 1485 CCGTCCCATATNSACCTAAACAAATCTTAATCTTGAATGATGATGATGATG 1544
Oy 1358 ATTTTCTCTGCTGAGAGCTCTCTGCTGCTTAATNTAGATGATGATGATG 1417
Db 1545 ATTTTCTCTGCTGAGAGCTCTCTGCTGCTTAATNTAGATGATGATGATG 1604
Oy 1418 TTGATTAAGTACTATCTTACTTATGCAAAAGGAGACATGATGATGATGATG 1477
|||||
```

```
Db 1605 TTGAATAGTGTACTATCTTACTTCAATGCAAAAGGACACATATGATGATTCATCA 1664
Oy 1478 CATGACACACAAATCTTAAGTCTAATTTGATTAATAGAGTTTATGATTAATATGAA 1537
Db 1665 CATGACACACAAATCTTAAGTCTAATTTGATTAATAGAGTTTATGATTAATATGAA 1724
Oy 1538 ATGCAAGKCCACACAGGGAATGTTATGGGACGTTTGAAGCTGGGATGTAAGA 1597
Db 1725 ATGCAAGKCCACACAGGGAATGTTATGGGACGTTTGAAGCTGGGATGTAAGA 1784
Oy 1598 AAGCAGGGAACCTTATGATATCTTAATATATCTTCAATTTCTTATCTTATACAA 1657
Db 1785 AAGCAGGGAACCTTATGATATCTTAATATATCTTCAATTTCTTATCTTATACAA 1844
Oy 1658 TATCCACACAGCTTTTCAACAGATTCATGACAGTGAATTCGCCAAGSTAACTTATCC 1717
Db 1845 TATCCACACAGCTTTTCAACAGATTCATGACAGTGAATTCGCCAAGSTAACTTATCC 1904
Oy 1718 ATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1777
Db 1905 ATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1964
Oy 1778 TGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1837
Db 1965 TGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2024
Oy 1838 AGGTTCACTCTCTGCAATTAAGATTTTACAAGA 1872
Db 2025 AGGTTCACTCTCTGCAATTAAGATTTTACAAGA 2059

RESULT 4
AAS64026
ID AAS64026 standard; cDNA; 3923 BP.
XX
AC AAS64026;
XX
DT 29-JAN-2002 (first entry)
XX
DE Human cDNA encoding DD3.
XX
KW Human; prostate cancer; ss; cytosolic; immunostimulant; tumour.
XX
OS Homo sapiens.
XX
PN WO200173032-A2.
XX
PD 04-OCT-2001.
XX
PE 27-MAR-2001; 2001WO-US09919.
XX
PR 27-MAR-2000; 2000US-0536857.
XX
PR 09-MAY-2000; 2000US-0568100.
XX
PR 12-MAY-2000; 2000US-0570737.
XX
PR 13-JUN-2000; 2000US-0593793.
XX
PR 27-JUN-2000; 2000US-0605783.
XX
PR 10-AUG-2000; 2000US-0636215.
XX
PR 29-AUG-2000; 2000US-0651236.
XX
PR 06-SEP-2000; 2000US-0657279.
XX
PR 02-OCT-2000; 2000US-0679426.
XX
PR 10-OCT-2000; 2000US-0685166.
XX
PA (CORI-) CORIXA CORP.
XX
PI Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Kalos MD;
PI Fanger GR, Retter MW, Stolk JA, Day CH, Vedvick TS, Carter D;
PI Li SX, Wang A, Skelky YAM, Hepler WT, Henderson RA;
XX
DR WPI: 2001-639232/73.
XX
PT New human prostate-specific polypeptides and polynucleotides useful for
XX the diagnosis and treatment of cancer, especially prostate cancer -
```

PS Claim 1; Page 473-474; 579pp; English.
XX The invention relates to isolated prostate-specific
CC polynucleotides, polypeptides, fusion proteins of the polypeptides,
CC antibodies raised against the polypeptides (or antigenic epitopes
CC derived from them) and antigen-presenting cells expressing the
CC polypeptides. The antibodies are useful for detecting the presence of
CC cancer, especially prostate cancer. The polypeptides, polynucleotides and
CC the antigen-presenting cells are useful for stimulating and/or expanding
CC T cells specific for a tumour protein, and for inhibiting the development
CC of cancer especially prostate cancer. Compositions comprising the
CC polynucleotide and/or polypeptide are useful for stimulating an immune
CC response, and for treating cancer. The oligonucleotide is useful for
CC detecting cancer. The present sequence is a prostate specific
CC polynucleotide of the invention.
XX
Sequence 3923 BP; 1157 A; 840 C; 740 G; 1186 T; 0 other;
Query Match 73.08; Score 1367; DB 22; Length 3923;
Best Local Similarly 99.58; Pred. No. 0;
Matches 1767; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
QY 98 GGTGAGAAATTAAGAAAGGCTGCTGACTTACCATCTGAGGCCACACATCTGCTGAATGG 157
DB 285 GGTGAGAAATTAAGAAAGGCTGCTGACTTACCATCTGAGGCCACACATCTGCTGAATGG 344
QY 158 AGATAATTAACATCACTAGAAAGAGAGAGATGACATATATATGCTAAGTAGTACATGT 217
DB 345 AGATAATTAACATCACTAGAAAGAGAGATGACATATATATGCTAAGTAGTACATGT 404
QY 218 TTTTGCACATTTCCAGCCCTTTAATATTCACACACACAGAGAAAGCAAAAGAGACAC 277
DB 405 TTTTGCACATTTCCAGCCCTTTAATATTCACACACACAGAGAAAGCAAAAGAGACAC 464
QY 278 AGAGATCCCTGGGAGAAATGCGCGCCGATCTGGTCATGATGATGAGCTGCGCTGT 337
DB 465 AGAGATCCCTGGGAGAAATGCGCGCCGATCTGGTCATGATGATGAGCTGCGCTGT 524
QY 338 GCGCTGTGCGCGCTGTGAGGAGAGAGATGAGAAATGATGATGCTTCTTAAGA 397
DB 525 GCGCTGTGCGCGCTGTGAGGAGAGAGATGAGAAATGATGATGCTTCTTAAGA 584
QY 398 TGGGCGAGAAACAGATCCCTGTTGTGATTTTATTTGAACGGGATTACAGATTTGAAT 457
DB 585 TGGGCGAGAAACAGATCCCTGTTGTGATTTTATTTGAACGGGATTACAGATTTGAAT 644
QY 458 GAAGTCACAAGTGAGCATTAACCAATGAGAGAAACAGAGAAATCTTGATGCTT 517
DB 645 GAAGTCACAAGTGAGCATTAACCAATGAGAGAAACAGAGAAATCTTGATGCTT 704
QY 518 CACAGACATGCAACAAACAAATGAATAGTGTGATGATGAGAGAGCAAGCTGGG 577
DB 705 CACAGACATGCAACAAACAAATGAATAGTGTGATGATGAGAGAGCAAGCTGGG 764
QY 578 AGAGATTAACAGAGGCGCAAGAGGTGAGATTTCTGGCCCTGCTGCTAACTGTGCTTC 637
DB 765 AGAGATTAACAGAGGCGCAAGAGGTGAGATTTCTGGCCCTGCTGCTAACTGTGCTTC 824
QY 638 ATAAACCAATCATTTCTATTTCTAAACCTCAAAACAAAGCTGTTGAATATCTGATCTC 697
DB 825 ATAAACCAATCATTTCTATTTCTAAACCTCAAAACAAAGCTGTTGAATATCTGATCTC 884
QY 698 TAGGTTCTCTTGGGCGCAACATTCATATATCCAGCCAGCACTATTTTAATTTT 757
DB 885 TAGGTTCTCTTGGGCGCAACATTCATATATCCAGCCAGCACTATTTTAATTTT 944
QY 758 AGTTCCAGATCTGCTACTGTGACCTTTCTACACTGTAAGATTAACATTTACATTTGCTTC 817
DB 945 AGTTCCAGATCTGCTACTGTGACCTTTCTACACTGTAAGATTAACATTTACATTTGCTTC 1004
QY 818 AAAGACCTTCTGTTGCTGCTAATATGATGATGATGATGATGATGATGATGATGATGATG 877
DB 1005 AAAGACCTTCTGTTGCTGCTAATATGATGATGATGATGATGATGATGATGATGATGATG 1064

QY 878 GCCAGGGATCTGTGAACAGAGCTGGAGACATCTCAAGATCTTTCCAGGGTTATACTTA 937
DB 1065 GCCAGGGATCTGTGAACAGAGCTGGAGACATCTCAAGATCTTTCCAGGGTTATACTTA 1124
QY 938 CTAGACACAGCATGATCATTAAGAGATTAATCTAATCAACATCATCTGATGCTT 997
DB 1125 CTAGACACAGCATGATCATTAAGAGATTAATCTAATCAACATCATCTGATGCTT 1184
QY 998 TTGGCCATCTGAATTCATTTCCCATTTTGGCCCATCTCTCAAGACCTCAAAATGTCA 1057
DB 1185 TTGGCCATCTGAATTCATTTCCCATTTTGGCCCATCTCTCAAGACCTCAAAATGTCA 1244
QY 1058 TTCCATTAATATCAAGATTAATCTTTTAAACCTGGAAGAAATTCATGTTACATG 1117
DB 1245 TTCCATTAATATCAAGATTAATCTTTTAAACCTGGAAGAAATTCATGTTACATG 1304
QY 1118 CAGCTATGGAAATTAATTAATATTTGTTTCCAGTGCAGAAAGATGACTAATCTTTA 1177
DB 1305 CAGCTATGGAAATTAATTAATATTTGTTTCCAGTGCAGAAAGATGACTAATCTTTA 1364
QY 1178 TTCCCTCCCTTGTGATTTTTCACATTAATGCTTAAGCTTACCTGTATCTG 1237
DB 1365 TTCCCTCCCTTGTGATTTTTCACATTAATGCTTAAGCTTACCTGTATCTG 1424
QY 1238 AGGCTGTATACAGACAGCCCTCCCATCCCTCCAGCTTATCTGATCACCATCAAC 1297
DB 1425 AGGCTGTATACAGACAGCCCTCCCATCCCTCCAGCTTATCTGATCACCATCAAC 1484
QY 1298 CCTCCCATTTTSACTTAACAAATCTAATCTGTAATCTCTTGAACATGTCAGAGCATAC 1357
DB 1485 CCTCCCATTTTSACTTAACAAATCTAATCTGTAATCTCTTGAACATGTCAGAGCATAC 1544
QY 1358 ATTATTCCTTCTGCTGAGAGAGCTCTCCCTGCTCTTAATCTAGATGATGATGATG 1417
DB 1545 ATTATTCCTTCTGCTGAGAGAGCTCTCCCTGCTCTTAATCTAGATGATGATGATG 1504
QY 1418 TTGAATTAAGTTGACTATCTACTTATCTATGATGAGAGAGACATATGATGATGATG 1477
DB 1605 TTGAATTAAGTTGACTATCTACTTATCTATGATGAGAGAGACATATGATGATGATG 1664
QY 1478 CATGAGACAGCAATTAATTAAGTGTATTTGATTTATGAGATTTGATTAATATGAA 1537
DB 1665 CATGAGACAGCAATTAATTAAGTGTATTTGATTTATGAGATTTGATTAATATGAA 1724
QY 1538 ATGCAAGACACAGAGAGAGATTTATGAGGAGACGCTTGTAGAGCTGGATGTAAGAA 1597
DB 1725 ATGCAAGACACAGAGAGAGATTTATGAGGAGACGCTTGTAGAGCTGGATGTAAGAA 1784
QY 1598 AAGGACAGGAACTCATATGATCTTAATTAATTAATTAATTAATTAATTAATTAAT 1657
DB 1785 AAGGACAGGAACTCATATGATCTTAATTAATTAATTAATTAATTAATTAATTAAT 1844
QY 1658 TATCCAAACAGCTTTTACAGAAATTCATGAGAGTCAATCCCAAGAGTAACTTATTC 1717
DB 1845 TATCCAAACAGCTTTTACAGAAATTCATGAGAGTCAATCCCAAGAGTAACTTATTC 1904
QY 1718 ATTTCATGCTGATGCTGCTTAAATTTTGGCAAAATCACTGCTACTATCTCAACTT 1777
DB 1905 ATTTCATGCTGATGCTGCTTAAATTTTGGCAAAATCACTGCTACTATCTCAACTT 1964
QY 1778 TGAGATGTGTTTGTCTTGTAGTTAATGGAAGAAATAGGCACTTGTGAGCACTTT 1837
DB 1965 TGAGATGTGTTTGTCTTGTAGTTAATGGAAGAAATAGGCACTTGTGAGCACTTT 2024
QY 1838 AGGCTTCACTCCCTGGCAATTAAGAAATTTACAAAGA 1872
DB 2025 AGGCTTCACTCCCTGGCAATTAAGAAATTTACAAAGA 2059
RESULT 5
AAH93861
ID AAH93861 standard; cdna: 3923 BP.

XX AAH93861;
AC 04-OCT-2001 (first entry)
DT XX
DE Gene DD3 cDNA sequence.
XX Human: prostate cancer: prostate-specific; diagnosis; vaccine;
KM cytosolic; gene therapy; metastasis; ss.
XX
OS Homo sapiens.
XX WO200151633-A2.
XX 19-JUL-2001.
XX
XX 16-JAN-2001; 2001WO-US01574.
XX 14-JAN-2000; 2000US-0483672.
XX (CORI-) CORIXA CORP.
XX Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Reed SG;
PI Kalos MD, Fanger GR, Day CH, Retter MW, Stolk JA, Skeiky YAW;
PI Wang A, Meagher MJ;
XX WPI: 2001-425873/45.
XX
XX New polynucleotide encoding a prostate-specific protein, for
PT diagnosing, monitoring and treating prostate cancer in a patient and
PT for use in vaccines -
XX
XX
XX Claim 1: Page 452-453; 543pp; English.
XX
XX The present invention describes polynucleotide sequences (I) which encode
CC prostate-specific proteins (II). (I) and (II) have cytostatic activity,
CC and can be used in vaccine production and gene therapy. (I), (II),
CC antibodies to (II), fusion proteins comprising (II), and isolated
CC T cells prepared using (I) or (II) are used treat cancer in a patient.
CC (I) and the antibodies are also used in the detection of cancer in a
CC patient. The cancer that is diagnosed or treated is particularly
CC prostate cancer. (I) and (II) can be used in vaccines. The antibodies or
CC (I) can be used for monitoring the progression of cancer in a patient.
CC (I) and (II) can also be used to improve diagnostic and therapeutic
CC methods for prostate cancer. They can indicate the level of metastasis
CC as well as the prostate volume. AAH93357 to AAH93944 and AAH01115 to
CC AAH01318 represent polynucleotide and amino acid sequences used in the
CC exemplification of the present invention.
XX
XX Sequence 3923 BP; 1157 A; 840 C; 740 G; 1186 T; 0 other;
SQ

Query Match 73.0%; Score 1367; DB 22; Length 3923;
Best Local Similarity 99.5%; Pred. No. 0;
Matches 1767; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Db 525 GCCTGTCGCCGCTTGAGAGGAGACATTAGAAATGAATTGATGTCTCTTAAGCA 584
QY 398 TGGGAGAGAAAAACAGATCCTGTGTGATATTATTGAAGGGATTACAGATTGAAAT 457
Db 585 TGGGAGAGAAAAACAGATCCTGTGTGATATTATTGAAGGGATTACAGATTGAAAT 644
QY 458 GAAAGTCACAAAGTGGAGCATTTACCATGAGAGAAACAGAGAAAAATCTTGATGGCT 517
Db 645 GAAAGTCACAAAGTGGAGCATTTACCATGAGAGAAACAGAGAAAAATCTTGATGGCT 704
QY 518 CACAAGACATGCACAAACAAATGAAATGATCTGTGATGACATGAGCAGCCAAAGCTGGGG 577
Db 705 CACAAGACATGCACAAACAAATGAAATGATCTGTGATGACATGAGCAGCCAAAGCTGGGG 764
QY 578 AGGAGATTAACCAAGGGGAGAGAGGTCTGAGGCTGTGCTTAACTGTCCGTTTC 637
Db 765 AGGAGATTAACCAAGGGGAGAGAGGTCTGAGGCTGTGCTTAACTGTCCGTTTC 824
QY 638 ATTAACCAATGATTTTCATATTCTTAACCTCAAAACAAAGGTTGTAATATCTGATGTC 697
Db 825 ATTAACCAATGATTTTCATATTCTTAACCTCAAAACAAAGGTTGTAATATCTGATGTC 884
QY 698 TAAGGTTCTCTTGGGCCCAACATTTCCATATATCCAGCCACACTATTTTAAATATT 757
Db 885 TAAGGTTCTCTTGGGCCCAACATTTCCATATATCCAGCCACACTATTTTAAATATT 944
QY 758 AGTTCCAGATCTGACTGTGACCTTTTACACTAGAAATACATTTACTATTTTGTTC 817
Db 945 AGTTCCAGATCTGACTGTGACCTTTTACACTAGAAATACATTTACTATTTTGTTC 1004
QY 818 AAAGACCTTGCTGTGGCTGCTAATATGAGCTGACAGCTTTTCCAGAGAGCTGTG 877
Db 1005 AAAGACCTTGCTGTGGCTGCTAATATGAGCTGACAGCTTTTCCAGAGAGCTGTG 1064
QY 878 GCCCAGGGGATCTGACAGAGCTGGGAGACATCCAAGATCTTCCAGGGTTATATCTTA 937
Db 1065 GCCCAGGGGATCTGACAGAGCTGGGAGACATCCAAGATCTTCCAGGGTTATATCTTA 1124
QY 938 CTAGACACAGATATATATGAGAGGAAATATCTATCAACATCTCATCTGCT 997
Db 1125 CTAGACACAGATATATATGAGAGGAAATATCTATCAACATCTCATCTGCT 1184
QY 998 TTGCCATACGAAATTCATTTCCCATTTTGGCCATTTCCAGACCTCAAAATGTC 1057
Db 1185 TTGCCATACGAAATTCATTTCCCATTTTGGCCATTTCCAGACCTCAAAATGTC 1244
QY 1058 TTGCATTAATACAGAGATTAACTTTTAACTGGAAGAAATTCATGTTACATG 1117
Db 1245 TTGCATTAATACAGAGATTAACTTTTAACTGGAAGAAATTCATGTTACATG 1304
QY 1118 CAGCTATGGGAATTTAATTACATATTTGTTTCCAGTGCACAAAGATGACTAAGTCTTTA 1177
Db 1305 CAGCTATGGGAATTTAATTACATATTTGTTTCCAGTGCACAAAGATGACTAAGTCTTTA 1364
QY 1178 TCCCTGCCCTTGTGATTTTTCAGAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGT 1237
Db 1365 TCCCTGCCCTTGTGATTTTTCAGAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGT 1424
QY 1238 AGGCTGTAAACAGACACCTCTCCCAATCCCTCAGGCTTATCTGTATCCATCCATCAC 1297
Db 1425 AGGCTGTAAACAGACACCTCTCCCAATCCCTCAGGCTTATCTGTATCCATCCATCAC 1484
QY 1298 CCCTCCATNTSACCTAAACAAATCTAATCTTAATCTTTGAACATGTGAGNCATAC 1357
Db 1485 CCCTCCATNTSACCTAAACAAATCTAATCTTTGAACATGTGAGNCATAC 1544
QY 1358 ATTTTCTCTGCTGGAAGAGCTCTCTCTCTCTTAANTCTGATGATGATGATGATGAT 1417
Db 1545 ATTTTCTCTGCTGGAAGAGCTCTCTCTCTCTTAANTCTGATGATGATGATGATGAT 1604
QY 1418 TTGAATTAAGTGAATATCTTACTTTCACAAAGAGGACATATGAGATTTCATCATCA 1477
Db 1605 TTGAATTAAGTGAATATCTTACTTTCACAAAGAGGACATATGAGATTTCATCATCA 1664

QY 1478 CATGACACCAATACTATAAGTGTATTTGATTATAGAGTTTACATAAATATATGAA 1537
|||
DB 1665 CATGAGACCAATACTATAAGTGTATTTGATTATAGAGTTTACATAAATATATGAA 1724
|||
QY 1538 ATGCAGACACCAAGAGGGAATGTTATGGGCGACGTTTAAAGCTGGATGTGAAGA 1597
|||
DB 1725 ATCCAAAGCCACAGAGGGAATGTTATGGGCGACGTTTAAAGCTGGATGTGAAGA 1784
|||
QY 1598 AAGGACGGAACCTCATAGTATCTTATATATATCTTCTATCTATCTATCAAA 1657
|||
DB 1785 AAGGACGGAACCTCATAGTATCTTATATATATCTTCTATCTATCTATCAAA 1844
|||
QY 1658 TATCCAAAGAGCTTTTACAGAAATTCATGAGTGAATCCCAAGAGTAACCTTATCC 1717
|||
DB 1845 TATCCAAAGAGCTTTTACAGAAATTCATGAGTGAATCCCAAGAGTAACCTTATCC 1904
|||
QY 1718 ATTTCATGTGATGGCTTTAGAAATTTGGCAAAATATCTGTCTATCTATCAACTT 1777
|||
DB 1905 ATTTCATGTGATGGCTTTAGAAATTTGGCAAAATATCTGTCTATCTATCAACTT 1964
|||
QY 1778 TCAGATGTGTTTCTCTTGTAGTTAATTTGAAGAATAGGCGACTTGTGAGCGCACTT 1837
|||
DB 1965 TCAGATGTGTTTCTCTTGTAGTTAATTTGAAGAATAGGCGACTTGTGAGCGCACTT 2024
|||
QY 1838 AGGCTTACTCTGCGCAATTAAGAATTTTACAAAGA 1872
|||
DB 2025 AGGCTTACTCTGCGCAATTAAGAATTTTACAAAGA 2059
|||

RESULT 6

ABK92196 ID ABK92196 standard; DNA; 3923 BP.

XX AC ABK92196;

XX DT 15-AUG-2002 (first entry)

XX DE Prostate cancer-associated DNA sequence #82.

XX KM Prostate cancer; prostate tumour tissue; human; mammal; cytostatic;

XX KM gene therapy; gene; ds.

XX OS Mammalia.

XX PN W0200230268-A2.

XX PD 18-APR-2002.

XX PF 12-OCT-2001; 2001WO-US32045.

XX PR 13-OCT-2000; 2000US-0687576.

XX PR 08-DEC-2000; 2000US-0733288.

XX PR 08-DEC-2000; 2000US-0733288.

XX PR 24-JAN-2001; 2001US-263957P.

XX PR 15-MAR-2001; 2001US-276791P.

XX PR 06-APR-2001; 2001US-276888P.

XX PR 24-APR-2001; 2001US-286214P.

XX PR 30-APR-2001; 2001US-0847046.

XX PR 04-MAY-2001; 2001US-288589P.

XX PA (EOSB-) EOS BIOTECHNOLOGY INC.

XX PI Gish KC, Mack DH, Wilson KE, Afari D, Hevezi P;

XX DR WPI; 2002-471335/50.

XX PT Detecting a prostate cancer-associated transcript in a cell in a

XX PT patient, useful for diagnosing prostate cancer (PC) or screening

XX PT modulators of PC, by determining if prostate cancer-associated genes

XX PT are expressed in a prostate tissue

PS Claim 22; Page 365-366; 436bp; English.
XX
CC The present invention relates to methods of detecting a prostate
CC cancer-associated transcript in a cell from a patient. The method
CC comprises contacting a biological sample from the patient with
CC prostate cancer-associated polynucleotides (designated PC genes) that
CC selectively hybridise to a sequence that is at least 80% identical
CC to them. The prostate cancer-associated polynucleotide sequences
CC are differentially expressed in prostate tumour tissue or in
CC prostate cancer and are derived from the tissues of various
CC organisms such as humans or other mammals (e.g. mice, sheep and dogs).
CC The methods of the invention are useful for diagnosing and treating
CC prostate cancer in mammals. The prostate cancer-associated genes are
CC useful for diagnosing or treating prostate cancer, as well as for
CC identifying modulators of prostate cancer or agents that inhibit
CC prostate cancer. The nucleic acid sequences are particularly useful
CC in gene therapy, as a vaccine or in antisense applications.
CC ABK92115-ABK92263 represent prostate cancer-associated polynucleotide
CC sequences.
XX
SQ Sequence 3923 BP; 1157 A; 840 C; 740 G; 1186 T; 0 other;

Query Match 73.0%; Score 1367; DB 24; Length 3923;
Best Local Similarity 99.5%; Pred. No. 0;
Matches 1767; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 98 GGTGAGAAATTAAGAAAGCTGCTGACTTTCATCTGAGGCGCACATCTGCGAAATGG 157
|||
DB 285 GGTGAGAAATTAAGAAAGCTGCTGACTTTCATCTGAGGCGCACATCTGCGAAATGG 344
|||
QY 158 AGATTAATTAACATCACTAGAAACGACAGATGACATATATGTCTTAAGTAGACATGT 217
|||
DB 345 AGATTAATTAACATCACTAGAAACGACAGATGACATATATGTCTTAAGTAGACATGT 404
|||
QY 218 TTTTGCACATTTCCAGCCCTTTAAATATCCACACACAGGAGCAACAAAGAAAGCAC 277
|||
DB 405 TTTTGCACATTTCCAGCCCTTTAAATATCCACACACAGGAGCAACAAAGAAAGCAC 464
|||
QY 278 AGAGATCCCTGGGAGAAATGCCGCCCATCTTGGCTCATCATGAGCCCTGCTG 337
|||
DB 465 AGAGATCCCTGGGAGAAATGCCGCCCATCTTGGCTCATCATGAGCCCTGCTG 524
|||
QY 338 GCCTGCTCCCGCTTTGAGGAGAAAGGACATTAGAAATGAATATATGTCTTAAAGA 397
|||
DB 525 GCCTGCTCCCGCTTTGAGGAGAAAGGACATTAGAAATGAATATATGTCTTAAAGA 584
|||
QY 398 TGGGCAAGAAACAGATCTGTTGTGAGATTTATTTGAACGCGATTACAGATTTGAAT 457
|||
DB 585 TGGGCAAGAAACAGATCTGTTGTGAGATTTATTTGAACGCGATTACAGATTTGAAT 644
|||
QY 458 GAAGTCACAAAGTGAGCATTACCAATGAGAGAAACAGACGAGAAATCTTGATGCTT 517
|||
DB 645 GAAGTCACAAAGTGAGCATTACCAATGAGAGAAACAGACGAGAAATCTTGATGCTT 704
|||
QY 518 CACAAGACATGCAACAAACAAATGGAATCTGTGATGACATGAGGACGCAAGCTGGGG 577
|||
DB 705 CACAAGACATGCAACAAACAAATGGAATCTGTGATGACATGAGGACGCAAGCTGGGG 764
|||
QY 578 AGGAGATTAACCAAGGCGGAGAGGATGAGATTTGCGCCCTGCTTAAACTGTGCTTC 637
|||
DB 765 AGGAGATTAACCAAGGCGGAGAGGATGAGATTTGCGCCCTGCTTAAACTGTGCTTC 824
|||
QY 638 ATAACCAAAATCATTTATATTTCTAAACCTCAAAACAAAGCTTGTATATGTGATCTC 697
|||
DB 825 ATAACCAAAATCATTTATATTTCTAAACCTCAAAACAAAGCTTGTATATGTGATCTC 884
|||
QY 698 TAGGTTCTTCTGGGCGGCAACATTTCTCCATATATCCAGCAGCATTTTAAATATTT 757
|||
DB 885 TAGGTTCTTCTGGGCGGCAACATTTCTCCATATATCCAGCAGCATTTTAAATATTT 944
|||
QY 758 AGTTCCAGATCTGTAAGTGTGACCTTTCTACACTGAGAAATTAACATTTACTTTTCTTC 817
|||
DB 945 AGTTCCAGATCTGTAAGTGTGACCTTTCTACACTGAGAAATTAACATTTACTTTTCTTC 1004
|||

QY	818	AAAAACCCCTTGTTGCTGGCTAATAATAGTAGCTGACCTGTTTTTTCCTAAGAAGTCTCTG	877
Db	1005	AAAACACCCCTTGTTGCTGGCTAATAATAGTAGCTGACCTGTTTTTTCCTAAGAAGTCTCTG	1064
QY	878	GCCCAAGGGAGTCTGTGAACAGGCTGAGGAGACATCTCAAGATCTTCTCCAGGCTATATCTTA	937
Db	1065	GCCCAAGGGAGTCTGTGAACAGGCTGAGGAGACATCTCAAGATCTTCTCCAGGCTATATCTTA	1122
QY	938	CTAGCACACAGCATGATCATTACGGAGTGAATTATCTAATCAACATCTCCAGTGTCT	997
Db	1125	CTAGCACACAGCATGATCATTACGGAGTGAATTATCTAATCAACATCTCCAGTGTCT	1184
QY	998	TTGGCCCAATACGAATTCATTCCCACTTTGTGGCCCTTTCGCAAGACCTCAAAATGTCA	1057
Db	1185	TTGGCCCAATACGAATTCATTCCCACTTTGTGGCCCTTTCGCAAGACCTCAAAATGTCA	1244
QY	1058	TTCCATTAAATATACAGAGATTAACTTTTTTTTTTAACCTGGAGAAATTCATATGTATCATG	1117
Db	1245	TTCCATTAAATATACAGAGATTAACTTTTTTTTTTAACCTGGAGAAATTCATATGTATCATG	1304
QY	1118	CAGCTATGGGAATTTAATTACATATTTTGTTTTCCAGTGCAGAAAGATCTAAGTCTTTTA	1177
Db	1305	CAGCTATGGGAATTTAATTACATATTTTGTTTTCCAGTGCAGAAAGATCTAAGTCTTTTA	1364
QY	1178	TTCCCTCCCTTTGTTGATTTTTTTTTTCCAGATATAAAGTTAAATGCTTAGCCTGTACTG	1237
Db	1365	TTCCCTCCCTTTGTTGATTTTTTTTTTCCAGATATAAAGTTAAATGCTTAGCCTGTACTG	1422
QY	1238	AGGCTGTATACAGACAGAGCTCTCCCAATCCCTCAGGCTTATGTGCATACCATCAAC	1297
Db	1425	AGGCTGTATACAGACAGAGCTCTCCCAATCCCTCAGGCTTATGTGCATACCATCAAC	1484
QY	1298	CCCTCCCAATNNSACCTTAACAAATNCTAATCTGTAAATCTCTGTAACATCTCAGGACATAC	1357
Db	1485	CCCTCCCAATNNSACCTTAACAAATNCTAATCTGTGTAAATCTCTGTAACATCTCAGGACATAC	1544
QY	1358	ATTATTCCCTCTGCGCTGAGAAAGCTCTTCCTGCTCTTAANTCTAAGATGTATGAATTT	1417
Db	1545	ATTATTCCCTCTGCGCTGAGAAAGCTCTTCCTGCTCTTAANTCTAAGATGTATGAATTT	1604
QY	1418	TTGATTAATAGTTGACTATCTTACTTCATGCAAAAGAGGACACATATGAGATTCAATCA	1477
Db	1605	TTGATTAATAGTTGACTATCTTACTTCATGCAAAAGAGGACACATATGAGATTCAATCA	1664
QY	1478	CATGAGACAGAAATACTAAAGGTAAATTTGATTAATATAGAGTTAGATTAATATATGAA	1537
Db	1665	CATGAGACAGAAATACTAAAGGTAAATTTGATTAATATAGAGTTAGATTAATATATGAA	1724
QY	1538	ATGCAAGAKCCACAGAGGGAATGTTTATGGGGACGTTTGTAAAGCCTGGAGTGTGAAMA	1597
Db	1725	ATGCAAGAGCCACAGAGGGAATGTTTATGGGGACGTTTGTAAAGCCTGGAGTGTGAAMA	1784
QY	1598	AAGGCAGAGGAACCATAGTATCTTATATATAATATCTCATCTTCATCTCATACAA	1657
Db	1785	AAGGCAGAGGAACCATAGTATCTTATATATAATATCTCATCTTCATCTCATACAA	1844
QY	1658	TATCAACAACAGCTTTTACAGAAATTCATGAGTGCCAATCCCAAGGTAAACCTTTATCC	1717
Db	1845	TATCAACAACAGCTTTTACAGAAATTCATGAGTGCCAATCCCAAGGTAAACCTTTATCC	1904
QY	1718	ATTTCAGAGGACAGGCTTTTAAAGAAATTTGGCAATCATATGCTGACTATATCAACTT	1777
Db	1905	ATTTCAGAGGACAGGCTTTTAAAGAAATTTGGCAATCATATGCTGACTATATCAACTT	1964
QY	1778	TGAGATGTGTTTGTCTCTGTAGTAAATTTGAAGAATAAGGCACTCTGTATAGCACACTT	1837
Db	1965	TGAGATGTGTTTGTCTCTGTAGTAAATTTGAAGAATAAGGCACTCTGTATAGCACACTT	2024
QY	1838	AGGCTTACATCTCTGGCAATTAAGAATTTACAAAG	1872
Db	2025	AGGCTTACATCTCTGGCAATTAAGAATTTACAAAG	2059

RESULT 7	
ABL95397	
ID	ABL95397 standard; cDNA: 3923 BP.
XX	
AC	ABL95397;
XX	
DT	19-JUL-2002 (first entry)
XX	
DE	
XX	Human DD3 cDNA sequence SEQ ID NO 690.
KM	Human; cancer; prostate cancer; vaccine; cytostatic; immunostimula
XX	gene therapy; gene; ss.
XX	
OS	Homo sapiens.
XX	
PN	US200202248-A1.
XX	
PD	21-FEB-2002.
XX	
PF	
XX	12-JAN-2001; 2001US-0759143.
XX	
PR	25-FEB-1997; 97US-0806099.
PR	01-AUG-1997; 97US-0904804.
PR	09-FEB-1998; 98US-0000956.
PR	25-FEB-1998; 98US-0030607.
PR	14-JUL-1998; 98US-0115453.
PR	23-SEP-1998; 98US-0159812.
PR	15-JAN-1999; 99US-0232149.
PR	09-APR-1999; 99US-0288946.
PR	13-JUL-1999; 99US-0352616.
PR	12-NOV-1999; 99US-0439313.
PR	18-NOV-1999; 99US-0443686.
PR	14-JAN-2000; 2000US-0483672.
PR	27-MAR-2000; 2000US-0536857.
PR	09-MAY-2000; 2000US-0568100.
PR	12-MAY-2000; 2000US-0570737.
PR	13-JUN-2000; 2000US-0593793.
PR	27-JUN-2000; 2000US-0605783.
PR	10-AUG-2000; 2000US-0636215.
PR	29-AUG-2000; 2000US-0651236.
PR	06-SEP-2000; 2000US-0657279.
PR	02-OCT-2000; 2000US-0679426.
PR	10-OCT-2000; 2000US-0685166.
XX	
PA	(XUJ/) XU J.
PA	(DILL/) DILLON D C.
PA	(MITC/) MITCHAM J L.
PA	(HARL/) HARLOCKER S L.
PA	(JTAN/) JTANG Y.
PA	(KALO/) KALOS M D.
PA	(FANG/) FANGER G R.
PA	(RETT/) RETTER M W.
PA	(STOL/) STOLK J A.
PA	(DAYC/) DAY C H.
PA	(VEDV/) VEDVICK T S.
PA	(CART/) CARTER D.
PA	(LISX/) LI S X.
PA	(WANG/) WANG A.
PA	(SKEI/) SKEIKY Y A W.
PA	(HEPL/) HEPLER W T.
PA	(HEND/) HENDERSON R A.
XX	
PI	Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jtang Y, Kalos MD;
PI	Fanger GR, Retter SM, Stolk JA, Day CH, Vedvick TS, Carter D;
PI	Li SX, Wang A, Skeiky YAW, Hepler WR, Henderson RA;
XX	
DR	WPI: 2002-255649/30.
XX	
PT	New prostate-specific polynucleotides for diagnosing and treating
PT	diseases, in particular prostate cancer, and as markers for the
PT	progression of cancer
XX	

PS Claim 1; SEQ ID NO 690; 87bp; English.

CC The present invention provides prostate-specific coding sequences and
CC their encoded proteins. These can be used in the diagnosis and treatment
CC of cancers, particularly prostate cancer. The present sequence is a cDNA
CC described in the invention.

XX Sequence 3923 BP; 1157 A; 840 C; 740 G; 1186 T; 0 other;

Query Match 73.0%; Score 1367; DB 24; Length 3923;

Best local similarity 99.5%; Pred. No. 0;

Matches 1767; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

```
QY 98 GGTGAGAAATTAAGAAAGGCTGCTGACCTTTACCATCTAGGCCACACATCTGCTGAATGG 157
DB 285 GGTGAGAAATTAAGAAAGGCTGCTGACCTTTACCATCTAGGCCACACATCTGCTGAATGG 344
QY 158 AGATAATTAACATCACTAGAAACAGCAAGATGACAAATATATGCTAAGTAGACATGT 217
DB 345 AGATAATTAACATCACTAGAAACAGCAAGATGACAAATATATGCTAAGTAGACATGT 404
QY 218 TTTTGCACATTTCCAGCCCTTTAAATATCCACACACAGCAAGCAAAAGGAAAGCAC 277
DB 405 TTTTGCACATTTCCAGCCCTTTAAATATCCACACACAGCAAGCAAAAGGAAAGCAC 464
QY 278 AGAGATCCCTGGGAGAAATCCCGGCCCATCTTGGGTGATGATGAGCCCTGCGCTGT 337
DB 465 AGAGATCCCTGGGAGAAATCCCGGCCCATCTTGGGTGATGATGAGCCCTGCGCTGT 524
QY 338 GCGTGTCCCGCTTGTGAGGAGGAGACATAGAAAATGAATGTGTTCTTTAAAGGA 397
DB 525 GCGTGTCCCGCTTGTGAGGAGGAGACATAGAAAATGAATGTGTTCTTTAAAGGA 584
QY 398 TGGGCGAGAAACAGATCTCTGTTGTGATATTTATTTGAAAGGGATTTACAGATTTGAAT 457
DB 585 TGGGCGAGAAACAGATCTCTGTTGTGATATTTATTTGAAAGGGATTTACAGATTTGAAT 644
QY 458 GAAGTCACAAGTAGACATTAACCAATGAGAGAAACAGAGCAAGAAATTTATGCTT 517
DB 645 GAAGTCACAAGTAGACATTAACCAATGAGAGAAACAGAGCAAGAAATTTATGCTT 704
QY 518 CACAGACATGACAAACAAATGGAATCTGTGATGACATGAGCGAGCAAGCTTGGG 577
DB 705 CACAGACATGACAAACAAATGGAATCTGTGATGACATGAGCGAGCAAGCTTGGG 764
QY 578 AGAGATTAACCAAGGGGAGAGGCTCAGATTTCTGGCCCTGCTGCTAACTGTGCTTC 637
DB 765 AGAGATTAACCAAGGGGAGAGGCTCAGATTTCTGGCCCTGCTGCTAACTGTGCTTC 824
QY 638 ATAAACCAATCAATTTATATTTTAAACCCCAAAACAAAGCTGTGTAATATCTGATCTC 697
DB 825 ATAAACCAATCAATTTATATTTTAAACCCCAAAACAAAGCTGTGTAATATCTGATCTC 884
QY 698 TAGGTTCTCTTGGGCCCAACATTTCTCATATATATCAGGCACACATCTTTTAAATTT 757
DB 885 TAGGTTCTCTTGGGCCCAACATTTCTCATATATATCAGGCACACATCTTTTAAATTT 944
QY 758 AGTTCCAGATCTGTACTGTGACCTTTTACACTGTAGAAATTAACATTAATCTGATTTG 817
DB 945 AGTTCCAGATCTGTACTGTGACCTTTTACACTGTAGAAATTAACATTAATCTGATTTG 1004
QY 818 AAAGACCTTCTGTTGCTGCTTAAATATGATGATGATGATTTTCTTAAGAGATGTTCTG 877
DB 1005 AAAGACCTTCTGTTGCTGCTTAAATATGATGATGATGATTTTCTTAAGAGATGTTCTG 1064
QY 878 GCCCAGGGATCTGTGAACAGGCTGGAGAGCATCTAAGATCTTCCAGGGTATATACCTTA 937
DB 1065 GCCCAGGGATCTGTGAACAGGCTGGAGAGCATCTAAGATCTTCCAGGGTATATACCTTA 1124
QY 938 CTAGACACAGCATGTATCTTACGGAAGTAATATCTAATCAACATCATCTCCAGTGTCT 997
DB 1125 CTAGACACAGCATGTATCTTACGGAAGTAATATCTAATCAACATCATCTCCAGTGTCT 1184
```

```
QY 998 TTGGCCATCTGAATTCATTTCCACCTTTTGGCCCATCTTCAAGACCTCAAAATGTCA 1057
DB 1185 TTGGCCATCTGAATTCATTTCCACCTTTTGGCCCATCTTCAAGACCTCAAAATGTCA 1244
QY 1058 TTCCATTAATATACAGGATTAATCTTTTAAACCTTGAGAAATTAATGTTACATG 1117
DB 1245 TTCCATTAATATACAGGATTAATCTTTTAAACCTTGAGAAATTAATGTTACATG 1304
QY 1118 CAGCTATGGAATTAATTAATATATTTTGTTCAGTGCAGAAAGATGATGATCTGTTA 1177
DB 1305 CAGCTATGGAATTAATTAATATATTTTGTTCAGTGCAGAAAGATGATGATCTGTTA 1364
QY 1178 TCCCTCCCTTTGTTGATTTTTCACATTAAGTTAAATGCTTACCTTGTACTG 1237
DB 1365 TCCCTCCCTTTGTTGATTTTTCACATTAAGTTAAATGCTTACCTTGTACTG 1424
QY 1238 AGGCTGTATACAGACAGCCTTCCCATCCCTCAGCCCTTATCTGATCAGACATCAAC 1297
DB 1425 AGGCTGTATACAGACAGCCTTCCCATCCCTCAGCCCTTATCTGATCAGACATCAAC 1484
QY 1298 CCCTCCCATNYSACCTTAACAAATCTAATCTTAAATCTCTGACATGTACAGNCATAC 1357
DB 1485 CCCTCCCATNYSACCTTAACAAATCTAATCTTAAATCTCTGACATGTACAGNCATAC 1544
QY 1358 ATTCTCTCTGCTGAGAGAGCTCTTCTGCTCTTAANTAGATATGTAAGTT 1417
DB 1545 ATTCTCTCTGCTGAGAGAGCTCTTCTGCTCTTAANTAGATATGTAAGTT 1604
QY 1418 TTGAATATGTTGACTCTTACTTCAATGCAAAAGGAGACATATGAGATTTATCATCA 1477
DB 1605 TTGAATATGTTGACTCTTACTTCAATGCAAAAGGAGACATATGAGATTTATCATCA 1664
QY 1478 CATGAGACAGCAAAATCTAAGTTGATTTAAGATTTAAGATTAATATATGAA 1537
DB 1665 CATGAGACAGCAAAATCTAAGTTGATTTAAGATTTAAGATTAATATATGAA 1724
QY 1538 ATGCAAGACCAAGAGGGAATGTTATGAGGAGACCTTGTAGCCCTGGATGTGAAGA 1597
DB 1725 ATGCAAGACCAAGAGGGAATGTTATGAGGAGACCTTGTAGCCCTGGATGTGAAGA 1784
QY 1598 AAGGAGGGAACCTCATAGTATCTTATATATATCTTCAATTTCTATCTATACAA 1657
DB 1785 AAGGAGGGAACCTCATAGTATCTTATATATATCTTCAATTTCTATCTATACAA 1844
QY 1658 TATCCAAAGCTTTTTCACAGAAATTCATGCAATGCAATCCCAAGATTAACCTTATCC 1717
DB 1845 TATCCAAAGCTTTTTCACAGAAATTCATGCAATGCAATCCCAAGATTAACCTTATCC 1904
QY 1718 ATTTCATGAGTGGAGTGGCTTTAAGATTTTGGCAAAATCATCTGTCATCTCAACTT 1777
DB 1905 ATTTCATGAGTGGAGTGGCTTTAAGATTTTGGCAAAATCATCTGTCATCTCAACTT 1964
QY 1778 TGAGATGTGTTTCTCTTGTAGTTAATTTGAAAGAAATAGGCACTCTTGAGCCACTTT 1837
DB 1965 TGAGATGTGTTTCTCTTGTAGTTAATTTGAAAGAAATAGGCACTCTTGAGCCACTTT 2024
QY 1838 AGGGTTCACCTCTGCAATTAAGAATTTACAAAGA 1872
DB 2025 AGGGTTCACCTCTGCAATTAAGAATTTACAAAGA 2059
```

RESULT 8
ACAS9834
ID ACAS9834 standard; cDNA; 3923 BP.
XX ACAS9834:
AC ACAS9834:
XX 10-JUN-2003 (first entry)
DE Prostate cancer therapy associated cDNA #545.
XX Prostate cancer; vaccine; gene therapy; cytostatic; fusion protein;
KW Immunogen; cancer; prostate specific antigen; PSA;

KW prostatic acid phosphatase; PAP; prostate specific membrane antigen;
XX PSM: gene: ss.
OS Homo sapiens.
XX US2002192763-A1.
XX
PD 19-DEC-2002.
XX
PF 29-JUN-2001; 2001US-0895793.
XX
PR 17-APR-2000; 2000US-157455P.
PR 04-OCT-2000; 2000US-0679272.
PR 28-MAR-2001; 2001US-0822827.
XX
PA (XUJ/) XU J.
PA (DILL/) DILLON D C.
PA (MITC/) MITCHAM J L.
PA (HARL/) HARLOCKER S L.
PA (JIAN/) JIANG Y.
PA (KALO/) KALOS M D.
PA (FANG/) FANGER G R.
PA (RETT/) RETTER M W.
PA (STOL/) STOLK J A.
PA (DAYC/) DAY C H.
PA (VEDV/) VEDVICK T S.
PA (CART/) CARTER D.
PA (LISX/) LI S X.
PA (WANG/) WANG A.
PA (SKEI/) SKEIKY Y A W.
PA (HEPL/) HEPLER M T.
PA (HEND/) HENDERSON R A.
PA (HURA/) HURAL J.
PA (MCNE/) MCNEILL P D.
PA (HOUT/) HOUTON R L.
PA (DBAS/) Y DE BASSOLS C V.
PA (FOYT/) FOY T M.
XX
PI Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Kalos MD;
PI Fanger GR, Retter MW, Stolk JA, Day CH, Vedvick TS, Carter D;
PI Li SX, Wang A, Skeiky YAW, Hepler MT, Henderson RA, Hural J;
PI Mcneill PD, Houghton RL, Y De Bassols CV, Foy TM;
XX
XX WPI: 2003-352711/33.
DR
XX
XX
PT New fusion protein comprising prostate-specific polypeptides, or its
PT immunogenic portions, useful for diagnosing, preventing and/or treating
PT cancer, particularly prostate cancer -
XX
XX
XX Example 16; SEQ ID NO 690; 85pp; English.
XX
CC The invention describes a fusion protein comprising at least one amino
CC acid sequence of immunogenic portions of any of the 3 sequences not
CC defined in the specification, or sequences having at least 70 or 90 %
CC sequence identity to any one of the 35 sequences defined in the USPO
CC web site, which is encoded by any of the 4 nucleotide sequences not
CC defined in the specification. The fusion protein, composition and
CC methods are useful for diagnosing, preventing and/or treating cancer,
CC particularly prostate cancer. The proteins are useful as markers to
CC indicate the presence or absence of cancer. This sequence
CC represents a prostate cancer therapy associated cDNA.
CC Note: The sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
CC from the US patent office at
CC segdata.uspto.gov/sequence.html?DocID=US20020192763.
XX
XX
SQ Sequence 3923 BP; 1157 A; 840 C; 740 G; 1186 T; 0 other;
Query Match 73.0%; Score 1367; DB 25; Length 3923;
Best Local Similarity 99.5%; Pred. No. 0;
Matches 1/67; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Db 285 GGTGAGAAATAGAAAGGCTGCTGACTTACCATCTGAGGCCACACATCTGCTGAATGG 344
QY 158 AGATATTTTACATCTAGTAAACAGCAGATACATATATAGTCTAGTACTGACATGT 217
Db 345 AGATATTTTACATCTAGTAAACAGCAGATACATATATAGTCTAGTACTGACATGT 404
QY 218 TTTTGACATTTCCAGCCCTTTAAATATCCACACACAGGAGACAAAAGGAAAGC 277
Db 405 TTTTGACATTTCCAGCCCTTTAAATATCCACACACAGGAGACAAAAGGAAAGC 464
QY 278 AGAGATCCCTGGGAGAAATGCCCGGCCATCTTGGGTCATGATGAGCTCGGCCCTGT 337
Db 465 AGAGATCCCTGGGAGAAATGCCCGGCCATCTTGGGTCATGATGAGCTCGGCCCTGT 524
QY 338 GCTTGTCCTGCTGCTGAGGAGGACATTTAGAAAATGATGATGCTTCTTAAAGGA 397
Db 525 GCTTGTCCTGCTGCTGAGGAGGACATTTAGAAAATGATGATGCTTCTTAAAGGA 584
QY 398 TGGGAGGAAACAGATCCCTGTTGAGATATTTTGAACGGGATTAACAGATTTGAAT 457
Db 585 TGGGAGGAAACAGATCCCTGTTGAGATATTTTGAACGGGATTAACAGATTTGAAT 644
QY 458 GAAGTCACAAAGTGAAGCATTTACCAATGAGAGGAAACAGAGGAAATCTTGATGGCTT 517
Db 645 GAAGTCACAAAGTGAAGCATTTACCAATGAGAGGAAACAGAGGAAATCTTGATGGCTT 704
QY 518 CACAAGACATGCAACAACAAATGGAATAGTGTGATGATGATGAGGAGGAGGAGG 577
Db 705 CACAAGACATGCAACAACAAATGGAATAGTGTGATGATGATGAGGAGGAGGAGG 764
QY 578 AGGAGATATACCAAGGGGCGAGGAGGATCTGGCCCTGCTTAACTGCTGCTTC 637
Db 765 AGGAGATATACCAAGGGGCGAGGAGGATCTGGCCCTGCTTAACTGCTGCTTC 824
QY 638 ATACCAATATCTTATTTCTTAACCTCAACCAACAAAGCTGTTGATATCTGATCTC 697
Db 825 ATACCAATATCTTATTTCTTAACCTCAACCAACAAAGCTGTTGATATCTGATCTC 884
QY 698 TACGGTTCCTTGGGGCCCAACATCTTCATATATTCACAGCAGCAGCTATTTTAAATTT 757
Db 885 TACGGTTCCTTGGGGCCCAACATCTTCATATATTCACAGCAGCAGCTATTTTAAATTT 944
QY 758 ACTTCCAGATCTGATCTGATCTGATCTTCTACACTGTAGATATACATTTTCTTCTC 817
Db 945 ACTTCCAGATCTGATCTGATCTGATCTTCTACACTGTAGATATACATTTTCTTCTC 1004
QY 818 AAGAGCCCTTGTGCTGCTTAAATATGATGATGATGATGATGATGATGATGATG 877
Db 1005 AAGAGCCCTTGTGCTGCTTAAATATGATGATGATGATGATGATGATGATGATG 1064
QY 878 GCCCAGGGAGTGTGACAGGCTGGGAGGATCTCAAGATCTTTCACAGGTTATATCTTA 937
Db 1065 GCCCAGGGAGTGTGACAGGCTGGGAGGATCTCAAGATCTTTCACAGGTTATATCTTA 1124
QY 938 CTAGACACAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 997
Db 1125 CTAGACACAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1184
QY 998 TTGGCCATTTACTGAAATTTCTTCCACCTTTTGGCCATTTCAAGACCTCAAAATGTCA 1057
Db 1185 TTGGCCATTTACTGAAATTTCTTCCACCTTTTGGCCATTTCAAGACCTCAAAATGTCA 1244
QY 1058 TTTCATTTATATCAGATGATGATGATGATGATGATGATGATGATGATGATGATG 1117
Db 1245 TTTCATTTATATCAGATGATGATGATGATGATGATGATGATGATGATGATGATG 1304
QY 1118 CAGCTATGGAATTTAT 1177
Db 1305 CAGCTATGGAATTTAT 1364
QY 1178 TCCCTTCCCTTGTGATTTTCTTCCAGTAAAGTTAAAGTCTTAAAGCTTAAAGCTTAA 1237

QY 697 CTAGGCTCTCTGGGCCAACATTCATATTCAGCAGCAGCATTTTATAT 756
 DB 1170 CTAGGCTCTCTGGGCCAACATTCATATTCAGCAGCAGCATTTTATAT 1111
 QY 757 TAGTCCAGATCTGTACTGTGACCTTCTACACTGTAGTAATACATTACTATTTGTT 816
 DB 1110 TAGTCCAGATCTGTACTGTGACCTTCTACACTGTAGTAATACATTACTATTTGTT 1051
 QY 817 CAAAGACCTTCGTGTGCTGCTTAATATGTAAGTACTGTTTCTTAAGAGTGTCT 876
 DB 1050 CAAAGACCTTCGTGTGCTGCTTAATATGTAAGTACTGTTTCTTAAGAGTGTCT 991
 QY 877 GACCCAGGAGATCTGTAACAGGCTGGGAGACATCTCAAGATCTTCCAGGTTTACTT 936
 DB 990 GACCCAGGAGATCTGTAACAGGCTGGGAGACATCTCAAGATCTTCCAGGTTTACTT 931
 QY 937 ACTAGCACAGACATGATCATTCAGAGTGAATTAATCAATCAATCATCTCAGTGT 996
 DB 930 ACTAGCACAGACATGATCATTCAGAGTGAATTAATCAATCAATCATCTCAGTGT 871
 QY 997 TTTGCCATCTAGGAATTCATTTCCACTTTTGTCCCATTTCTCAAGACCTCAAAATGTC 1056
 DB 870 TTTGCCATCTAGGAATTCATTTCCACTTTTGTCCCATTTCTCAAGACCTCAAAATGTC 811
 QY 1057 ATTCATTAATATTCACAGATTAATTTTAACTTTTAACTGGAAGAAATTCATGTTACT 1116
 DB 810 ATTCATTAATATTCACAGATTAATTTTAACTTTTAACTGGAAGAAATTCATGTTACT 751
 QY 1117 GCAGCTATGGAATTAATTAATTAATTTTGTTCAGTGCAGAAAGATGTAAGTCTTT 1176
 DB 750 GCAGCTATGGAATTAATTAATTAATTTTGTTCAGTGCAGAAAGATGTAAGTCTTT 691
 QY 1177 ATCCCTCCCTTTTGTGTTATTTTTCAGATTAATTAATTAATTTTGTGTTACT 1236
 DB 690 ATCCCTCCCTTTTGTGTTATTTTTCAGATTAATTAATTAATTTTGTGTTACT 631
 QY 1237 GAGGCTGTATACAG 1251
 DB 630 GAGGCTGTATACAG 616
 RESULT 10
 AAS63898/c
 ID AAS63898 standard; cDNA; 2426 BP.
 XX
 AC AAS63898;
 XX
 DT 29-JAN-2002 (first entry)
 XX
 DE Human prostate cDNA sequence #432.
 XX
 KW Human; prostate cancer; ss; cytosolic; immunostimulant; tumour.
 XX
 OS Homo sapiens.
 XX
 PN W0200173032-A2.
 PD 04-OCT-2001.
 XX
 PF 27-MAR-2001; 2001WO-US09919.
 XX
 PR 27-MAR-2000; 2000US-0536857.
 PR 09-MAY-2000; 2000US-0568100.
 PR 12-MAY-2000; 2000US-0570737.
 PR 13-JUN-2000; 2000US-0593793.
 PR 27-JUN-2000; 2000US-0605783.
 PR 10-AUG-2000; 2000US-0636215.
 PR 29-AUG-2000; 2000US-0651236.
 PR 06-SEP-2000; 2000US-0652729.
 PR 02-OCT-2000; 2000US-0679426.
 PR 10-OCT-2000; 2000US-0685166.
 XX

PA (CORI-) CORIXA CORP.
 XX
 PI Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Kalos MD;
 PI Fanger GR, Reiter WM, Stolk JA, Day CH, Vedrick TS, Carter D;
 PI Li SX, Wang A, Skelky YAW, Hepler WT, Henderson RA;
 DR WPI: 2001-639232/73.
 XX
 PT New human prostate-specific polypeptides and polynucleotides useful for
 PT the diagnosis and treatment of cancer, especially prostate cancer -
 PS
 XX
 XX
 CC
 CC The invention relates to isolated prostate-specific
 CC polynucleotides, polypeptides, fusion proteins of the polypeptides,
 CC antibodies raised against the polypeptides (or antigenic epitopes
 CC derived from them) and antigen-presenting cells expressing the
 CC polypeptides. The antibodies are useful for detecting the presence of
 CC cancer, especially prostate cancer. The polypeptides, polynucleotides and
 CC the antigen-presenting cells are useful for stimulating and/or expanding
 CC T cells specific for a tumour protein, and for inhibiting the development
 CC of cancer especially prostate cancer. Compositions comprising the
 CC polynucleotide and/or polypeptide are useful for stimulating an immune
 CC response, and for treating cancer. The oligonucleotide is useful for
 CC detecting cancer. The present sequence is a prostate specific
 CC polynucleotide of the invention.
 XX
 SQ Sequence 2426 BP; 717 A; 476 C; 548 G; 685 T; 0 other;
 Query Match 61.7%; Score 1155; DB 22; Length 2426;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1155; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 97 AGGTGAGAAATTAAGAAAGGCTGCTGACTTTACCATCTGAGCCACACATCTGTAATG 156
 DB 1770 AGGTGAGAAATTAAGAAAGGCTGCTGACTTTACCATCTGAGCCACACATCTGTAATG 1711
 QY 157 GAGATTAATTAATCATCTAGAAAGCAAGCAAGATGAAATTAATGTTAGTGTGATG 216
 DB 1710 GAGATTAATTAATCATCTAGAAAGCAAGCAAGATGAAATTAATGTTAGTGTGATG 1651
 QY 217 TTTTTCACATTTCCAGCCCTTTAAATATCCACACACACAGAGCAACAAAGAGAGA 276
 DB 1650 TTTTTCACATTTCCAGCCCTTTAAATATCCACACACACAGAGCAACAAAGAGAGA 1591
 QY 277 CAGAGATCCCTGGGAGAAATGCGCGGCCCATCTTGGGTATGATGATGAGCTGCCCTG 336
 DB 1590 CAGAGATCCCTGGGAGAAATGCGCGGCCCATCTTGGGTATGATGATGAGCTGCCCTG 1531
 QY 337 TGCCGTGTCGCCCTGTGAGGAGAGACATTTGAAATGAATGATGATGTTTCTTAAGG 396
 DB 1530 TGCCGTGTCGCCCTGTGAGGAGAGACATTTGAAATGAATGATGATGTTTCTTAAGG 1471
 QY 397 ATGGCAGAGAAACAGATCCCTGTGATGATTTATTTGAACGGGATTAAGATTTGAAA 456
 DB 1470 ATGGCAGAGAAACAGATCCCTGTGATGATTTATTTGAACGGGATTAAGATTTGAAA 1411
 QY 457 TGAAGTCAAGAGTGAAGATTTCCATGAGAGAGAAACAGACAGAAATCTTGATGGCT 516
 DB 1410 TGAAGTCAAGAGTGAAGATTTCCATGAGAGAGAAACAGACAGAAATCTTGATGGCT 1351
 QY 517 TCACAAGACATGCAACAAACAAATGGAATGATGATGATGATGAGGAGGACCAACTGGG 576
 DB 1350 TCACAAGACATGCAACAAACAAATGGAATGATGATGATGATGAGGAGGACCAACTGGG 1291
 QY 577 GAGGAGATTAACGAGGAGGAGGATTCAGGATTTGCGCCCTGCTCTAACTGCGCTT 636
 DB 1290 GAGGAGATTAACGAGGAGGAGGATTCAGGATTTGCGCCCTGCTCTAACTGCGCTT 1231
 QY 637 CATTAACCAATCATTTTCAATTTTCAACCTCAAAACAAAGCTGTTGTAATATCTGATCT 696
 DB 1230 CATTAACCAATCATTTTCAATTTTCAACCTCAAAACAAAGCTGTTGTAATATCTGATCT 1171

QY 697 CTACGGTTCCTCGGGCCCAACATCTCCATATATCCAGCACACATCTTTATAT 756
DB 1170 CTACGGTTCCTCGGGCCCAACATCTCCATATATCCAGCACACATCTTTATAT 1111
QY 757 TAGTCCAGATCTGTACTGTGACCTTCTACACTGTAGATATACATTTACTTTGTT 816
DB 1110 TAGTCCAGATCTGTACTGTGACCTTCTACACTGTAGATATACATTTACTTTGTT 1051
QY 817 CAAGACCCCTTCGTTGCTGCTTAATATGTAGCTGACTTTTCTTAAGAGCTTCT 876
DB 1050 CAAGACCCCTTCGTTGCTGCTTAATATGTAGCTGACTTTTCTTAAGAGCTTCT 991
QY 877 GGCCCAAGGATCTGTATACAGGTGGAGACATCTAAGATCTTCCAGGTTACTT 936
DB 990 GGCCCAAGGATCTGTATACAGGTGGAGACATCTAAGATCTTCCAGGTTACTT 931
QY 937 ACTAGCACAGCATGTATCATACGAGTGAATATATCATCATCATCTCAGTGT 996
DB 930 ACTAGCACAGCATGTATCATACGAGTGAATATATCATCATCATCTCAGTGT 871
QY 997 TTTGCCATACGTGAATTCATTTCCACTTTTGCCCATCTCCAGACCTCAAAATGTC 1056
DB 870 TTTGCCATACGTGAATTCATTTCCACTTTTGCCCATCTCCAGACCTCAAAATGTC 811
QY 1057 ATTCCATTAAATACAGAGATTAATCTTTTCTTAACCTGGAAAGATTCATTTGAT 1116
DB 810 ATTCCATTAAATACAGAGATTAATCTTTTCTTAACCTGGAAAGATTCATTTGAT 751
QY 1117 GCAGCTATGGGAATTTAATATATTTGTTTCCAGTCAAGATGACTAAGTCTT 1176
DB 750 GCAGCTATGGGAATTTAATATATTTGTTTCCAGTCAAGATGACTAAGTCTT 691
QY 1177 ATCCCTCCCTTTGTTGATTTTCTCCAGTAAAGTTAAATGCTTACCTGTACT 1236
DB 690 ATCCCTCCCTTTGTTGATTTTCTCCAGTAAAGTTAAATGCTTACCTGTACT 631
QY 1237 GAGGCTGTATACAGC 1251
DB 630 GAGGCTGTATACAGC 616

RESULT 11
AAH93805/c
ID AAH93805 standard; cDNA; 2426 BP.
AC AAH93805;
XX 04-OCT-2001 (first entry)
DE Human prostate-specific cDNA sequence P710P #3.
XX
KW Human; prostate cancer; prostate-specific; diagnosis; vaccine;
cytostatic; gene therapy; metastasis; ss.
OS Homo sapiens.
XX
PN WO200151633-A2.
XX 19-JUL-2001.
PD 16-JAN-2001; 2001MO-US01574.
PF 14-JAN-2000; 2000US-0483672.
PR (CORI-) CORIXA CORP.
XX
PA
XX
PI Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Reed SG;
PI Kalos MD, Fanger GR, Day CH, Retter MW, Stolk JA, Skelky YAM;
PI Wang A, Meagher MJ;
XX
DR WPI; 2001-425873/45.
PT New polynucleotide encoding a prostate-specific protein, for

PT diagnosing, monitoring and treating prostate cancer in a patient and
XX for use in vaccines -
PS
XX Claim 1: Page 384-385; 543pp; English.
CC The present invention describes polynucleotide sequences (I) which encode
CC prostate-specific proteins (II). (I) and (II) have cytostatic activity,
CC and can be used in vaccine production and gene therapy. (I), (II),
CC antibodies to (II), fusion proteins comprising (II), and isolated
CC T cells prepared using (I) or (II) are used to treat cancer in a patient.
CC (I) and the antibodies are also used in the detection of cancer in a
CC patient. The cancer that is diagnosed or treated is particularly
CC prostate cancer. (I) and (II) can be used in vaccines. The antibodies or
CC (I) can be used for monitoring the progression of cancer in a patient.
CC (I) and (II) can also be used to improve diagnostic and therapeutic
CC methods for prostate cancer. They can indicate the level of metastasis
CC as well as the prostate volume. AAH93357 to AAH93944 and AAH01115 to
CC AAH01318 represent polynucleotide and amino acid sequences used in the
CC exemplification of the present invention.
XX
SQ Sequence 2426 BP; 717 A; 476 C; 548 G; 685 T; 0 other;
Query Match 61.7%; Score 1155; DB 22; Length 2426;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1155; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 97 AGGTGAGAAATTAAGAAAGGCTGCTGACTTACCATCTGAGCCACACATCTGTAATG 156
DB 1770 AGGTGAGAAATTAAGAAAGGCTGCTGACTTACCATCTGAGCCACACATCTGTAATG 1711
QY 157 GAGTATATTAACATCACTACAAACAGCAGATGACATATATGTCTAAGTACTGACATG 216
DB 1710 GAGTATATTAACATCACTACAAACAGCAGATGACATATATGTCTAAGTACTGACATG 1651
QY 217 TTTTGGACATTTCCAGCCCTTTAAATATCCACACACAGAGAGACAAAGAGCA 276
DB 1650 TTTTGGACATTTCCAGCCCTTTAAATATCCACACACAGAGAGACAAAGAGCA 1591
QY 277 CAGAGATCCCTGGGAGAAATGCCGGCCCATCTTGCGTCATCGATGAGCCCTGCGCTG 336
DB 1590 CAGAGATCCCTGGGAGAAATGCCGGCCCATCTTGCGTCATCGATGAGCCCTGCGCTG 1531
QY 337 TGGCTGGTCCCGCTGTGAGGAGAAAGCATTAAGAAATGATGTGTCTTAAAG 396
DB 1530 TGGCTGGTCCCGCTGTGAGGAGAAAGCATTAAGAAATGATGTGTCTTAAAG 1471
QY 397 ATGGCAGAGAAACAGATCTCTGTGTGATTTATTTGAAGGATTAACAGATTGAAA 456
DB 1470 ATGGCAGAGAAACAGATCTCTGTGTGATTTATTTGAAGGATTAACAGATTGAAA 1411
QY 457 TGAAGTCACAAATGAGCATTTACCAATGAGAGGAAACAGACGAGAAATCTTGATGCT 516
DB 1410 TGAAGTCACAAATGAGCATTTACCAATGAGAGGAAACAGACGAGAAATCTTGATGCT 1351
QY 517 TCACAAGACATGCAACAAACAAATGAAATGATGTGATGACATGAGGAGCCAGGTGGG 576
DB 1350 TCACAAGACATGCAACAAACAAATGAAATGATGTGATGACATGAGGAGCCAGGTGGG 1291
QY 577 GAGGAGATAACACAGGGGAGAGGATCTGGCCCTGCTGCTAAAGTGTGCTT 636
DB 1290 GAGGAGATAACACAGGGGAGAGGATCTGGCCCTGCTGCTAAAGTGTGCTT 1231
QY 637 CATACCAAAATCATTTTCAATTTTCAACCCCTCAAAACAAAGCTGTTGTAATATCTGATCT 696
DB 1230 CATACCAAAATCATTTTCAATTTTCAACCCCTCAAAACAAAGCTGTTGTAATATCTGATCT 1171
QY 697 CTACGGTTCCTCGGGCCCAACATCTCCATATATCCAGCACACATCTTTATAT 756
DB 1170 CTACGGTTCCTCGGGCCCAACATCTCCATATATCCAGCACACATCTTTATAT 1111
QY 757 TAGTCCAGATCTGTACTGTGACCTTCTACACTGTAGATATACATTTACTTTGTT 816
DB 1110 TAGTCCAGATCTGTACTGTGACCTTCTACACTGTAGATATACATTTACTTTGTT 1051

QY	817	CAAGACCCCTGCTGCTGCTGCTCCCTAATATGTAGCTGACTGTTTTTCTTAAGAGTGTCT	876
Db	1050	CAAGAGCCCTTCGTGTGCTGCTCCCTAATATGTAGCTGACTGTTTTTCTTAAGAGAGTCTCT	991
QY	877	GGCCGAGGGATCTGTGAACAGAGCGGGGAGACATCTCAAGATCTTCCAGGGTTATCTT	936
Db	990	GGCCGAGGGATCTGTGAACAGAGCGGGGAGACATCTCAAGATCTTCCAGGGTTATCTT	931
QY	937	ACTAGCACACAGCATGATCATTTACGAGGTGAATTATCTAATCAACATCATCTCCAGTGC	996
Db	930	ACTAGCACACAGCATGATCATTTACGAGGTGAATTATCTAATCAACATCATCTCCAGTGC	871
QY	997	TTTGCCCATCTGAATTCATTTCCACTTTTGGCCCATCTCTCAAGACGCTCAAAATGC	1056
Db	870	TTTGCCCATCTGAATTCATTTCCACTTTTGGCCCATCTCTCAAGACGCTCAAAATGC	811
QY	1057	ATTCATTAATATATCAGAGATTAACTTTTTTTTAAACCTGGAGAAATTCATGTTACAT	1118
Db	810	ATTCATTAATATATCAGAGATTAACTTTTTTTTAAACCTGGAGAAATTCATGTTACAT	751
QY	1117	GCACCTATGGGAATTTAATTCATATTTTGTTCACGTGCAGAAAGTACTAAGTCCTTT	1178
Db	750	GCACCTATGGGAATTTAATTCATATTTTGTTCACGTGCAGAAAGTACTAAGTCCTTT	691
QY	1177	ATCCCTGCCCCCTTGTGTGATTTTTTTTCCACTATATAAGTTAAATAGCTTAGCCTGTACT	1236
Db	690	ATCCCTGCCCCCTTGTGTGATTTTTTTTCCACTATATAAGTTAAATAGCTTAGCCTGTACT	631
QY	1237	GAGGCTGTATACAGC 1251	
Db	630	GAGGCTGTATACAGC 616	

CC	RESULT 12
XX	AAH85119/c
ID	AAH85119 standard; cDNA; 2426 BP.
XX	
AC	AAH85119;
XX	
DT	25-SEP-2001 (first entry)
XX	
DE	Human prostate-specific cDNA sequence P710P #3.
XX	
KW	Human; prostate cancer; therapy; diagnosis; cat eye syndrome;
KW	Chromosome 22q11.2; prostate-specific protein; chromosome 1;
KW	prostate specific antigen; PSA; ss.
XX	
OS	Homo sapiens.
XX	
PN	WO200134802-A2.
XX	
PD	17-MAY-2001.
XX	
PF	09-NOV-2000; 2000WO-US30904.
XX	
PR	12-NOV-1999; 99US-0439313.
PR	18-NOV-1999; 99US-0443686.
XX	
PA	(CORI-) CORIXA CORP.
XX	
PI	Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Reed SG;
PI	Kalos MD, Retter MW, Stolk JA, Day CH, Skeiky YAM, Wang A;
XX	WPI; 2001-308785/32.
DR	
XX	
PT	Isolated polypeptide comprising at least an immunogenic portion of a
PT	prostate-specific protein, useful in the diagnosis and therapy of
PT	prostate cancer -
XX	
PS	Claim 5; Page 284; 325pp; English.
XX	
CC	The present invention describes an isolated polypeptide (P1) comprising

at least an immunogenic portion of a prostate-specific protein, or its variant. Also described are polynucleotides (N1) encoding (P1). (P1) and (N1) have cytostatic activity and can be used in vaccine production. The polypeptides, nucleic acids and antibodies from the present invention are useful in the diagnosis and therapy of prostate cancer. Prostate specific genes P704P, P712P, P714P, P775P and B305D are located in a genomic region on chromosome 22q11.2 known as the Cat Eye Syndrome region. Prostate specific antigen (PSA) P501S was located on chromosome 1. AAH84671 to AAH5143 and AAG99000 to AAG99077 represent polynucleotide and polypeptide sequences used in the exemplification of the present invention.

Sequence 2426 BP; 717 A; 476 C; 548 G; 685 T; 0 other;

Query Match 61.78; Score 1155; DB 22; Length 2426;

```

Matches 1155; Conservative 0; Indels 0; Gaps 0;

```

QY	97	AGGTGAGAAATAGAAAGCGCTGCAGACTTTACCATCTGAGGCCACACATCTGCTGAATG	156
Db	1770	AGGTGAGAAATAGAAAGCGCTGCAGACTTTACCATCTGAGGCCACACATCTGCTGAATG	1711

157 GAGATAATTAAACATCAGTGAACACGCAAGATGACATATATAATGTCTAAGTAGTGACATG 216

Db 1710 GAGATAATTACATCACTAGAACACGACAGATGACAATATTAATGCTCTAAGTAGTGACATG 16511

217 TTTTGCACATTTCCAGCCCTTAAATATCCACACACAGGAGCACAAAGAAGCA 276

Db 1650 TTTTGCACATTTCCAGCCCTTTAAATATCCACACACAGGAGCACAAAGGAGCA 1591

277 CAGAGATCCCTGGGAGAAATGCCCGGCCCATCTTGGTCAATGATGAGCCTGCCCTG 336

Db 1590 CAGAGATCCCTGGGAGAATGCCCGCCCATCTTGGGTGATGATGAGCCCTGCCCTG 1531

337 TGCCTGGTCCCGCTTGAGGGAAGACATTAGAAATGAATTGATGTTCTTAAAG 396

Db 1530 TGCCTGTCCTGTTGTGAGGGAAGACATTAGAAATGAATTGATGTCTTCTTAAGG 1471

QY 397 ATGGGCAAGAAACAGATCCTGTTGTGGATATTTATTTGAACGGGATTACAGATTGAAA 456

Db 1470 ATGGCAGGAAACAGATCCTGTTGTGGATATTATTGGAACGGGATTACAGATTGCAA 1411

457 TGAAGTCACAAAGTGAGCATTACCAATGAGAGGAAACAGACGAGAAATCTTGATGGCT 516

Db 1410 TGAAGTCACCAAGTGAGCATTACCAATGAGAGGAAACAGACGAGAAATCTTGATGGCT 1351

517 TCACAAGACATGCAACAACAAATGGAATACTGTGATGACATGAGGCAGGCCAAGCTGGG 576

Db 1350 TCACAAGACATGCCAACAAATGGAATACTGTGATGACATGAGGCAGCCAAGCTGGG 1291

QY 577 GAGGAGTAAACCACGGGGCAGAGGCTCAGGATTCTGGCCCTGCTGCCCTAAACTGTGCGTT 636

Db 1290 GAGGATTAACCCAGGGGCGAGGGCTCAGATTCTGGCCCTGCTGCCCTAAACTGTGCGTT 1231

QY 637 CATAACCAATCATTTTCATATTTCTAACCCCTCAAAACAAGCTGTTGTAATATCTGATCT 696

Db 1230 CATAACCAATCATTTTCATATTTCTAACCCCTCAAACCAAGCTGTGTAATATCTGATCT 1171

QY 697 CTACGGTTCCTTCTGGGCCCAACATTTCTCCATATATCCAGCCACACTCATTTTAAATATT 756

Db 1170 CTACGGTTCCTTCTGGGCCCAACATTTCTCCATATATCCAGCCACACTCATTTTAAATATT 1111

757 TAGTCCAGATCTGTACTGTGACCTTTCTACACTGTAGAATAACATTACTCATTTTGT 816

Db 1110 TAGTCCAGATCTGACTGTGACCTTCTACACTGTAGAATAACATTACTCATTTTGT 1051

817 CAAGACCTTCGTGTGCTGCCTAATATGTAGCTGACTGTTTTCCTAAGGAGTGTCT 876

Db 1050 CAAGACCCTTGGTGTGCTGCCTAATATGTAGCTGACTGTTTTCCTAAGGAGTGTCT 991

877 GGGCCAGGGATCTGTGAACAGGCTGGGAAGCATCTCAAGATCTTCCAGGGTTATACTT 936

Db 990 GGGCCAGGGGATCTGTGAACAGGCTGGGAAGCATCTCAAGATCTTCCAGGGTTATACTT 931

Db 810 ATTCCATTATATACAGAGATTAACTTTTTTTTAACTGGAAGAAATTCATGTTACAT 751
OY 1117 GCAGCTATGGAATTAATTAATATTTTGTTCAGTGAAGATGACTAGTCTTT 1176
Db 750 GCAGCTATGGAATTAATTAATATTTTGTTCAGTGAAGATGACTAGTCTTT 691
OY 1177 ATCCCTCCCTTTGTTGATTTTTTTTCCAGTATAAGTTAAAGTCTAGCTGTGACT 1236
Db 690 ATCCCTCCCTTTGTTGATTTTTTTTCCAGTATAAGTTAAAGTCTAGCTGTGACT 631
OY 1237 GAGGCTGTATACAC 1251
Db 630 GAGGCTGTATACAGC 616

RESULT 14

AAF86948/C
ID AAF86948 standard: cDNA: 2426 BP.

AAF86948:

XX 06-JUL-2001 (first entry)

XX Human P710P Inventive antigen coding sequence SEQ ID NO: 344.

XX Human: mouse; immunotherapy: cancer; leukaemia; WTI: Wilms' tumour gene;
XX chromosome 11p13; zinc finger transcription factor; ss.

OS Homo sapiens.

PN WO200125273-A2.

XX 12-APR-2001.

PE 04-OCT-2000; 2000WO-US27465.

PR 04-OCT-1999; 99US-0157459.

PA (CORI-) CORIXA CORP.

PI Skelky YAW, Xu J, Cheever MA, Reed SG;

XX WPI: 2001-328324/34.

PT Polypeptide comprising part of the Wilms' Tumour gene product sequence is
PT used in the diagnosis and treatment of malignant diseases e.g. Leukemia
PT and cancer associated with WTI

PS Disclosure: Page 219-220; 228pp: English.

XX The present invention describes compositions comprising peptides derived
XX from the Wilms' tumour protein WTI and methods for their use in treating
XX malignant diseases. Peptides derived from both the murine and human WTI
XX proteins are provided. The human WTI gene is found on chromosome 11p13,
XX and the protein was shown to be a zinc finger transcription factor. The
XX immunogenic peptides of the invention are particularly useful in the
XX diagnosis and treatment of cancer and leukaemia. The present sequence is
XX a coding sequence used in the exemplification of the invention.

XX Sequence 2426 BP; 717 A; 476 C; 548 G; 685 T; 0 other;

XX Query Match 61.7%; Score 1155; DB 22; Length 2426;

XX Best Local Similarity 100.0%; Pred. No. 0; Mismatches 0; Indels 0; Gaps 0;

XX Matches 1155; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 97 AGGTGGAATAAGAAAGCTGCTGACTTTACATCTGAGCCACACATCTGCTGAATG 156
Db 1770 AGGTGGAATAAGAAAGCTGCTGACTTTACATCTGAGCCACACATCTGCTGAATG 1711
OY 157 GAGATTAATTAACATCTGTAAGAAAGCAAGATGACATTAATGTTAAGTGTGACATG 216
Db 1710 GAGATTAATTAACATCTGTAAGAAAGCAAGATGACATTAATGTTAAGTGTGACATG 1651

OY 217 TTTTTCACATTTTCCAGCCCTTTAAATATCCACACACAGAGAACCAAAAGAGCA 276
Db 1650 TTTTTCACATTTTCCAGCCCTTTAAATATCCACACACAGAGAACCAAAAGAGCA 1591
OY 277 CAGAGATCCCTGGGAGAAATGCCCGCCCATCTTGGGTCAATCATGATGAGCTCCGCCCG 336
Db 1590 CAGAGATCCCTGGGAGAAATGCCCGCCCATCTTGGGTCAATCATGATGAGCTCCGCCCG 1531
OY 337 TGCCTGTCCCGTTTGTGAGGAGAGACATTAAGAAATGAATTTGATGTCTTCTTAAG 396
Db 1530 TGCCTGTCCCGTTTGTGAGGAGAGACATTAAGAAATGAATTTGATGTCTTCTTAAG 1471
OY 397 ATGGCAGAGAAAACAGATCCTGTTGATATTTATTTGACGGGATTCAGATTGAA 456
Db 1470 ATGGCAGAGAAAACAGATCCTGTTGATATTTATTTTACGGGATTCAGATTGAA 1411
OY 457 TGAAGTCACAAAGTGAGCATTTACAAATGAGAGAAAAACAGAGAAAAATCTTGATGCT 516
Db 1410 TGAAGTCACAAAGTGAGCATTTACAAATGAGAGAAAAACAGAGAAAAATCTTGATGCT 1351
OY 517 TCACAAAGACATGCAACAAACAAATGGAATCTGTGATGACATGAGGCCACCAAGCTGG 576
Db 1350 TCACAAAGACATGCAACAAACAAATGGAATCTGTGATGACATGAGGCCACCAAGCTGG 1291
OY 577 GAGGAGATTAACCAAGGGGAGAGAGGATTCAGGATTCGGCCCTGCTTAACCTGTGCTG 636
Db 1290 GAGGAGATTAACCAAGGGGAGAGAGGATTCAGGATTCGGCCCTGCTTAACCTGTGCTG 1231
OY 637 CATTAACCAATCATTTATTTCTTAACCCCAAAACAAAGCTGTTGAATATCTGATCT 696
Db 1230 CATTAACCAATCATTTATTTCTTAACCCCAAAACAAAGCTGTTGAATATCTGATCT 1171
OY 697 CTACGCTTCTTCTGGGCCCAACATTTCTCATATATCCAGCCACACTATTTTAATAT 756
Db 1170 CTACGCTTCTTCTGGGCCCAACATTTCTCATATATCCAGCCACACTATTTTAATAT 1111
OY 757 TAGTCCAGATCTGTACTGTGACCTTTCTACACCTGATAATATACATTTCTCATTTGTT 816
Db 1110 TAGTCCAGATCTGTACTGTGACCTTTCTACACCTGATAATATACATTTCTCATTTGTT 1051
OY 817 CAAAGACCTTGGTGGCTTAATATGATGATGATGATGATGATGATGATGATGATGAT 876
Db 1050 CAAAGACCTTGGTGGCTTAATATGATGATGATGATGATGATGATGATGATGATGAT 921
OY 877 GGCCCAAGGAGATCTGGAACAGGCTGGGAGACATCTCAAGATCTTCCAGGTTATCTT 936
Db 921 GGCCCAAGGAGATCTGGAACAGGCTGGGAGACATCTCAAGATCTTCCAGGTTATCTT 931
OY 937 ACTAGACACAGATGATCATTAAGGAGATTAATCATCAACATCAATCCAGCTGTC 996
Db 930 ACTAGACACAGATGATCATTAAGGAGATTAATCATCAACATCAATCCAGCTGTC 871
OY 997 TTTGGCCATTAAGAAATTTCCACTTTTGGCCCAATTCACAGACCTCAAAATGTC 1056
Db 870 TTTGGCCATTAAGAAATTTCCACTTTTGGCCCAATTCACAGACCTCAAAATGTC 811
OY 1057 ATTCATTATATACAGAGATTAATTTTAACTGTAAGATTAATTAATTAATTAATTAAT 1116
Db 810 ATTCATTATATACAGAGATTAATTTTAACTGTAAGATTAATTAATTAATTAATTAAT 751
OY 1117 GCAGCTATGGAATTAATTAATATTTTGTTCAGTGAAGATGACTAGTCTTT 1176
Db 750 GCAGCTATGGAATTAATTAATATTTTGTTCAGTGAAGATGACTAGTCTTT 691
OY 1177 ATCCCTCCCTTTGTTGATTTTTTTTCCAGTATAAGTTAAAGTCTAGCTGTGACT 1236
Db 690 ATCCCTCCCTTTGTTGATTTTTTTTCCAGTATAAGTTAAAGTCTAGCTGTGACT 631
OY 1237 GAGGCTGTATACAC 1251
Db 630 GAGGCTGTATACAGC 616

RESULT: 15
ABL95269/C
ID ABL95269 standard; CDNA: 2426 BP.
XX
AC ABL95269;
XX
DT 19-JUL-2002 (first entry)
XX
DE Human P710P CDNA sequence SEQ ID NO 470.
XX
KW Human; cancer; prostate cancer; vaccine; cytostatic; immunostimulant;
KM gene therapy; gene; ss.
XX
OS Homo sapiens.
XX
PN US2002022248-A1.
XX
PD 21-FEB-2002.
XX
PF 12-JAN-2001; 2001US-0759143.
XX
PR 25-FEB-1997; 97US-0806099.
PR 01-AUG-1997; 97US-0904804.
PR 09-FEB-1998; 98US-0020956.
PR 25-FEB-1998; 98US-0030607.
PR 14-JUL-1998; 98US-0115453.
PR 23-SEP-1998; 98US-0159812.
PR 15-JAN-1999; 99US-0232149.
PR 09-APR-1999; 99US-0288946.
PR 13-JUL-1999; 99US-0352616.
PR 12-NOV-1999; 99US-0439313.
PR 18-NOV-1999; 99US-0443686.
PR 14-JAN-2000; 2000US-0483672.
PR 27-MAR-2000; 2000US-0536857.
PR 09-MAY-2000; 2000US-0568100.
PR 12-MAY-2000; 2000US-0570737.
PR 13-JUN-2000; 2000US-0593793.
PR 27-JUN-2000; 2000US-0605783.
PR 10-AUG-2000; 2000US-0636215.
PR 29-AUG-2000; 2000US-0651236.
PR 06-SEP-2000; 2000US-0657279.
PR 02-OCT-2000; 2000US-0679426.
PR 10-OCT-2000; 2000US-0685166.
XX
PA (XUJ/) XU J.
PA (DILL/) DILLON D C.
PA (MITC/) MITCHAM J L.
PA (HARL/) HARLOCKER S L.
PA (JIAN/) JIANG Y.
PA (KALO/) KALOS M D.
PA (FRNG/) FANGER G R.
PA (RETT/) RETTER M W.
PA (STOL/) STOLK J A.
PA (DAYC/) DAY C H.
PA (VEDV/) VEDVICK T S.
PA (CART/) CARTER D.
PA (LISX/) LI S X.
PA (WANG/) WANG A.
PA (SKEI/) SKEIKY Y A W.
PA (HEPL/) HEPLER W T.
PA (HEND/) HENDERSON R A.
XX
PI Xu J, Dillon DC, Mitcham JT, Harlocker SL, Jiang Y, Kalos MD;
PI Fanger GR, Retter MW, Stolk JA, Day CH, Vedvick TS, Carter D;
PI Li SX, Wang A, Skeiky YAW, Hepler WT, Henderson RA;
XX
DR WPI: 2002-255649/30.
XX
XX
PT New prostate-specific polynucleotides for diagnosing and treating
PT diseases, in particular prostate cancer, and as markers for the
PT progression of cancer
XX
PS Claim 1; SEQ ID NO 470; 87bp; English.

XX The present invention provides prostate-specific coding sequences and
CC their encoded proteins. These can be used in the diagnosis and treatment
CC of cancers, particularly prostate cancer. The present sequence is a CDNA
CC described in the invention.
XX
SQ Sequence 2426 BP; 717 A; 476 C; 548 G; 685 T; 0 other:

Query Match 61.7%; Score 1155; DB 24; Length 2426;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1155; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 97 AGGTGAGAAATFAGAAAGGCTGCTGACTTTACATCTGAGGCCACACATCTGCTGAATG 156
DB 1770 AGGTGAGAAATFAGAAAGGCTGCTGACTTTACATCTGAGGCCACACATCTGCTGAATG 1711
QY 157 GAGTAAATTAACATCCTAGAAACAGACAGATGCAATATATATGCTAACTAGACATG 216
DB 1710 GAGTAAATTAACATCCTAGAAACAGACAGATGCAATATATATGCTAACTAGACATG 1651
QY 217 TTTTGGACATTTCCAGCCCTTTAAATATCCACACACAGAGAACCAAAAGAGACA 276
DB 1650 TTTTGGACATTTCCAGCCCTTTAAATATCCACACACAGAGAACCAAAAGAGACA 1591
QY 277 CAGAGATCCCTGGAGAAATGCCGCCCATCTTGGGTATCATGATGACCTCGCCCTG 336
DB 1590 CAGAGATCCCTGGAGAAATGCCGCCCATCTTGGGTATCATGATGACCTCGCCCTG 1531
QY 337 TGCCTGTCGCCGCTTGAGAGAAAGACATTAGAAATGAATTGATGTGCTCTAAAG 396
DB 1530 TGCCTGTCGCCGCTTGAGAGAGACATTAGAAATGAATTGATGTGCTCTAAAG 1471
QY 397 ATGGGAGAGAAACAGATCCCTGTTGTGATATTTATTTGAACGGGATTACAGATTTGAAA 456
DB 1470 ATGGGAGAGAAACAGATCCCTGTTGTGATATTTATTTGAACGGGATTACAGATTTGAAA 1411
QY 457 TGAAGTACAAAAGGACATTACCAATGAGAGAAAACACACAGAAATCTTGATGCT 516
DB 1410 TGAAGTACAAAAGGACATTACCAATGAGAGAAAACACACAGAAATCTTGATGCT 1351
QY 517 TCACAAAGACATGCACAAACAAATGGAATAGCTGTGATGACATGAGAGCCCAAGCTGG 576
DB 1350 TCACAAAGACATGCACAAACAAATGGAATAGCTGTGATGACATGAGAGCCCAAGCTGG 1291
QY 577 GAGGATTAACCAACGGGGGAGAGGCTCAGATTCTGGCCCTGCTTAACCTGTGGCT 636
DB 1290 GAGGATTAACCAACGGGGGAGAGGCTCAGATTCTGGCCCTGCTTAACCTGTGGCT 1231
QY 637 CATRACCAATCATTTATATTTCTTAACCTCAAAACAAAGCTGTTATATCTGATCT 696
DB 1230 CATRACCAATCATTTATATTTCTTAACCTCAAAACAAAGCTGTTATATCTGATCT 1171
QY 697 CTACGGTCTCTTGGGCCCAACATTTCTCATATATCCAGCCACACTCATTTTAATAT 756
DB 1170 CTACGGTCTCTTGGGCCCAACATTTCTCATATATCCAGCCACACTCATTTTAATAT 1111
QY 757 TAGTCCAGATCTGTAAGTGAACCTTTCTACACTGATGAATATACATTAATCTATTT 816
DB 1110 TAGTCCAGATCTGTAAGTGAACCTTTCTACACTGATGAATATACATTAATCTATTT 1051
QY 817 CAAGAGCCCTTCTGTTGCTGCTCAATATATGACTGACTGTTTCTTAAGAGTGTCT 876
DB 1050 CAAGAGCCCTTCTGTTGCTGCTCAATATATGACTGACTGTTTCTTAAGAGTGTCT 991
QY 877 GGCCCGAGGATCTGTAACAGCTGGGAGCAATCTCAAGATCTTCCAGAGTTAATCT 936
DB 990 GGCCCGAGGATCTGTAACAGCTGGGAGCAATCTCAAGATCTTCCAGAGTTAATCT 931
QY 937 ACTAGCACAGCATGATCTTACGAGAGTAATATATCAATCAATCATCCAGAGTGC 996
DB 930 ACTAGCACAGCATGATCTTACGAGAGTAATATATCAATCAATCATCCAGAGTGC 871
QY 997 TTGGCCCATAGTAATTCATTTCCACTTTTGTGCCCATTCACAGACCTCAAAATGTC 1056

```
Db      870  |||||  
         TTGGCCATGAAATTCATTCCACTTTGTGCCCATCTCTCAAGACCTCAAAATGTC 811  
QY      1057 ATTCATTAAATCCACAGGATTACTTTTATTACCTGGAGAAATTCATGTTACAT 1116  
         |||||  
Db      810  ATTCATTAAATCCACAGGATTACTTTTATTACCTGGAGAAATTCATGTTACAT 751  
QY      1117 GCAGCTATGGGAATTTAATTAATTTGTTTCCAGTGCAGAAAGATGACTAAGTCCCTT 1176  
         |||||  
Db      750  GCAGCTATGGGAATTTAATTAATTTGTTTCCAGTGCAGAAAGATGACTAAGTCCCTT 691  
QY      1177 ATCCCTCCCTTTGTTGATTTTTCAGATAAAGTTAAATGCTTAGCCTGTACT 1236  
         |||||  
Db      690  ATCCCTCCCTTTGTTGATTTTTCAGATAAAGTTAAATGCTTAGCCTGTACT 631  
QY      1237 GAGGCTGTATACAGC 1251  
         |||||  
Db      630  GAGGCTGTATACAGC 616
```

Search completed: September 26, 2003, 22:20:44
Job time : 494.581 secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 26, 2003, 21:40:03 : Search time 107,441 Seconds
(without alignments)
7690,430 Million cell updates/sec

Title: US-09-402-713A-3

Perfect score: 1872

Sequence: 1 agaagctgctcagaaaaa.....caataaagattacaaga 1872

Scoring table:

Gapop 60.0 , Gapext 60.0

Searched: 569978 seqs, 220691566 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : Issued Patents_NA:*

1: /cgn2_6/ptodata/1/lna/5A.COMB.seq:*
2: /cgn2_6/ptodata/1/lna/5B.COMB.seq:*
3: /cgn2_6/ptodata/1/lna/6A.COMB.seq:*
4: /cgn2_6/ptodata/1/lna/6B.COMB.seq:*
5: /cgn2_6/ptodata/1/lna/PCTOS.COMB.seq:*
6: /cgn2_6/ptodata/1/lna/Backfile1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	1155	61.7	2426	4	US-09-439-313-470 Sequence 470, App
C 2	1155	61.7	2426	4	US-09-352-616A-470 Sequence 470, App
C 3	1155	61.7	3112	4	US-09-439-313-468 Sequence 468, App
C 4	1155	61.7	3112	4	US-09-352-616A-468 Sequence 468, App
C 5	1034	55.2	2229	4	US-09-439-313-469 Sequence 469, App
C 6	1034	55.2	2229	4	US-09-352-616A-469 Sequence 469, App
C 7	812	43.4	812	4	US-09-439-313-471 Sequence 471, App
C 8	812	43.4	812	4	US-09-352-616A-471 Sequence 471, App
C 9	257	13.7	718	4	US-09-439-313-313 Sequence 313, App
C 10	257	13.7	718	4	US-09-352-616A-313 Sequence 313, App
C 11	257	13.7	718	4	US-09-232-149A-313 Sequence 313, App
C 12	179	9.6	301	4	US-09-439-313-287 Sequence 287, App
C 13	179	9.6	301	4	US-09-352-616A-287 Sequence 287, App
C 14	179	9.6	301	4	US-09-232-149A-287 Sequence 287, App
C 15	26	1.4	1379	4	US-09-620-312D-791 Sequence 791, App
C 16	26	1.4	1462	4	US-09-620-312D-789 Sequence 789, App
C 17	26	1.4	1519	4	US-09-620-312D-789 Sequence 789, App
C 18	20	1.1	1664976	4	US-08-916-421B-1 Sequence 1, Appl
C 19	19	1.0	161	1	US-08-450-834-3 Sequence 10, Appl
C 20	19	1.0	98844	4	US-09-791-211-10 Sequence 10, Appl
C 21	18	1.0	3645	2	US-08-663-112-1 Sequence 1, Appl
C 22	18	1.0	4527	2	US-08-944-448-8 Sequence 8, Appl
C 23	18	1.0	4527	4	US-09-353-362-8 Sequence 8, Appl
C 24	18	1.0	8930	4	US-09-077-096A-1 Sequence 1, Appl
C 25	18	1.0	17000	4	US-09-679-299A-18 Sequence 18, Appl
C 26	18	1.0	72604	4	US-09-268-992-7 Sequence 7, Appl
C 27	18	1.0	72604	4	US-09-657-474-7 Sequence 7, Appl

C 28	18	1.0	99500	4	US-09-798-096-10 Sequence 10, Appl
C 29	17	0.9	157	1	US-08-392-678-11 Sequence 11, Appl
C 30	17	0.9	157	1	US-08-457-304A-11 Sequence 11, Appl
C 31	17	0.9	157	1	US-08-456-701A-11 Sequence 11, Appl
C 32	17	0.9	157	4	US-08-684-932A-11 Sequence 11, Appl
C 33	17	0.9	426	4	US-09-328-352+2225 Sequence 2225, Ap
C 34	17	0.9	590	4	US-09-364-206-25 Sequence 25, Appl
C 35	17	0.9	659	2	US-08-454-115-1 Sequence 1, Appl
C 36	17	0.9	831	1	US-08-450-834-5 Sequence 5, Appl
C 37	17	0.9	981	4	US-09-134-001C-982 Sequence 982, App
C 38	17	0.9	1017	4	US-09-328-475C-104 Sequence 104, App
C 39	17	0.9	1242	2	US-08-454-115-4 Sequence 4, Appl
C 40	17	0.9	2196	1	US-08-313-274-1 Sequence 1, Appl
C 41	17	0.9	2389	4	US-09-228-986-1 Sequence 1, Appl
C 42	17	0.9	2427	1	US-08-490-099-1 Sequence 1, Appl
C 43	17	0.9	2920	4	US-08-976-259-10 Sequence 10, Appl
C 44	17	0.9	3247	3	US-08-718-388-4 Sequence 4, Appl
C 45	17	0.9	3661	3	US-08-718-388-5 Sequence 5, Appl

ALIGNMENTS

RESULT 1									
US-09-439-313-470/c									
; Sequence 470, Application US/09439313									
; Patent No. 6329505									
; GENERAL INFORMATION:									
; APPLICANT: Xu, Jiangchun									
; APPLICANT: Dillon, David C.									
; APPLICANT: Mitcham, Jennifer L.									
; APPLICANT: Harlocker, Susan Louise									
; APPLICANT: Jiang Yugu									
; APPLICANT: Reed, Steven G.									
; APPLICANT: Fanger, Gary									
; APPLICANT: Retter, Mark									
; APPLICANT: Solk, John									
; APPLICANT: Day, Craig									
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND									
; FILE REFERENCE: 210121.427C9									
; CURRENT APPLICATION NUMBER: US/09/439, 313									
; CURRENT FILING DATE: 1999-11-12									
; NUMBER OF SEQ ID NOS: 575									
; SOFTWARE: FastSeq for Windows Version 3.0									
; SEQ ID NO 470									
; LENGTH: 2426									
; TYPE: DNA									
; ORGANISM: Homo sapiens									
; US-09-439-313-470									
Query Match									
Best Local Similarity 100.0%; Pred. No. 0;									
Matches 1155; Conservative 0; Mismatches 0; Indels 0; Gaps 0;									
QY	97	AGGTGGAATTAAGAAAGGCTGCTGACTTACCACCTGTGAGCCACACATCTCTGAATG	156						
DB	1770	AGGTGGAATTAAGAAAGGCTGCTGACTTACCACCTGTGAGCCACACATCTCTGAATG	1711						
QY	157	GAGTAATTAACATCACTGAGAAAGCAAGATGACAAATTAATGCTAAGTGACATG	216						
DB	1710	GAGTAATTAACATCACTGAGAAAGCAAGATGACAAATTAATGCTAAGTGACATG	1651						
QY	217	TTTTTGCAATTTCCAGCCCTTTAATATCCACACACAGAGCAACAAAGAGACA	276						
DB	1650	TTTTTGCAATTTCCAGCCCTTTAATATCCACACACAGAGCAACAAAGAGACA	1591						
QY	277	CAGAGATCCCTGGAGAAATGCGCGCCGCACTTTGGTCAATGATGACCTCGCCCTG	336						
DB	1590	CAGAGATCCCTGGAGAAATGCGCGCCGCACTTTGGTCAATGATGACCTCGCCCTG	1531						
QY	337	TGCCGTGTCCTGTTGTAGGAGACATTTGAAATATGATGCTTCCCTTAAAGC	396						

OY	937	ACTGACACAGCAGTGATCATTTAGGGAGTGAATTAATCAATCAATCATCTCAGTGTG	996
Db	930	ACTGACACACAGCAGTATCATTTAGGGAGTGAATTAATCAATCAATCATCTCAGTGTG	871
OY	997	TTTCCCATCTACTGAAATTCATTTCCACTTTTGTGCCCCATCTCAGACCTCAAAATGTC	1056
Db	870	TTTGCCCATCTGAAATTCATTTCCACTTTTGTGCCCCATCTCAGACCTCAAAATGTC	811
OY	1057	ATTCATTAATATCACAGGATTAACCTTTTTTTTTTAACCTGGAGAAATTCATGTTACAT	1118
Db	810	ATTCATTAATATCACAGGATTAACCTTTTTTTTTTAACCTGGAGAAATTCATGTTACAT	751
OY	1117	GCAGTATGGGAATTTTAATTCATATTTTGTTCCTCAGTGGAAAGATGACTAAGTCCTT	1176
Db	750	GCAGTATGGGAATTTTAATTCATATTTTGTTCCTCAGTGGAAAGATGACTAAGTCCTT	691
OY	1177	ATCCCTCCCTCTTGTGTGATTTTTTTTCCAGTATAAAGTTAAATGCTTAGCCTGTACT	1236
Db	690	ATCCCTCCCTCTTGTGTGATTTTTTTTCCAGTATAAAGTTAAATGCTTAGCCTGTACT	631
OY	1237	GAGGCTGTATACAGC 1251	
Db	630	GAGGCTGTATACAGC 616	
RESULT 3			
US-09-439-313-468			
Sequence 468, Application US/09439313			
Patent No. 6329505			
GENERAL INFORMATION:			
APPLICANT: Xu, Jiangchun			
APPLICANT: Dillon, Devin C.			
APPLICANT: Mitcham, Jennifer L.			
APPLICANT: Harlocker, Susan Louise			
APPLICANT: Jiang Yuqul			
APPLICANT: Reed, Steven G.			
APPLICANT: Kalos, Michael			
APPLICANT: Fanger, Gary			
APPLICANT: Retter, Mark			
APPLICANT: Solk, John			
APPLICANT: Day, Craig			
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND			
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER			
FILE REFERENCE: 210121.427C9			
CURRENT APPLICATION NUMBER: US/09/439,313			
CURRENT FILING DATE: 1999-11-12			
NUMBER OF SEQ ID NOS: 575			
SOFTWARE: FastSeq for Windows Version 3.0			
SEQ ID NO 468			
LENGTH: 3112			
TYPE: DNA			
ORGANISM: Homo sapiens			
US-09-439-313-468			
Query Match 61.7%; Score 1155; DB 4; Length 3112;			
Best Local Similarity 100.0%; Pred. No. 0;			
Matches 1155; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
OY	97	AGGTGAGAAATGAAGAAAGCTGCTGACTTTTACCATCTGAGGCCACACATCTGCTGAATG	156
Db	1312	AGGTGAGAAATGAAGAAAGCTGCTGACTTTTACCATCTGAGGCCACACATCTGCTGAATG	137
OY	157	GAGTAATTAATCAATCACTAGAAAGACAGACAAGATGACAAATATATGTCCTAAGTAGACATG	216
Db	1372	GAGTAATTAATCAATCACTAGAAAGACAGACAAGATGACAAATATATGTCCTAAGTAGACATG	143
OY	217	TTTTTGACATTTCTCAGGCCCTTTAAATATATCACACACAGAGGAAGACAAAGAGACGA	276
Db	1432	TTTTTGACATTTCTCAGGCCCTTTAAATATATCACACACAGAGGAAGACAAAGAGACGA	149
OY	277	CAGAGATCCCTGGGAGAAATGCCGGCCGACATCTTGGGTATGATGATGAGCCTGGCCCTG	336
Db	277	CAGAGATCCCTGGGAGAAATGCCGGCCGACATCTTGGGTATGATGATGAGCCTGGCCCTG	336

Db	1492	CAGAGATCCCTGGGAGAAATGCTCCGGCCGACATCTTGGGTGATGATGAGGCTCGCCTG	151
QY	337	TGCTCGGTCCCGCTTTGTGAGGGAAGGACATTAGAAAAATGAATGTATGTCTTTAAAG	396
Db	1552	TGCCTGTGGTCCCGCTTGTGAGGGAAGGACATTAGAAAAATGAATGTATGTCTTTAAAG	1611
QY	397	ATGGGAGGAAACAGATCCTGTGTGGATTTTATTTGAACGGGATTTACGATTTGAA	456
Db	1612	ATGGGAGGAAACAGATCCTGTGTGGATTTTATTTGAACGGGATTTACGATTTGAA	1671
QY	457	TGAAGTCACAAAGTGAGCATTTACCAATGAGAGAAAAAGACGAGAAAAATTTGATGCT	516
Db	1672	TGAGTGACCAAGTGAGCATTTACCAATGAGAGAAAAAGACGAGAAAAATTTGATGCT	1731
QY	517	TCACAGACATGCAACAAACAAAATGGAATCTGTGATGACATGAGGACGCAAGCTGGG	576
Db	1732	TCACAGACATGCAACAAACAAAATGGAATCTGTGATGACATGAGGACGCAAGCTGGG	1791
QY	577	GAGGAGATTAACACAGGGGACAGAGGTACAGATTTGGGCCCGTGGCTAAACGTGGGT	636
Db	1792	GAGGAGATTAACACAGGGGACAGAGGTACAGATTTGGGCCCGTGGCTAAACGTGGGT	1851
QY	637	CATAACCAATCATTTTCATTTTTCATACCCCTCAACAAACAAAGCTTTGTAATCTGATCT	696
Db	1852	CATAACCAATCATTTTCATTTTTCATACCCCTCAACAAACAAAGCTTTGTAATCTGATCT	1911
QY	697	CTAGCGTTCCCTTGTGGGCCCAACATTTCTCATATATCCAGCCACATCTATTTTAATTT	756
Db	1912	CTAGCGTTCCCTTGTGGGCCCAACATTTCTCATATATCCAGCCACATCTATTTTAATTT	1971
QY	757	TAGTTCCCAATCTGTGACTGTGACCTTTCTACACTGTAGAAATACATTACTCATTTTGT	816
Db	1972	TAGTTCCCAATCTGTGACTGTGACCTTTCTACACTGTAGAAATACATTACTCATTTTGT	2031
QY	817	CAAGACCCCTCGTGTGTGCTCCCTAATATGAGCTGACTGTTTTCCTAAGAGATGTCT	876
Db	2032	CAAGACCCCTCGTGTGTGCTCCCTAATATGAGCTGACTGTTTTCCTAAGAGATGTCT	2091
QY	877	GGCCGAGGGATCTGTGAACAGGCTGGGAGACATCTCAGATCTTTCAGGGTATACTT	936
Db	2092	GGCCGAGGGATCTGTGAACAGGCTGGGAGACATCTCAGATCTTTCAGGGTATACTT	2151
QY	937	ACTAGCACACGACATGATCATTTAGGAGTGAATTATCTAATCAACATCATCTCTAGTCT	996
Db	2152	ACTAGCACACGACATGATCATTTAGGAGTGAATTATCTAATCAACATCATCTCTAGTCT	2211
QY	997	TTTGCCCACTAGTAATTCATTTCCACTTTTGGCCCATCTCTCAGACCTCAAAATGTC	1056
Db	2212	TTTGCCCACTAGTAATTCATTTCCACTTTTGGCCCATCTCTCAGACCTCAAAATGTC	2271
QY	1057	ATTCACATTAATACAGAGATTAACTTTTTTTTTTAAACCTGAGAAATTCATCTTACAT	1116
Db	2272	ATTCACATTAATACAGAGATTAACTTTTTTTTTTAAACCTGAGAAATTCATCTTACAT	2331
QY	1117	GCAGCTATGGAAATTTAATTACATATTTTGTTCACGTGCAAAAGATGACTATGCTTT	1176
Db	2332	GCAGCTATGGAAATTTAATTACATATTTTGTTCACGTGCAAAAGATGACTATGCTTT	2391
QY	1177	ATCCCTCCCTTTGTGTGATTTTTTTTTCGATATAAAGTTAAATGCTTAGCCTTGACT	1236
Db	2392	ATCCCTCCCTTTGTGTGATTTTTTTTTCGATATAAAGTTAAATGCTTAGCCTTGACT	2451
QY	1237	GAGGCTGTATACAGC 1251	
Db	2452	GAGGCTGTATACAGC 2466	

APPLICANT: Harlocker, Susan Louise
APPLICANT: Jiang, Yugu
APPLICANT: Xu, Jiangchun
APPLICANT: Mitcham, Jennifer Lynn
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
FILE REFERENCE: 210121.427C8
CURRENT APPLICATION NUMBER: US/09/352.616A
NUMBER OF FILING DATE: 1999-07-13
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 468
LENGTH: 3112
TYPE: DNA
ORGANISM: Homo sapiens
US-09-352-616A-468

Query Match 61.7%; Score 1155; DB 4; Length 3112;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1155; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 97 AGGTGAGAAATTAAGAAAGGCTGCTGACTTACATCTGAGGCCACACATCTGCTGAATG 156
DB 1312 AGGTGAGAAATTAAGAAAGGCTGCTGACTTACATCTGAGGCCACACATCTGCTGAATG 1371
QY 157 GAGATAATTAACATCACTAGAAACAGAGATGCAATATATGCTAAGTAGACATG 216
DB 1372 GAGATAATTAACATCACTAGAAACAGAGATGCAATATATGCTAAGTAGACATG 1431
QY 217 TTTTGGACATTTCCACCCCTTAAATATCCACACACAGGAAACAAAGAGCA 276
DB 1432 TTTTGGACATTTCCACCCCTTAAATATCCACACACAGGAAACAAAGAGCA 1491
QY 277 CAGAGATCCCTGGGAGAAATGCCCGGCCCATCTTGGGTCATGATGAGCCTCGCCTG 336
DB 1492 CAGAGATCCCTGGGAGAAATGCCCGGCCCATCTTGGGTCATGATGAGCCTCGCCTG 1551
QY 337 TGCTGGTCCCGCTGTGTGAGGAAAGCATTAAGAAATGAATGATGTCTTCTTAAAG 366
DB 1552 TGCTGGTCCCGCTGTGTGAGGAAAGCATTAAGAAATGAATGATGTCTTCTTAAAG 1611
QY 397 ATGGGCGAGAAACAGATCCCTGTGTGATATTTATTTGAACGGGATTAAGATTGAAA 456
DB 1612 ATGGGCGAGAAACAGATCCCTGTGTGATATTTATTTGAACGGGATTAAGATTGAAA 1671
QY 457 TGAAGTCACAAGTACATTAACATGAGAGGAAACAGACGAGAAATCTTGATGCT 516
DB 1672 TGAAGTCACAAGTACATTAACATGAGAGGAAACAGACGAGAAATCTTGATGCT 1731
QY 517 TCACAAACATGCAACAAACAAATGGAATGATGTGATGACATGAGCAGCCAAAGCTGG 576
DB 1732 TCACAAACATGCAACAAACAAATGGAATGATGTGATGACATGAGCAGCCAAAGCTGG 1791
QY 577 GAGAGATACCAACGAGGAGAGGATGAGATTCCTGCGCTGCTTAAACGTGGCT 636
DB 1792 GAGAGATACCAACGAGGAGAGGATGAGATTCCTGCGCTGCTTAAACGTGGCT 1851
QY 637 CATACCAATTCATTTCTAATTTCTAACCCTCAAAACAAAGCTGTTTAAATCTGATCT 696
DB 1852 CATACCAATTCATTTCTAATTTCTAACCCTCAAAACAAAGCTGTTTAAATCTGATCT 1911
QY 697 CTACGGTCTCTGCGGCCCAACATCTTCATATATCCAGCCACATCTTTTAAATAT 756
DB 1912 CTACGGTCTCTGCGGCCCAACATCTTCATATATCCAGCCACATCTTTTAAATAT 1971
QY 757 TAATTCACAGATCTGATCTGACCTTTCTACACTGAGATAACATTAACATTTTGT 816
DB 1972 TAATTCACAGATCTGATCTGACCTTTCTACACTGAGATAACATTAACATTTTGT 2031
QY 817 CAAAGACCTTCTGTGTGCTGCTAATATATGATGATGATGATGATGATGATGATGAT 876
DB 2032 CAAAGACCTTCTGTGTGCTGCTAATATATGATGATGATGATGATGATGATGATGAT 2091

QY 877 GCGCCAGGAGATCTGTGACAGCGCTGGGAAACATCTCAAGATCTTCCAGGTTACTT 936
DB 2092 GCGCCAGGAGATCTGTGACAGCGCTGGGAAACATCTCAAGATCTTCCAGGTTACTT 2151
QY 937 ACTAGCACACAGCATGATCATTTACGAGTGAATATATCAACATCATCTGAGTGC 996
DB 2152 ACTAGCACACAGCATGATCATTTACGAGTGAATATATCAACATCATCTGAGTGC 2211
QY 997 TTTGCCATCTAGTAAATTCATTTTCCACTTTTGGCCATTTCTCAAGCTCAAAATGTC 1056
DB 2212 TTTGCCATCTAGTAAATTCATTTTCCACTTTTGGCCATTTCTCAAGCTCAAAATGTC 2271
QY 1057 ATTCATTAATATACAGAGATTAACCTTTTTTTTAACTGAGAAATTAATGTTACAT 1116
DB 2272 ATTCATTAATATACAGAGATTAACCTTTTTTTTAACTGAGAAATTAATGTTACAT 2331
QY 1117 GCAGCTATGGGAATTTAATTAATTTGTTTCCAGTGCAGAGATGACTAAGTCTT 1176
DB 2332 GCAGCTATGGGAATTTAATTAATTTGTTTCCAGTGCAGAGATGACTAAGTCTT 2391
QY 1177 ATCCCTCCCTTTGTTGATTTTTTCCAGTATTAAGTTAAATGCTTAGCCTGTACT 1236
DB 2392 ATCCCTCCCTTTGTTGATTTTTTCCAGTATTAAGTTAAATGCTTAGCCTGTACT 2451
QY 1237 GAGGCTGTATACAGC 1251
DB 2452 GAGGCTGTATACAGC 2466

RESULT 5

US-09-439-313-469/c
Sequence 469, Application US/09439313
Patent No. 6329505
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan Louise
APPLICANT: Jiang Yugu
APPLICANT: Reed, Steven G.
APPLICANT: Kalos, Michael
APPLICANT: Fanger, Gary
APPLICANT: Retter, Mark
APPLICANT: Solk, John
APPLICANT: Day, Craig
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
FILE REFERENCE: 210121.427C9
CURRENT APPLICATION NUMBER: US/09/439, 313
NUMBER OF FILING DATE: 1999-11-12
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 469
LENGTH: 2229
TYPE: DNA
ORGANISM: Homo sapiens
US-09-439-313-469

Query Match 55.2%; Score 1034; DB 4; Length 2229;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1154; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 97 AGGTGAGAAATTAAGAAAGGCTGCTGACTTACATCTGAGGCCACACATCTGCTGAATG 156
DB 1776 AGGTGAGAAATTAAGAAAGGCTGCTGACTTACATCTGAGGCCACACATCTGCTGAATG 1717
QY 157 GAGATAATTAACATCACTAGAAACAGAGATGCAATATATGCTAAGTAGACATG 216
DB 1716 GAGATAATTAACATCACTAGAAACAGAGATGCAATATATGCTAAGTAGACATG 1657
QY 217 TTTTGGACATTTCCACCCCTTAAATATCCACACACAGAGAGCAAAAGAGCA 276
DB 1656 TTTTGGACATTTCCACCCCTTAAATATCCACACACAGAGAGCAAAAGAGCA 1597

QY	277	CAGAGATCCCTGGGAGAAATGCCCGGCCCATCTTGGGTATGATGAGCCTCGCCCTG	336
Db	1596	CAGAGATCCCTGGGAGAAATGCCCGGCCCATCTTGGGTATGATGAGCCTCGCCCTG	1537
QY	337	TGCCCTGGGCCGCTTGAGGAGGAGCAATAGAAAAATGAATGTGATGCTCTTAAGG	396
Db	1536	TGCCCTGGGCCGCTTGAGGAGGAGCAATAGAAAAATGAATGTGATGCTCTTAAGG	1477
QY	397	ATGGGCGAGAAAACAGATCCGTGTGTGATATTTATTTGAAAGGGATTACAGATTTGAA	456
Db	1476	ATGGGCGAGAAAACAGATCCGTGTGTGATATTTATTTGAACGGGATTACAGATTTGAA	1417
QY	457	TGAAGTCACAAAGTGAGCATTACCAATGAGAGGAAAACAGCGAGAAATCTTGATGCT	516
Db	1416	TGAAGTCACAAAGTGAGCATTACCAATGAGAGGAAAACAGCGAGAAATCTTGATGCT	1357
QY	517	TCACAAACATGCAACAACAAAATGGAATTCGTGATGATGACATGAGGACGCAACGTGG	576
Db	1356	TCACAAACATGCAACAACAAAATGGAATTCGTGATGATGACATGAGGACGCAACGTGG	1297
QY	577	GAGAGATTAACCAACGGGGCAGAGGGTCAGGATTCGTGGCCCTGCTGCTAACTGTGCTT	636
Db	1296	GAGAGATTAACCAACGGGGCAGAGGGTCAGGATTCGTGGCCCTGCTGCTAACTGTGCTT	1237
QY	637	CATTAACCAATTCATTTTATTTTCTAAACCCCAAAACAAGCTGTGTAATCTGATCT	696
Db	1236	CATTAACCAATTCATTTTATTTTCTAAACCCCAAAACAAGCTGTGTAATCTGATCT	1177
QY	697	CTACGGTTCCTCTTGGGGCCCAACATTCCTCATATATCAGGCACACATCTTTTAATTT	756
Db	1176	CTACGGTTCCTCTTGGGGCCCAACATTCCTCATATATCAGGCACACATCTTTTAATTT	1117
QY	757	TAGTTCCAGATCTGTACTGTGACCTTTCTACACTGTAAGATTAACATTCATTTGTT	816
Db	1116	TAGTTCCAGATCTGTACTGTGACCTTTCTACACTGTAAGATTAACATTCATTTGTT	1057
QY	817	CAAAGACCCTTCGGTGTGCTGCCCTAATATGATGAGTGAAGTCTGTTTCTCAAGAGCTGCT	876
Db	1056	CAAAGACCCTTCGGTGTGCTGCCCTAATATGATGAGTGAAGTCTGTTTCTCAAGAGCTGCT	997
QY	877	GGCCAGAGGGATCTGTGTAAACAGGCTGGGAACATCTCAAGATCTTCCAGGGTATACTT	936
Db	996	GGCCAGAGGGATCTGTGTAAACAGGCTGGGAACATCTCAAGATCTTCCAGGGTATACTT	937
QY	937	ACTAGCACACAGCATGATCATTTACGAGTGAATATCTAATCAACATCATCTCAGTGTG	996
Db	936	ACTAGCACACAGCATGATCATTTACGAGTGAATATCTAATCAACATCATCTCAGTGTG	877
QY	997	TTTTCGCATCTGAAATTCATTTTCCCACTTTTGGCCATCTCAAGACCTCAAAATGTC	1056
Db	876	TTTTCGCATCTGAAATTCATTTTCCCACTTTTGGCCATCTCAAGACCTCAAAATGTC	817
QY	1057	ATTCCATTAAATCACAGATTAACCTTTTCTTAAACCTGGAGAAATTCATGTACAT	1116
Db	816	ATTCCATTAAATCACAGATTAAC-CTTTTCTTAAACCTGGAGAAATTCATGTACAT	758
QY	1117	GCAGCTATGGGAATTTAATTCATATTTTGTTTCCAGTGCAGAAAGATGACTAAGTCTTT	1176
Db	757	GCAGCTATGGGAATTTAATTCATATTTTGTTTCCAGTGCAGAAAGATGACTAAGTCTTT	698
QY	1177	ATCCCTCCCTTGTGTGATTTTTTTTCCAGTATAAAGTTAAATGCTTACCTGTACT	1236
Db	697	ATCCCTCCCTTGTGTGATTTTTTTTCCAGTATAAAGTTAAATGCTTACCTGTACT	638
QY	1237	GAGGCTGTATACAGC 1251	
Db	637	GAGGCTGTATACAGC 623	

RESULT 6
US-09-352-616A-469/c
; Sequence 469, Application US/09352616A

```

? Patent No.6395278
? GENERAL INFORMATION:
? APPLICANT: Dillon, Davin C.
? APPLICANT: Harlocker, Susan Louise
? APPLICANT: Jiang, Yuguai
? APPLICANT: Xu, Jiangchun
? APPLICANT: Mitcham, Jennifer Lynn
? TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
? TITLE OF INVENTION: OF PROSTATE CANCER AND METHODS FOR THEIR USE
? FILE REFERENCE: 210121.427C8
? CURRENT APPLICATION NUMBER: US/09/352.616A
? CURRENT FILING DATE: 1999-07-13
? NUMBER OF SEQ ID NOS: 472
? SOFTWARE: FastSeq for Windows Version 3.0
? SEQ ID NO 469
? LENGTH: 2229
? TYPE: DNA
? ORGANISM: Homo sapiens
? US-09-352-616A-469

```

Query Match	Score	DB	Length
55.28;	1034;	4;	2229;

Best Local Similarity	99.96;	Pred.No. 0;
Matches 1154;	Conservative	0;
Mismatches	0;	Indels 1;
		Gaps 1;

97 AGGTGAGAAATAGAAAGGCTGCTGACTTTACCATCTGAGAGGCCACACATCTGCTGAAATG 156

1776 ACCTACAGAAATTAAGAAACCCGCGCGACGTTTACGATCGCGACCGCGACACATCGCGCGAATAC 1717

[illegible]

157 GAGCAATTTAACATCACACAGAAACAGCAAGATGACATATATAATGTCATAGTAGTGACATG 216

Db 1716 GAGATAATTACATCAGCTAGAAACAGCAAGATGACATATATATGCTTAAGTAGTGACATG 1657

217 TTTTTCACATTTCACAGCCCTTAAATATCCACACACAGCAAGCAAAAGGAGCA 276

Db 1656 TTTTTCACATTTCACAGCCCTTTAAATATCGACACACAGGAACCAAAAAGGAAGCA 1597

277 CAGAGATCCCTGGGAGAAATGCCCGCCCATCTTGGTCATCGATGAGCCTCGCCCTG 336

Db 1596 CAGAGATCCCTGGGAGAAATGCCCGGCGCGCATCTTGGGTCATGATGAGCCGCGCCG 1537

337 TTCTTCCCTCCTTCCTGACAGCAATTTACAAATAACAATTCTCTCTTAAAGCG 306

[illegible]

Db 1536 TGCCTGGTCCCGCTTGTGAGGGAAGACATTAGAAATGAATTGAATGTTCCCTAAAGG 1477

397 ATGGCGAGAAACAGATCTGTGTGGATATTTATTTCACGGGATTTACAGATTTGAAA 456

Db 1476 ATGGCAGGAAACAGATCTTGTGTGATATTATTGACGGGATTACAGATTGAAA 1417

457 TGAAGTCACAAAGTGAGCA TTACCAATGAGAGGAAACAGACGAGAAAATCTTGATGGCT 516

Db 1416 TGAAGTCACAAAGTGAGCACTTACCAATGAGAGCAAAACAGACGAGAAAAATCTTGATGGCT 1357

517 TCACAGACATGCAACACAATAATGGAATACCTGTGATGACATGAGCCAGCCAAAGCTGGG 576

Dh
1356 TTTCTGACATCCAGCAACAACAATCATCAGTCCAGCGAAGCGG 1297

[illegible]

QY 5' / GAGAGCAATACCCAGGGGATCAGAGATCTGGCCCTGCTGCCAATCTGTGCGTT 636

Db 1296 GAGGAGATTAACCCAGGGGTCAGGATTCGGCCCTGCTGCCTAAACTGTGGCTT 1237

637 CATACCAATCATTTTCATATTTCTAACCCCAAAACAAGCTGTGTAATATCTGATCT 696

Db 1236 CATTACCAATCATTTTCATATTCTTAACCGTCAAAACAAAGCTGTGTATATCTGATCT 1177

697 CTACGGTTCCTTCGCGCCACACATTCCTCATATATCCAGCCACACTCATTTTAAATATT 756

Db 1176 CTACGGTTCCTTCTGGGCGCAACA^{TTTCT}CA^{TATAT}CAAGCACA^{CTCA^{TTTTTTT}AA^{TAT}}TTT 1117

[illegible][illegible]

DB 1116 TAGTTCACAGATCTGACCTTCTACACGTAGAGATACACTTACCTATTCTT 1057

817 CAAAGACCCCTTCGTGTTGCTGCCTAATATATGTAGCTGACTGTTTTTCCTAAGGAGCTGTCT 876

Best Local Similarity 100.0%; Pred. No. 0;
Matches 812; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY 6 CTGGATCAGAAAAACAGAGGGAGATTTGTGCTGCTGACCCGAGGGAGACAGAGA 65
DB 812 CTGGATCAGAAAAACAGAGGGAGATTTGTGCTGCTGACCCGAGGGAGACAGAGA 753
QY 66 TCTGATGTTGGGAGGACCTGATATACAGAGTGAGAGAAATAAAGAGGCTGACACT 125
DB 752 TCTGATGTTGGGAGGACCTGATATACAGAGTGAGAGAAATAAAGAGGCTGACACT 693
QY 126 TACCATCTGAGGCCACACATCTGCTGAATAGAGATTAATTAACATCAGTAAGACGCA 185
DB 692 TACCATCTGAGGCCACACATCTGCTGAATAGAGATTAATTAACATCAGTAAGACGCA 633
QY 186 GATGACAAATTAATGCTTAAGTAGTACATGTTTTTGCACATTTCCAGCCCTTTAAATA 245
DB 632 GATGACAAATTAATGCTTAAGTAGTACATGTTTTTGCACATTTCCAGCCCTTTAAATA 573
QY 246 TCCACACACAGAGAGCAAAAAAGSAGCAGACAGATCCCTGGAGAAATGCCGGCCG 305
DB 572 TCCACACACAGAGAGCAAAAAAGSAGCAGACAGATCCCTGGAGAAATGCCGGCCG 513
QY 306 CCATCTTGGTCAATGATGAGCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 365
DB 512 CCATCTTGGTCAATGATGAGCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 453
QY 366 TTGAAATTAATGATGATGCTGCTTAAAGATGGGACAGAAACAGATCCTGTTGTGGA 425
DB 452 TTGAAATTAATGATGATGCTGCTTAAAGATGGGACAGAAACAGATCCTGTTGTGGA 393
QY 426 TATTAATTTGAACGGGATTTACAGATTTGAATGAATGAATGAATGAATGAATGAATGA 485
DB 332 TATTAATTTGAACGGGATTTACAGATTTGAATGAATGAATGAATGAATGAATGAATGA 333
QY 486 GAGGAAAAACAGACGAGAAATCTTGATGCTTACACAGACATGCAACAAACAAATGGA 545
DB 332 GAGGAAAAACAGACGAGAAATCTTGATGCTTACACAGACATGCAACAAACAAATGGA 273
QY 546 TACTGTGATGACATGAGCAGCAGCTGGGGAGAGATTAACACAGGGGACAGAGGCTCAG 605
DB 272 TACTGTGATGACATGAGCAGCAGCTGGGGAGAGATTAACACAGGGGACAGAGGCTCAG 213
QY 606 GATTCGCGCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 665
DB 212 GATTCGCGCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 153
QY 666 CTCAAAACAAAGCTGTTGTAATCTGATCTCTACGTTCTCTGCGGCCCAACAATCTTC 725
DB 152 CTCAAAACAAAGCTGTTGTAATCTGATCTCTACGTTCTCTGCGGCCCAACAATCTTC 93
QY 726 CATATATCCAGCAGCAGCTGATTTTAATATTTAGTCCAGATCTGTAAGCTGACCTTTC 785
DB 92 CATATATCCAGCAGCAGCTGATTTTAATATTTAGTCCAGATCTGTAAGCTGACCTTTC 33
QY 786 TACACTGTAGATATACATTACTCATTTTGTTC 817
DB 32 TACACTGTAGATATACATTACTCATTTTGTTC 1

RESULT 9
US-09-439-313-313
; Sequence 313, Application US/09439313
; Patent No. 6329505
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan Louise
; APPLICANT: Jiang Yuxui
; APPLICANT: Reed, Steven G.
; APPLICANT: Kalos, Michael
; APPLICANT: Fanger, Gary
```

```
; APPLICANT: Retter, Mark
; APPLICANT: Solk, John
; APPLICANT: Day, Craig
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
; FILE REFERENCE: 210121.427C9
; CURRENT APPLICATION NUMBER: US/09/439,313
; CURRENT FILING DATE: 1999-11-12
; NUMBER OF SEQ ID NOS: 575
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 313
; LENGTH: 718
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(718)
; OTHER INFORMATION: n = A,T,C or G
US-09-439-313-313

Query Match 13.7%; Score 257; DB 4; Length 718;
Best Local Similarity 99.4%; Pred. No. 1,1e-114;
Matches 357; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 42 TGCAGCCGAGGAGACAGGAAGATCTGATGCTGGAGGACCTGATGATACAGAGTG 101
DB 17 TGCAGCCGAGGAGACAGGAAGATCTGATGCTGGAGGACCTGATGATACAGAGTG 76
QY 102 AGAAATTAAGAAAGCTGCTGACTTTACATCTGAGGCCACACATCTGCTGAATGAGAT 161
DB 77 AGAAATTAAGAAAGCTGCTGACTTTACATCTGAGGCCACACATCTGCTGAATGAGAT 136
QY 162 AATTAACATCACTAGAAACAGACATGACATTAATATGCTTAAGTAGACATGTTTTT 221
DB 137 AATTAACATCACTAGAAACAGACATGACATTAATATGCTTAAGTAGACATGTTTTT 196
QY 222 GCACATTTCCAGCCCTTTAATATCCACACACAGAGAGCAAAAGAGACAGAG 281
DB 197 GCACATTTCCAGCCCTTTAATATCCACACACAGAGAGCAAAAGAGACAGAG 256
QY 282 ATCCCTGGAGAAATGCCCCGCCCATCTTGATCATGATGAGCCTCGCCCTGCT 341
DB 257 ATCCCTGGAGAAATGCCCCGCCCATCTTGATCATGATGAGCCTCGCCCTGCT 316
QY 342 GGTCCCGCTTGAGAGGAGACATTAAGAAATGAATGATGCTTCTTAAGATG 400
DB 317 GNTCCCGCTTGAGAGGAGACATTAAGAAATGAATGATGCTTCTTAAGATG 375

RESULT 10
US-09-352-616A-313
; Sequence 313, Application US/09352616A
; Patent No. 6395278
; GENERAL INFORMATION:
; APPLICANT: Dillon, Davin C.
; APPLICANT: Harlocker, Susan Louise
; APPLICANT: Jiang, Yuxui
; APPLICANT: Xu, Jiangchun
; APPLICANT: Mitcham, Jennifer Lynn
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
; FILE REFERENCE: 210121.427C8
; CURRENT APPLICATION NUMBER: US/09/352,616A
; CURRENT FILING DATE: 1999-07-13
; NUMBER OF SEQ ID NOS: 472
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 313
; LENGTH: 718
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(718)
```


OTHER INFORMATION: n = A,T,C or G
US-09-352-616A-313

Query Match	13.78;	Score 257;	DB 4;	Length 718;
Best Local Similarity	99.48;	Pred. No. 1.1e-114;		
Matches 357;	Conservative	0;	Mismatches 2;	Indels 0;
				Gaps 0;

QY	42	TGAGCGGAGGAGACACAGAAAGATCGATGCTGGGAAGGACCTGATGATACAGAGTG	102
Db	17	TGAGCGGAGGAGACACAGAAAGATCGATGCTGGGAAGGACCTGATGATACAGAGTG	76
QY	102	AGAAATAGAAAGGCTGCTGACTTTACATCTGAGGCCACACATCTGCTGAATAGAGAT	162
Db	77	AGAAATAGAAAGGCTGCTGACTTTACATCTGAGGCCACACATCTGCTGAATAGAGAT	132
QY	162	AATTAACATCAGTACAGAAACAGACAGATGATATATATGCTAACTAGTGCATGTTTT	222
Db	137	AATTAACATCAGTACAGAAACAGACAGATGATATATATGCTAACTAGTGCATGTTTT	192
QY	222	GCACATTTCCAGCCCTTTAAATATCCACACACACAGGAAGCAGAAAGAACACAGAG	282
Db	197	GCACATTTCCAGCCCTTTAAATATCCACACACAGGAAGCAGAAAGAACACAGAG	252
QY	282	ATACCTGGGAGAAATGCCGCCGCATTTGGGTCATGATGAGACCTCGCCCTGTGGCT	342
Db	257	ATCCTGGGAGAAATGCCGCCGCATTTGGGTCATGATGAGACCTCGCCCTGTGGCT	312
QY	342	GGTCGCCGCTTGAGGGAAGAGCATTTAGAAAATGAATTGATGTCTTCTTAAAGATGG	400
Db	317	GGTCGCCGCTTGAGGGAAGAGCATTTAGAAAATGAATTGATGTCTTCTTAAAGATGG	375

RESULT 11
US-09-232-149A-313
: Sequence 313, Application US/09232149A

```

GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer Lynn
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE
TITLE OF INVENTION: CANCER AND METHODS FOR THEIR USE
FILE REFERENCE: 210121.427C6
CURRENT APPLICATION NUMBER: US/09/232,149A
CURRENT FILING DATE: 1999-01-15
NUMBER OF SEQ ID NOS: 338
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 313
LENGTH: 718
TYPE: DNA
ORGANISM: Homo sapien
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)..(718)
OTHER INFORMATION: n = A,T,C or G
US-09-232-149A-313

```

Query Match	13.7%	Score 257;	DB 4;	Length 718;
Best Local Similarity	99.48;	Pred. No. 1.1e-114;		
Matches 357; Conservative	0;	Mismatches 2;	Indels 0;	Gaps 0;

[illegible]

QY	222	GCACATTTTCAGCCCTTTAAATATTCACACACAGAAACACAAAAAGAAACACAG	281
	197	GCACATTTTCAGCCCTTTAAATATTCACACACACAGAAACACAAAAAGAAACACAG	256
QY	282	ATCCCTGGGGAATATCCCGCCGCAATCTTGGGTATCGATGAGCCCTGCCCTGTACCT	341
	257	ATCCCTGGGGAATATCCCGCCGCAATCTTGGGTATCGATGAGCCCTGCCCTGTACCT	316
QY	342	GATCCCGCTGTGAGGGAAGACATTTAGAAAAATGAAATGATGTATCTTAAAGATGG	400
	317	GATCCCGCTGTGAGGGAAGACATTTAGAAAAATGAAATGATGTATCTTAAAGATGG	375

RESULT 12
US-09-439-313-287/c
; Sequence 287, Application US/09439313

```

GENERATED INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan Louise
APPLICANT: Jiang Yuqi
APPLICANT: Reed, Steven G.
APPLICANT: Kalos, Michael
APPLICANT: Fanger, Gary
APPLICANT: Retter, Mark
APPLICANT: Solk, John
APPLICANT: Day, Craig
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.42769
CURRENT APPLICATION NUMBER: US/09/439,313
CURRENT FILING DATE: 1999-11-12
NUMBER OF SEQ ID NOS: 575
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 287
LENGTH: 301
TYPE: DNA
ORGANISM: Homo sapien
US-09-439-313--287

```

Query Match	9.68;	Score 179;	DB 4;	Length 301;
Best Local Similarity	99.68;	Pred. No. 6.2e-77;		
Matches 229;	Conservative 0;	Mismatches 1;	Indels 0;	Gaps 0

QY	472	AGCATTTACCAATGAGAGGAAAAACACACAGAAAATCTTGATGGCTTCAACAAGACATCCAA	531
Db	301	AGCATTTACCAATGAGAGGAAAAACACACAGAAAATCTTGATGGCTTCAACAAGACATCCAA	242
QY	532	CAAAACAAAATGGAAATPACTGTGATGACATGAGGACGACCAAGCTGGGGAGGAGATPACACG	591
Db	241	CAAAACAAAATGGAAATCTGTGATTAACATGAGGACGACCAAGCTGGGGAGGAGATPACACG	182
QY	592	GGGCAGAGGGTCAGAGTTCTGGCCCTGCTGCCTTAACTGTGCGTTTCATTAACCAATTCATT	651
Db	181	GGGCAACAGGGTCAGAGTTCTGGCCCTGCTGCCTTAACTGTGCGTTTCATTAACCAATTCATT	122
QY	652	TCCATATTTCCAAACCCCAAAACAAAGCGTTGTAAATCAGATCCGTAACG	701
Db	121	TCCATATTTCCAAACCCCAAAACAAAGCGTTGTAAATCAGATCCGTAACG	72

RESULT 13
US-09-352-616A-287/c
; Sequence 287, Application US/09352616A

```

: GENERAL INFORMATION:
: APPLICANT: Dillon, Davin C.
: APPLICANT: Harlocker, Susan Louise
: APPLICANT: Jiang, Yuyu
: APPLICANT: Xu, Jiaqun
: APPLICANT: Mitcham, Jennifer Lynn

```



```
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
; FILE OF INVENTION: OF PROSTATE CANCER AND METHODS FOR THEIR USE
; CURRENT FILING DATE: 1999-07-13
; CURRENT FILING DATE: 1999-07-13
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 287
; LENGTH: 301
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-352-616A-287
```

```
Query Match          9.6%; Score 179; DB 4; Length 301;
Best Local Similarity 99.6%; Pred. No. 6,2e-77;
Matches 229; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 472 AGCATTACCAATGAGAGGAAACAGACGAGAAATCTTGATGGCTTACACAGATGCA 531
    |||||||
DB 301 AGCATTACCAATGAGAGGAAACAGACGAGAAATCTTGATGGCTTACACAGATGCA 242

QY 532 CAAACAAAATGGAATGACTGTGTGATGACATGAGCGACCAAGCTGGGAGAGATTAACACG 591
    |||||||
DB 241 CAAACAAAATGGAATGACTGTGTGATGACATGAGCGACCAAGCTGGGAGAGATTAACACG 182

QY 592 GGGCAGAGGGTCTGAGATTCCTGCGCTGCTGCTAAACCTGGCTTCAATCAACCAATCATT 651
    |||||||
DB 181 GGGCAGAGGGTCTGAGATTCCTGCGCTGCTGCTTAACTGCTGCTTCAATCAACCAATCATT 122

QY 652 TCATATTTCTAACCCTCAAAACCAAGCTGTGTAAATCTGATCTCTACG 701
    |||||||
DB 121 TCATATTTCTAACCCTCAAAACCAAGCTGTGTAAATCTGATCTCTACG 72
```

```
RESULT 14
US-09-232-149A-287/c
; Sequence 287, Application US/09232149A
; Patent No. 6465611
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, David C.
; APPLICANT: Mitcham, Jennifer Lynn
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE
; FILE OF INVENTION: CANCER AND METHODS FOR THEIR USE
; CURRENT FILING DATE: 1999-01-15
; CURRENT FILING DATE: 1999-01-15
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 287
; LENGTH: 301
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-232-149A-287
```

```
Query Match          9.6%; Score 179; DB 4; Length 301;
Best Local Similarity 99.6%; Pred. No. 6,2e-77;
Matches 229; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 472 AGCATTACCAATGAGAGGAAACAGACGAGAAATCTTGATGGCTTACACAGATGCA 531
    |||||||
DB 301 AGCATTACCAATGAGAGGAAACAGACGAGAAATCTTGATGGCTTACACAGATGCA 242

QY 532 CAAACAAAATGGAATGACTGTGTGATGACATGAGCGACCAAGCTGGGAGAGATTAACACG 591
    |||||||
DB 241 CAAACAAAATGGAATGACTGTGTGATGACATGAGCGACCAAGCTGGGAGAGATTAACACG 182

QY 592 GGGCAGAGGGTCTGAGATTCCTGCGCTGCTGCTAAACCTGGCTTCAATCAACCAATCATT 651
    |||||||
DB 181 GGGCAGAGGGTCTGAGATTCCTGCGCTGCTGCTTAACTGCTGCTTCAATCAACCAATCATT 122

QY 652 TCATATTTCTAACCCTCAAAACCAAGCTGTGTAAATCTGATCTCTACG 701
    |||||||
```

DB 121 TCATATTTCTAACCCTCAAAACCAAGCTGTGTAAATCTGATCTCTACG 72

```
RESULT 15
US-09-620-312D-791
; Sequence 791, Application US/09620312D
; Patent No. 6569662
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Zhang, Jie
; APPLICANT: Ren, Feiyun
; APPLICANT: Chen, Rui-hong
; APPLICANT: Zhao, Qing A.
; APPLICANT: Wehrman, Tom
; APPLICANT: Xue, Aldong J.
; APPLICANT: Yang, Yonghong
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Zhou, Ping
; APPLICANT: Ma, Yundong
; APPLICANT: Wang, Dairui
; APPLICANT: Wang, Zhiwei
; APPLICANT: John Tillinghast
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: No. 6569662el Nucleic Acids and
; FILE REFERENCE: 784CIP2B
; CURRENT APPLICATION NUMBER: US/09/620,312D
; CURRENT FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: 09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/488,725
; PRIOR FILING DATE: 2000-01-21
; NUMBER OF SEQ ID NOS: 1105
; SOFTWARE: PL_FL_genes Version 1.0
; SEQ ID NO 791
; LENGTH: 1379
; TYPE: DNA
; ORGANISM: Homo sapiens
; NAME/KEY: CDS
; LOCATION: (109)..(789)
US-09-620-312D-791
```

```
Query Match          1.4%; Score 26; DB 4; Length 1379;
Best Local Similarity 100.0%; Pred. No. 0.0066;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 977 TCACATCATCTCCTCAGTGTCTTTGCC 1002
    |||||||
DB 335 TCACATCATCTCCTCAGTGTCTTTGCC 360
```

Search completed: September 27, 2003, 11:43:52
Job time : 110.441 secs

THIS PAGE BLANK (CONFIDENTIAL)

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 26, 2003, 21:44:18 : Search time 433.819 Seconds
(without alignments)
10742.554 Million cell updates/sec

Title: US-09-402-713A-3

Perfect score: 1872

Sequence: 1 agaagctgcgtcagcaaaaa.....caataaagaattaccaga 1872

Scoring table:

Gapop 60.0, Gapext 60.0

Searched: 1678620 seqs, 1244745471 residues

Word size: 0

Total number of hits satisfying chosen parameters: 3357240

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database: Published Applications_NA:*

1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/2/pubpna/PCr_NEW_PUB.seq:*
3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
6: /cgn2_6/ptodata/2/pubpna/PCrUS_PUBCOMB.seq:*
7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
9: /cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:*
10: /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
13: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
14: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
15: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
16: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
17: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1367	73.0	3923	9 US-09-759-143-690	Sequence 690, App
2	1367	73.0	3923	9 US-09-780-669-690	Sequence 690, App
3	1367	73.0	3923	9 US-09-822-827-690	Sequence 690, App
4	1367	73.0	3923	10 US-09-895-793-690	Sequence 690, App
5	1367	73.0	3923	10 US-09-895-814-690	Sequence 690, App
6	1367	73.0	3923	12 US-10-144-678A-690	Sequence 690, App
7	1367	73.0	3923	13 US-10-012-896-690	Sequence 690, App
8	1367	73.0	3923	14 US-10-205-823-316	Sequence 316, App
9	1367	73.0	3923	9 US-09-759-143-470	Sequence 470, App
10	1155	61.7	2426	9 US-09-780-669-470	Sequence 470, App
11	1155	61.7	2426	9 US-09-822-827-470	Sequence 470, App
12	1155	61.7	2426	10 US-09-895-793-470	Sequence 470, App
13	1155	61.7	2426	10 US-09-895-814-470	Sequence 470, App
14	1155	61.7	2426	12 US-10-144-678A-470	Sequence 470, App
15	1155	61.7	2426	13 US-10-012-896-470	Sequence 470, App
16	1155	61.7	2426	14 US-10-010-940-470	Sequence 470, App

17	1155	61.7	2426	14 US-10-205-823-448	Sequence 448, App
18	1155	61.7	3112	9 US-09-759-143-468	Sequence 468, App
19	1155	61.7	3112	9 US-09-780-669-468	Sequence 468, App
20	1155	61.7	3112	9 US-09-822-827-468	Sequence 468, App
21	1155	61.7	3112	10 US-09-895-793-468	Sequence 468, App
22	1155	61.7	3112	10 US-09-895-814-468	Sequence 468, App
23	1155	61.7	3112	12 US-10-144-678A-468	Sequence 468, App
24	1155	61.7	3112	13 US-10-012-896-468	Sequence 468, App
25	1155	61.7	3112	14 US-10-010-940-468	Sequence 468, App
26	1034	55.2	2229	9 US-09-759-143-469	Sequence 469, App
27	1034	55.2	2229	9 US-09-780-669-469	Sequence 469, App
28	1034	55.2	2229	9 US-09-822-827-469	Sequence 469, App
29	1034	55.2	2229	10 US-09-895-793-469	Sequence 469, App
30	1034	55.2	2229	10 US-09-895-814-469	Sequence 469, App
31	1034	55.2	2229	12 US-10-144-678A-469	Sequence 469, App
32	1034	55.2	2229	13 US-10-012-896-469	Sequence 469, App
33	1034	55.2	2229	14 US-10-010-940-469	Sequence 469, App
34	835	44.6	876	11 US-09-957-708-3	Sequence 3, App11
35	812	43.4	812	9 US-09-759-143-471	Sequence 471, App
36	812	43.4	812	9 US-09-780-669-471	Sequence 471, App
37	812	43.4	812	9 US-09-822-827-471	Sequence 471, App
38	812	43.4	812	10 US-09-895-793-471	Sequence 471, App
39	812	43.4	812	10 US-09-895-814-471	Sequence 471, App
40	812	43.4	812	12 US-10-144-678A-471	Sequence 471, App
41	812	43.4	812	13 US-10-012-896-471	Sequence 471, App
42	812	43.4	812	14 US-10-010-940-471	Sequence 471, App
43	473	25.3	597	12 US-10-195-730-46	Sequence 46, App1
44	467	24.9	1102	14 US-10-198-846-11000	Sequence 11000, A
45	465	24.8	1036	14 US-10-198-846-13213	Sequence 13213, A

ALIGNMENTS

RESULT 1

US-09-759-143-690
Sequence 690, Application US/09759143

Patent No. US2002002248A1

GENERAL INFORMATION:

APPLICANT: Xu, Jlangchun

APPLICANT: Dillon, Davin C.

APPLICANT: Mitcham, Jennifer L.

APPLICANT: Harlocker, Susan L.

APPLICANT: Jiang, Yuqui

APPLICANT: Henderson, Robert A.

APPLICANT: Fanger, Gary R.

APPLICANT: Retter, Marc W.

APPLICANT: Stolk, John A.

APPLICANT: Day, Craig H.

APPLICANT: Veddyck, Thomas S.

APPLICANT: Carter, Darriick

APPLICANT: Wang, Aljun

APPLICANT: Li, Samuel

APPLICANT: Skeiky, Yasir A.W.

APPLICANT: Hepler, William

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND

TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER

FILE REFERENCE: 210121.427C23

CURRENT APPLICATION NUMBER: US/09/759,143

CURRENT FILING DATE: 2001-01-12

NUMBER OF SEQ ID NOS: 934

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 690

LENGTH: 3923

TYPE: DNA

ORGANISM: Homo sapien

US-09-759-143-690

Query Match 73.0%; Score 1367; DB 9; Length 3923;
Best Local Similarity 99.5%; Pred. No. 0;
Matches 1767; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 98 GGTGAGAAATAGAAAGCTGCTGACCTTAAACATCTGAGGCCACACATCTGCTGAAATGG 157
 |||||||
 Db 285 GGTGAGAAATAGAAAGCTGCTGACCTTAAACATCTGAGGCCACACATCTGCTGAAATGG 344
 QY 158 AGATAATTAACATACATAGAAAGCAAGATGACAAATTAATATGCTAAGTGTACATGT 217
 |||||||
 Db 345 AGATAATTAACATACATAGAAAGCAAGATGACAAATTAATATGCTAAGTGTACATGT 404
 QY 218 TTTTGCACATTTCCAGCCCTTTTAAATATCCACACACAGAGAGACAAAGAGAACAC 277
 |||||||
 Db 405 TTTTGCACATTTCCAGCCCTTTTAAATATCCACACACAGAGAGACAAAGAGAACAC 464
 QY 278 AGAGATCCCTGGAGAAATGCCGCCCATCTTGGGTGATGATGACCTGCGCTGT 337
 |||||||
 Db 465 AGAGATCCCTGGAGAAATGCCGCCCATCTTGGGTGATGATGACCTGCGCTGT 524
 QY 338 GCGCTGTCGGCTGTGAGGGAAGGACATTAAGAAATGATGATGCTTCCCTTAAGGA 397
 |||||||
 Db 525 GCGCTGTCGGCTGTGAGGGAAGGACATTAAGAAATGATGATGCTTCCCTTAAGGA 584
 QY 398 TGGGCAAGAAACAGATCCTGTTGTGATATTTATTTGAACGGGATTCAGATTTGAAT 457
 |||||||
 Db 585 TGGGCAAGAAACAGATCCTGTTGTGATATTTATTTGAACGGGATTCAGATTTGAAT 644
 QY 458 GAAGTCAACAAGTACGATTAACAATGAGAGAGAAACAGACAGAAATCTGTGCTT 517
 |||||||
 Db 645 GAAGTCAACAAGTACGATTAACAATGAGAGAGAAACAGACAGAAATCTGTGCTT 704
 QY 518 CACAAAGACATGCAACAAACAAATGAAATCTGATGATGACATGAGGACCAAGCTGGG 577
 |||||||
 Db 705 CACAAAGACATGCAACAAACAAATGAAATCTGATGATGACATGAGGACCAAGCTGGG 764
 QY 578 AGAGATTAACACAGGGGACAGAGGTACAGATTCGGCCCTGCTGCTTAACTGTGCTTC 637
 |||||||
 Db 765 AGAGATTAACACAGGGGACAGAGGTACAGATTCGGCCCTGCTGCTTAACTGTGCTTC 824
 QY 638 ATAAACCAATCATTTCTATTTCTTAACCTCAACCAACAAAGCTGTTGAATCTGATCTC 697
 |||||||
 Db 825 ATAAACCAATCATTTCTATTTCTTAACCTCAACCAACAAAGCTGTTGAATCTGATCTC 884
 QY 698 TAGCGTTCCTTGGGGCCCAACATTCCTCATATATCCAGCCACACATCTTAAATTT 757
 |||||||
 Db 885 TAGCGTTCCTTGGGGCCCAACATTCCTCATATATCCAGCCACACATCTTAAATTT 944
 QY 758 AGTTCCAGATCTGTACTGTGACCTTCTACACTGTAGAAATACATTAATCTTTGCTTC 817
 |||||||
 Db 945 AGTTCCAGATCTGTACTGTGACCTTCTACACTGTAGAAATACATTAATCTTTGCTTC 1004
 QY 818 AAAGACCCCTGCTGCTGCTGCTAATATGAGCGATGTTTCCTAAGGAGGCTCTG 877
 |||||||
 Db 1005 AAAGACCCCTGCTGCTGCTGCTAATATGAGCGATGTTTCCTAAGGAGGCTCTG 1064
 QY 878 GCCCAGGGGATCTGTGAACAGGCTGGGAGACATCTCAAGATCTTCCAGGGTTATACTTA 937
 |||||||
 Db 1065 GCCCAGGGGATCTGTGAACAGGCTGGGAGACATCTCAAGATCTTCCAGGGTTATACTTA 1124
 QY 938 CTAGCACACAGCATGATCATTTAGGAGTGAATATCTAATCAACATCATCTCAAGTGT 997
 |||||||
 Db 1125 CTAGCACACAGCATGATCATTTAGGAGTGAATATCTAATCAACATCATCTCAAGTGT 1184
 QY 998 TTGGCCATCTGAATTCATTTCCCATTTTGTGCCCATCTCAAGACCTCAAAATGTCA 1057
 |||||||
 Db 1185 TTGGCCATCTGAATTCATTTCCCATTTTGTGCCCATCTCAAGACCTCAAAATGTCA 1244
 QY 1058 TTCCATTAATATCAGAGATTAACCTTTTAACTGGAAGAAATCAATGTTACATG 1117
 |||||||
 Db 1245 TTCCATTAATATCAGAGATTAACCTTTTAACTGGAAGAAATCAATGTTACATG 1304
 QY 1118 CACCTATGGGAATTAATTAATATTTTGTTCACAGTGAAGAGTCAAGTCTCTTTA 1177
 |||||||
 Db 1305 CACCTATGGGAATTAATTAATATTTTGTTCACAGTGAAGAGTCAAGTCTCTTTA 1364
 QY 1178 TCCCTCCCTTTTGTGATTTTTCCTCAATATAAGTTAAATGCTTACCTTGTACTG 1237

Db 1365 TCCCTCCCTTTGTTGATTTTTCACATATAAGTTAAATGCTTACCTTGTACTG 1424
 QY 1238 AGCGTATACAGACAGCCCTCCCATCCCTCCACCTTATCTGCATCACATCAAC 1297
 |||||||
 Db 1425 AGCGTATACAGACAGCCCTCCCATCCCTCCACCTTATCTGCATCACATCAAC 1484
 QY 1298 CCGTCCCATVNSACTTAACAAATCACTTAATCTTGAATCTTGAACATGTCAAGNCATAC 1357
 |||||||
 Db 1485 CCGTCCCATVNSACTTAACAAATCACTTAATCTTGAATCTTGAACATGTCAAGNCATAC 1544
 QY 1358 ATTCTCTCTGCTGAGAGAGCTCTTCTGCTCTTAANTCAGATGATGAAAGTT 1417
 |||||||
 Db 1545 ATTATCTCTGCTGAGAGAGCTCTTCTGCTCTTAANTCAGATGATGAAAGTT 1604
 QY 1418 TTGAATAGTTGACTATCTTCACTTCAATGACAAAGAGGACACATATGATTCATCA 1477
 |||||||
 Db 1605 TTGAATAGTTGACTATCTTCACTTCAATGACAAAGAGGACACATATGATTCATCA 1664
 QY 1478 CATGAGACAGCAATATAAGTGTAAATTTGATTAATAGAGTTTGAATATAATAGAA 1537
 |||||||
 Db 1665 CATGAGACAGCAATATAAGTGTAAATTTGATTAATAGAGTTTGAATATAATAGAA 1724
 QY 1538 ATGCAAGKCCACAGAGGGAATGTTATGGGCACTTTTAACCCCTGGATGTGAAGAA 1597
 |||||||
 Db 1725 ATGCAAGKCCACAGAGGGAATGTTATGGGCACTTTTGAAGCCTGGGATGTGAAGCA 1784
 QY 1598 AAGGACAGGAACCTCATAGTATCTTATATATATCTTCACTTCTATCTATCAAA 1657
 |||||||
 Db 1785 AAGGACAGGAACCTCATAGTATCTTATATATATCTTCACTTCTATCTATCAAA 1844
 QY 1658 TATCCAAAGAGCTTTTACAGAAATTCATGCAAGTGAACATCCCAAGAGTAACTTATCC 1717
 |||||||
 Db 1845 TATCCAAAGAGCTTTTACAGAAATTCATGCAAGTGAACATCCCAAGAGTAACTTATCC 1904
 QY 1718 ATTTCAATGAGAGGCGCTTAGAATTTTGGCAATCAATCTGCTCACTATCTCAACTT 1777
 |||||||
 Db 1905 ATTTCAATGAGAGGCGCTTAGAATTTTGGCAATCAATCTGCTCACTATCTCAACTT 1964
 QY 1778 TGAGATGTGTTTGTCTTCTTGTAGTTAAATGAAAGAAATAGGCACTTGTGAGCCACTTT 1837
 |||||||
 Db 1965 TGAGATGTGTTTGTCTTCTTGTAGTTAAATGAAAGAAATAGGCACTTGTGAGCCACTTT 2024
 QY 1838 AGGGTCACTCTGCGCAATTAAGAAATTTACAAAGA 1872
 |||||||
 Db 2025 AGGGTCACTCTGCGCAATTAAGAAATTTACAAAGA 2059
 |||||||
 RESULT 2
 US-09-780-669-690
 ; Sequence 690, Application US/09780669
 ; Patent No. US20020051977A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Xu, Jiangchun
 ; APPLICANT: Dillon, Davin C.
 ; APPLICANT: Mitcham, Jennifer L.
 ; APPLICANT: Harlocker, Susan L.
 ; APPLICANT: Jiang, Yuxui
 ; APPLICANT: Henderson, Robert A.
 ; APPLICANT: Kalos, Michael D.
 ; APPLICANT: Fanger, Gary R.
 ; APPLICANT: Retter, Marc W.
 ; APPLICANT: Stolk, John A.
 ; APPLICANT: Day, Craig H.
 ; APPLICANT: Vedvick, Thomas S.
 ; APPLICANT: Carter, Darrick
 ; APPLICANT: Li, Samuel
 ; APPLICANT: Wang, Aljun
 ; APPLICANT: Skeiky, Yasir A.W.
 ; APPLICANT: Hepler, William
 ; APPLICANT: Hural, John
 ; APPLICANT: McNeill, Patricia D.
 ; APPLICANT: Houghton, Raymond L.

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C24
; CURRENT APPLICATION NUMBER: US/09/780,669
; CURRENT FILING DATE: 2001-02-09
; NUMBER OF SEQ ID NOS: 943
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 690
; LENGTH: 3923
; TYPE: DNA
; ORGANISM: Homo sapien
; US-09-780-669-690

Query Match 73.0%; Score 1367; DB 9; Length 3923;
Best Local Similarity 99.5%; Pred. No. 0;
Matches 1767; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 98 GGTGAAATATGAAAGGCTGCTGACTTTACCATCTGAGGCCACACATCTGCTGAATGG 157
DB 285 GGTGAAATATGAAAGGCTGCTGACTTTACCATCTGAGGCCACACATCTGCTGAATGG 344
QY 158 AGATATTTACATCTCTGAAACAGCAAGATGACATATTAATGTCTAAGTAGTGCATGT 217
DB 345 AGATATTTACATCTCTGAAACAGCAAGATGACATATTAATGTCTAAGTAGTGCATGT 404
QY 218 TTTTGACATTTCCAGCCCTTTTAATATCCACACACAGCAAGCAACAAAAGAACAC 277
DB 405 TTTTGACATTTCCAGCCCTTTTAATATCCACACACAGCAAGCAACAAAAGAACAC 464
QY 278 AGAGATCCCTGGAGAAATGCCCGCCGCATCTTGCTGATCATGATGAGCCCTGCCCTGT 337
DB 465 AGAGATCCCTGGAGAAATGCCCGCCGCATCTTGCTGATCATGATGAGCCCTGCCCTGT 524
QY 338 GCCTGCTCCCGCTGTGAGGGAAGACATTAAGAAATGAATGATGTGTCTTAAAGGA 397
DB 525 GCCTGCTCCCGCTGTGAGGGAAGACATTAAGAAATGAATGATGTGTCTTAAAGGA 584
QY 398 TGGGAGGAAAAAGATCCTGTGTGATATTATTTAGAGGGATTTACAGATTGAAAT 457
DB 584 TGGGAGGAAAAAGATCCTGTGTGATATTATTTAGAGGGATTTACAGATTGAAAT 644
QY 458 GAAGTCACAAAGTNGCATTTACCAATGAGAGAAAAACAGAGAGAAAAATCTTGATGCTT 517
DB 644 GAAGTCACAAAGTNGCATTTACCAATGAGAGAAAAACAGAGAGAAAAATCTTGATGCTT 704
QY 518 CACAAGACATGCAACAAACAAATGGAATFACTGTGATGACATGAGCCAGCCAGCTGGGG 577
DB 704 CACAAGACATGCAACAAACAAATGGAATFACTGTGATGACATGAGCCAGCCAGCTGGGG 764
QY 705 AGGAGATTAACACAGGGGGGAGAGGGGTCAGGATTTGGCCCTGCTGCTAAAGCTGCTTC 637
DB 824 AGGAGATTAACACAGGGGGGAGAGGGGTCAGGATTTGGCCCTGCTGCTAAAGCTGCTTC 824
QY 638 ATAAACCAATCATTTTCAATTTTCTTAACCTCAAAAAGAGCTGTGTAATATCTGATCTC 697
DB 884 ATAAACCAATCATTTTCAATTTTCTTAACCTCAAAAAGAGCTGTGTAATATCTGATCTC 884
QY 698 TACGGTTCTTCTGGGCCCAACATTTCTCATATATTCACAGCAACACTATTTTAAATTT 757
DB 885 TACGGTTCTTCTGGGCCCAACATTTCTCATATATTCACAGCAACACTATTTTAAATTT 944
QY 758 AGTTCCAGATCTGACTGTGACCTTTTACAGCTGAATAAATCACTTCTCATTTTGTTC 817
DB 945 AGTTCCAGATCTGACTGTGACCTTTTACAGCTGAATAAATCACTTCTCATTTTGTTC 1004
QY 818 AAAGACCTTCTGTGTGCTGCTAATATATGACTGACTGTGTTTCTTAAGAGTGTCTG 877
DB 1005 AAAGACCTTCTGTGTGCTGCTAATATATGACTGACTGTGTTTCTTAAGAGTGTCTG 1064
QY 878 GCCCAGGGGATCTGTGAACAGGCTGGGAAGCATCTCAAGATCTTTCCAGGGTTAACTTA 937
DB 1065 GCCCAGGGGATCTGTGAACAGGCTGGGAAGCATCTCAAGATCTTTCCAGGGTTAACTTA 1124

QY 938 CTAGCAGACAGCATGATCATTTACGAGGATTAATCTATATCAATCATCTCAGTGTCT 997
DB 1125 CTAGCAGACAGCATGATCATTTACGAGGATTAATCTATATCAATCATCTCAGTGTCT 1184
QY 998 TTGCCCATACAGAAATTCATTTCCAGCTTTTGGCCATTTCTCAAGACCTCAAAATGTCA 1057
DB 1185 TTGCCCATACAGAAATTCATTTCCAGCTTTTGGCCATTTCTCAAGACCTCAAAATGTCA 1244
QY 1058 TTCCATTAATATACAGAGATTAATCTTTTATTTTAACTCGGAAGATTCATGTTACATG 1117
DB 1245 TTCCATTAATATACAGAGATTAATCTTTTATTTTAACTCGGAAGATTCATGTTACATG 1304
QY 1118 CAGCTATGGAATTAATTAATCAATTTTGTGTTTCCAGTGAAGATGATGATGCTTTA 1177
DB 1305 CAGCTATGGAATTAATTAATCAATTTTGTGTTTCCAGTGAAGATGATGATGCTTTA 1364
QY 1178 TCCCTCCCTTTGTTGATTTTTCAGATTAAGTTAAATCTTAAGCTTTAGCTG 1237
DB 1365 TCCCTCCCTTTGTTGATTTTTCAGATTAAGTTAAATCTTAAGCTTTAGCTG 1424
QY 1238 AGGCTGTATACAGCAGCCTCTCCCATCTCCCTCAGCCTTATCTGTATCAACATCAAC 1297
DB 1425 AGGCTGTATACAGCAGCCTCTCCCATCTCCCTCAGCCTTATCTGTATCAACATCAAC 1484
QY 1298 CCCCTCCATNTSACCTAAACAAATCTAATCTGTAATCTTGAACATGTCAGSCATAC 1357
DB 1485 CCCCTCCATNTSACCTAAACAAATCTAATCTGTAATCTTGAACATGTCAGSCATAC 1544
QY 1358 ATTTTCCTTCTGCTGAGAGCTCTCTCTGCTCTTAANTCTGAATGATGTAAGTT 1417
DB 1545 ATTTTCCTTCTGCTGAGAGCTCTCTCTGCTCTTAANTCTGAATGATGTAAGTT 1604
QY 1418 TTGAATTAAGTTGACTATCTTACTGTCAAGAAAGGACACATATGAGATTCATCAATCA 1477
DB 1605 TTGAATTAAGTTGACTATCTTACTGTCAAGAAAGGACACATATGAGATTCATCAATCA 1664
QY 1478 CATGAGACAGCAAAATGTAAGATTAATGATTAATGATTAATGATTAATGATTAATGATTA 1537
DB 1665 CATGAGACAGCAAAATGTAAGATTAATGATTAATGATTAATGATTAATGATTAATGATTA 1724
QY 1538 ATGCAAGACCAAGAGGAAATGTTTATGGGACAGTTTGTGAAGCTGGATGTAAGAA 1597
DB 1725 ATGCAAGACCAAGAGGAAATGTTTATGGGACAGTTTGTGAAGCTGGATGTAAGAA 1784
QY 1598 AAGCGAGGAACCTATATGATCTTAATATATCTTCAATCTTCTATCTATACAA 1657
DB 1785 AAGCGAGGAACCTATATGATCTTAATATATCTTCAATCTTCTATCTATACAA 1844
QY 1658 TATCCAAAGCTTTTACAGAAATCATGCAAGTGAATCCCAAGGTAACCTTATCC 1717
DB 1845 TATCCAAAGCTTTTACAGAAATCATGCAAGTGAATCCCAAGGTAACCTTATCC 1904
QY 1718 ATTTTCATGTTAGTGGCTTTAGAAATTTTGGCAATCACTAGTCAATCTTCAAGCT 1777
DB 1905 ATTTTCATGTTAGTGGCTTTAGAAATTTTGGCAATCACTAGTCAATCTTCAAGCT 1964
QY 1778 TGAGATGTGTTTCTTGTGATTAATTAAGAAATAGGCGACTTGTGAGCCACTTT 1837
DB 1965 TGAGATGTGTTTCTTGTGATTAATTAAGAAATAGGCGACTTGTGAGCCACTTT 2024
QY 1838 AGGTTCACTCTGCGCAATTAAGAAATTTACAAAGA 1872
DB 2025 AGGTTCACTCTGCGCAATTAAGAAATTTACAAAGA 2059

RESULT 3
US-09-822-827-690
; Sequence 690. Application US/09822827
; Patent No. US20020081680A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; DIAGNOSIS OF PROSTATE CANCER

```
FILE REFERENCE: 210121.534C1
CURRENT APPLICATION NUMBER: US/09/822.827
CURRENT FILING DATE: 2001-03-28
NUMBER OF SEQ ID NOS: 982
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 690
LENGTH: 3923
TYPE: DNA
ORGANISM: Homo sapien
US-09-822-827-690

Query Match      73.0% Score 1367; DB 9; Length 3923;
Best Local Similarity 99.5% P-Val. No. 0;
Matches 1767; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 98 GGTGAGAAATAGAAAGGCTGTGACTTACATCTGAGGCCACACATCTGCTGAATGG 157
DB 285 GGTGAGAAATAGAAAGGCTGTGACTTACATCTGAGGCCACACATCTGCTGAATGG 344
QY 158 AGATTAATTAACATCAGTAAGAACAGACATGACATATTAATGCTTAAGTAGACATGT 217
DB 345 AGATTAATTAACATCAGTAAGAACAGACATGACATATTAATGCTTAAGTAGACATGT 404
QY 218 TTTTGCACATTTCCAGCCCTTTAAATATCCACACACAGAGAAAGCAAAAGGAACAC 277
DB 405 TTTTGCACATTTCCAGCCCTTTAAATATCCACACACAGAGAAAGCAAAAGGAACAC 464
QY 278 AGAGATCCCTGGGAGAAATCCCGGCCCATCTTGGGTCATGATGAGCCCTGCTGT 337
DB 465 AGAGATCCCTGGGAGAAATCCCGGCCCATCTTGGGTCATGATGAGCCCTGCTGT 524
QY 338 GCGTGTCCCGCTTGTGAGGAGAGACATTAAGAAATGAATGTGATGCTTAAAGGA 397
DB 525 GCGTGTCCCGCTTGTGAGGAGAGACATTAAGAAATGAATGTGATGCTTAAAGGA 584
QY 398 TGGGCAAGAAACAGATCCTGTTGTGATATTTGAACGGGATTAAGATTTGAAT 457
DB 585 TGGGCAAGAAACAGATCCTGTTGTGATATTTGAACGGGATTTACGATTTGAAT 644
QY 458 GAAATCACAAGTGAGCATTTACCAATGAGAGAAACAGAGAAATCTTGATGCTT 517
DB 645 GAAATCACAAGTGAGCATTTACCAATGAGAGAAACAGAGAAATCTTGATGCTT 704
QY 518 CACAAGACATGCAACAACAAATGGAATCTGTGATGATGAGCAGCCAAAGCTGGG 577
DB 705 CACAAGACATGCAACAACAAATGGAATCTGTGATGATGAGCAGCCAAAGCTGGG 764
QY 578 AGGAGATTAACGAGGGGAGAGGGTCAAGATCTGGGCCCTGCTAAACCTGCGCTT 637
DB 765 AGGAGATTAACGAGGGGAGAGGGTCAAGATCTGGGCCCTGCTAAACCTGCGCTT 824
QY 638 ATAAACCAATCATTTTATATTTCTAAACCTCAAAACAAAGCTTGTGAATATCTGATC 697
DB 825 ATAAACCAATCATTTTATATTTCTAAACCTCAAAACAAAGCTTGTGAATATCTGATC 884
QY 698 TACGATGCTTCTGGGCCCCAACAATCTCCATATATCCAGCCACATCTTTTAATATT 757
DB 885 TACGATGCTTCTGGGCCCCAACAATCTCCATATATCCAGCCACATCTTTTAATATT 944
QY 758 AGTTCCAGATCTGTACTGTGACCTTCTACACTGTAGAAATTAACATTACATTTGTTT 817
DB 945 AGTTCCAGATCTGTACTGTGACCTTCTACACTGTAGAAATTAACATTACATTTGTTT 1004
QY 818 AAAGACCTTCTGTGCTGCTTAAATATGATGATGATGCTGTTTTCCTAAAGAGTGTCTG 877
DB 1005 AAAGACCTTCTGTGCTGCTTAAATATGATGATGATGCTGTTTTCCTAAAGAGTGTCTG 1064
QY 878 GCCCAGGGGATCTGTGAACAGGCTGGGAACATCTCAAGATCTTCCAGGGTTATCTTA 937
DB 1065 GCCCAGGGGATCTGTGAACAGGCTGGGAACATCTCAAGATCTTCCAGGGTTATCTTA 1124
QY 938 CTAGCACAAGCATGATCATTTAGGAGTGAATATCTAATCAACATCATCTCAGTGTCT 997
```

```
DB 1125 CTAGCACAAGCATGATCATTTAGGAGTGAATATCTAATCAACATCATCTCAGTGTCT 1184
QY 998 TTGCCATAGTGAATTCATTTCCCATCTTTGTGCCCATCTCAAGACCTCAAAATGTCA 1057
DB 1185 TTGCCATAGTGAATTCATTTCCCATCTTTGTGCCCATCTCAAGACCTCAAAATGTCA 1244
QY 1058 TTCCATTAATATCAACAGATTAACCTTTTTTTTTTAAACCTGGAAGATTCATGTACATG 1117
DB 1245 TTCCATTAATATCAACAGATTAACCTTTTTTTTTTAAACCTGGAAGATTCATGTACATG 1304
QY 1118 CAGCTATGGAATTTAATTCATATTTTGTTCCTCCAGTGAAGATGACATACCTCTTA 1177
DB 1305 CAGCTATGGAATTTAATTCATATTTTGTTCCTCCAGTGAAGATGACATACCTCTTA 1364
QY 1178 TCCCTCCCTTGTGATTTTTCCTCAATATTAAGTTAAATGCTGTAGCCCTGTACTG 1237
DB 1365 TCCCTCCCTTGTGATTTTTCCTCAATATTAAGTTAAATGCTGTAGCCCTGTACTG 1424
QY 1238 AGGCTGTATACAGACAGCCTTCCCATCCCTCCAGCCTTATCTGTATCACCATCAAC 1297
DB 1425 AGGCTGTATACAGACAGCCTTCCCATCCCTCCAGCCTTATCTGTATCACCATCAAC 1484
QY 1298 CCCCTCCATNYSCTTAAACAAATCTAATCTGTAATCTCTGAACATGTCAGGNCATAC 1357
DB 1485 CCCCTCCATNYSCTTAAACAAATCTAATCTGTAATCTCTGAACATGTCAGGNCATAC 1544
QY 1358 ATTATTCCTTCTCCCTGAGAGCTCTTCTGCTCTTAATCTGAATGATGTAAGTT 1417
DB 1545 ATTATTCCTTCTCCCTGAGAGCTCTTCTGCTCTTAATCTGAATGATGTAAGTT 1604
QY 1418 TTGAATTAAGTTGACTATCTTACTTATGCAAAAGAGGACATATGAGATTTATATCA 1477
DB 1605 TTGAATTAAGTTGACTATCTTACTTATGCAAAAGAGGACATATGAGATTTATATCA 1664
QY 1478 CATGAGACAGCAATTAATTAAGTGTATTTGAATTAAGATTTAGATTAATATGAA 1537
DB 1665 CATGAGACAGCAATTAATTAAGTGTATTTGAATTAAGATTTAGATTAATATGAA 1724
QY 1538 ATGCAAGACACAGAGGGAATGTTATGAGGACAGCTTTGTAAAGCTGGAGTGAAGAA 1597
DB 1725 ATGCAAGACACAGAGGGAATGTTATGAGGACAGCTTTGTAAAGCTGGAGTGAAGAA 1784
QY 1598 AAGGACAGGACCTCATAGTATCTTATATATATCTTCACTTCTATCTATCAACA 1657
DB 1785 AAGGACAGGACCTCATAGTATCTTATATATATCTTCACTTCTATCTATCAACA 1844
QY 1658 TATCCAAACAAGCTTTTCAAGAAATTCATGACAGAGCAAAATCCCAAGGTAACTTATCC 1717
DB 1845 TATCCAAACAAGCTTTTCAAGAAATTCATGACAGAGCAAAATCCCAAGGTAACTTATCC 1904
QY 1718 ATTTCAATGATGAGTGGCTTTAGAAATTTGGCAAAATCATAGTGTACTTATCTCAACT 1777
DB 1905 ATTTCAATGATGAGTGGCTTTAGAAATTTGGCAAAATCATAGTGTACTTATCTCAACT 1964
QY 1778 TGAGATGCTGTTGCTTGTAGTTAATGGAAGAAATAGGGCAGCTTGTGAGCCACTTT 1837
DB 1965 TGAGATGCTGTTGCTTGTAGTTAATGGAAGAAATAGGGCAGCTTGTGAGCCACTTT 2024
QY 1838 AGGGTTCACCTCCGCAATTAAGATTTTCAAGA 1872
DB 2025 AGGGTTCACCTCCGCAATTAAGATTTTCAAGA 2059

RESULT 4
US-09-895-793-690
Sequence 690, Application US/09895793
Publication No. US20020192763A1
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Jiang, Yujun
```

```

; APPLICANT: Kalos, Michael D.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedicik, Thomas S.
; APPLICANT: Carter, Darlick
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Vinals de Bassols, Carlota
; APPLICANT: Foy, Teresa
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.534C2
; CURRENT APPLICATION NUMBER: US/09/895,793
; NUMBER OF SEQ ID NOS: 982
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 690
; LENGTH: 3923
; TYPE: DNA
; ORGANISM: Homo saplen
; US-09-895-793-690

Query Match      73.0%  Score 1367:  DB 10:  Length 3923:
Best Local Similarity 99.5%:  Pred No. 0:
Matches 1767:  Conservative  0:  Mismatches  8:  Indels  0:  Gaps  0:

OY  98 GGTGGAATAAGAAAGCTGCTGACTTACCATCTGAGCCACACATCTGCTGAATGG 157
    |||||
DB  285 GGTGGAATAAGAAAGCTGCTGACTTACCATCTGAGCCACACATCTGCTGAATGG 344
OY  158 AGATATTAACATCTCTAGAAACAGACAGATGACATATATAGTCTAGTACATCT 217
    |||||
DB  345 AGATATTAACATCTCTAGAAACAGACAGATGACATATATAGTCTAGTACATCT 404
OY  218 TTTTCACATTTCCAGCCCTTTAATATCCACACACAGAGAGACACAAAAGAAAGC 277
    |||||
DB  405 TTTTCACATTTCCAGCCCTTTAATATCCACACACAGAGAGACACAAAAGAAAGC 464
OY  278 AGAGATCCCTGGGAGAAATGCCGGCCGCATCTTGGGTCAATGATGAGCCCTGCT 337
    |||||
DB  465 AGAGATCCCTGGGAGAAATGCCGGCCGCATCTTGGGTCAATGATGAGCCCTGCT 524
OY  338 GCTGTGCTCCCTGTGTGAGGGAAGACATTAAGAAATGATGATGTCTCTTAAAGGA 397
    |||||
DB  525 GCTGTGCTCCCTGTGTGAGGGAAGACATTAAGAAATGATGATGTCTCTTAAAGGA 584
OY  398 TGGGAGAGAAACAGATCCTGTTGAGATATTATTTGAACGGGATTACAGATTGAAT 457
    |||||
DB  585 TGGGAGAGAAACAGATCCTGTTGAGATATTATTTGAACGGGATTACAGATTGAAT 644
OY  458 GAAGTCACAAAGTAGCATTTACCAATGAGAGAGAAACAGACGAGAAATCTTGATGCTT 517
    |||||
DB  645 GAAGTCACAAAGTAGCATTTACCAATGAGAGAGAAACAGACGAGAAATCTTGATGCTT 704
OY  518 CACAAGACATGCAACAAACAAATGGAATACGTGATGACATGAGAGCCCAAGCTGGGG 577
    |||||
DB  705 CACAAGACATGCAACAAACAAATGGAATACGTGATGACATGAGAGCCCAAGCTGGGG 764
OY  578 AGAGATTAACACAGGGGGAGAGAGTCTGAGATTCTGGCCCTGCTTAACCTGCTGTC 637
    |||||
DB  765 AGAGATTAACACAGGGGGAGAGAGTCTGAGATTCTGGCCCTGCTTAACCTGCTGTC 824
OY  638 ATACCAATATCATTTTCATATTTCTAACCCTCAAAACAAAGCTGTTGTAATCTGATCTC 697
    |||||
DB  825 ATACCAATATCATTTTCATATTTCTAACCCTCAAAACAAAGCTGTTGTAATCTGATCTC 884
```

```

OY  698 TACGGTCCCTCTGGGGCCCAACATCTCCATATACAGCCACACATTTTAAATTT 757
    |||||
DB  885 TACGGTCCCTCTGGGGCCCAACATCTCCATATATCCAGCCACATCTTTTAAATTT 944
OY  758 AGTTCCAGATCTGACTGTGACCTTTACACTGTAGAAATTAACATTTACTATTTGCTC 817
    |||||
DB  945 AGTTCCAGATCTGACTGTGACCTTTACACTGTAGAAATTAACATTTACTATTTGCTC 1004
OY  818 AAAGACCTTCTGTTGCTGCTTAATATGCTGACCTGCTTTTCCTAAGAGTGTCTG 877
    |||||
DB  1005 AAAGACCTTCTGTTGCTGCTTAATATGCTGACCTGCTTTTCCTAAGAGTGTCTG 1064
OY  878 GCCCAGGGGATCTGTGAAACAGGCTGGGAAGCAATCCAGATCTTCCAGAGTTACTACTA 937
    |||||
DB  1065 GCCCAGGGGATCTGTGAAACAGGCTGGGAAGCAATCCAGATCTTCCAGAGTTACTACTA 1124
OY  938 CTAGCACACAGATGATCATTTACAGAGTAATATCTAATCAACATCATCTCAGTCT 997
    |||||
DB  1125 CTAGCACACAGATGATCATTTACAGAGTAATATCTAATCAACATCATCTCAGTCT 1184
OY  998 TTGCCCATCTGAATTCATTTCCACTTTTGCCCATTTCAAGACCTCAAAATGTCA 1057
    |||||
DB  1185 TTGCCCATCTGAATTCATTTCCACTTTTGCCCATTTCAAGACCTCAAAATGTCA 1244
OY  1058 TTCCATTAATACACAGATTAACCTTTTTTAACTGGAAGAAATTCATGTTTACATG 1117
    |||||
DB  1245 TTCCATTAATACACAGATTAACCTTTTTTAACTGGAAGAAATTCATGTTTACATG 1304
OY  1118 CAGCTATGGGAATTAATACATATTTTCCAGTCAAGAAAGATGATGATGCTTTA 1177
    |||||
DB  1305 CAGCTATGGGAATTAATACATATTTTCCAGTCAAGAAAGATGATGATGCTTTA 1364
OY  1178 TCCCTCCCTTTGTTGATTTTTCAGATTAAGTTAAATGCTAAGCTGTGATG 1237
    |||||
DB  1365 TCCCTCCCTTTGTTGATTTTTCAGATTAAGTTAAATGCTAAGCTGTGATG 1424
OY  1238 AGGCTGTATACAGACAGCCCTGCCCATCCCTCCAGCTTTCCTGTCACCAATCAAC 1297
    |||||
DB  1425 AGGCTGTATACAGACAGCCCTGCCCATCCCTCCAGCTTTCCTGTCACCAATCAAC 1484
OY  1298 CCTCCCATATNSACCTAAACAAATCTAATCTGTAATCTCTGAACATGTCAAGNCATAC 1357
    |||||
DB  1485 CCTCCCATATNSACCTAAACAAATCTAATCTGTAATCTCTGAACATGTCAAGNCATAC 1544
OY  1358 ATTTTCTCTTGCCTGAGAGCTCTCTCTGTCTTAATCTGATGATGTAAGTT 1417
    |||||
DB  1545 ATTTTCTCTTGCCTGAGAGCTCTCTCTGTCTTAATCTGATGATGTAAGTT 1604
OY  1418 TTGAATAGTTGACTATCTTACTTCATGCAAGAAAGGGACATATGATTCATCATCA 1477
    |||||
DB  1605 TTGAATAGTTGACTATCTTACTTCATGCAAGAAAGGGACATATGATTCATCATCA 1664
OY  1478 CATGAGACAGCAAAATCTAATAAGTGAATTTAATAGATTTAGATTAATATGA 1537
    |||||
DB  1665 CATGAGACAGCAAAATCTAATAAGTGAATTTAATAGATTTAATAGATTAATATGA 1724
OY  1538 ATGCAAGACCAACAGAGGAATGTTATGGGACGCTTTGTAAGCTGGGATGTAAGAA 1597
    |||||
DB  1725 ATGCAAGACCAACAGAGGAATGTTATGGGACGCTTTGTAAGCTGGGATGTAAGAA 1784
OY  1598 AAGGACGGGAACTCATAGTATCTTATATATATATCTTCAATCTCTATCATCA 1657
    |||||
DB  1785 AAGGACGGGAACTCATAGTATCTTATATATATATCTTCAATCTCTATCATCA 1844
OY  1658 TATCCAAACAGCTTTTACAGAGATTCATGACAGTGAAGAAATCCCAAGGTAACCTTATCC 1717
    |||||
DB  1845 TATCCAAACAGCTTTTACAGAGATTCATGACAGTGAAGAAATCCCAAGGTAACCTTATCC 1904
OY  1718 ATTTATGCTGAGTGGCTTTTGAATTTTGGCAATCATCTGCTGCTATCTCACT 1777
    |||||
DB  1905 ATTTATGCTGAGTGGCTTTTGAATTTTGGCAATCATCTGCTGCTATCTCACT 1964
```


|||||
Db 1665 CATGAGACGCAAACTAAAGTGTATTTGATATATAAGATTAGATTAATATATGCA 1724
QY 1358 ATGCAGAKCCACAGAGGAAATGTTTATGGGACGTTTGAAGCCTGGATGTGAAGA 1597
Db 1725 ATGCAGAGCCACAGAGGAAATGTTTATGGGACGTTTGAAGCCTGGATGTGAAGA 1784
QY 1598 AAGGAGGGAACCCATAGTATCTATATATATATCTCATTTCTCTATCTATACACA 1657
Db 1785 AAGGAGGGAACCCATAGTATCTATATATATATCTCATTTCTCTATCTATACACA 1844
QY 1658 TATCCAAACAGCTTTTCACAGATTCAGTGAATCCCAAGGAACCTTATCC 1717
Db 1845 TATCCAAACAGCTTTTCACAGATTCAGTGAATCCCAAGGAACCTTATCC 1904
QY 1718 ATTTGATGAGTACGTCGCTTTAGAAATTTTGGCAATCATCTGCTACTTATCTCACTT 1777
Db 1905 ATTTGATGAGTACGTCGCTTTAGAAATTTTGGCAATCATCTGCTACTTATCTCACTT 1964
QY 1778 TGAGATGTGTTGTCCTTGTAGTTAATGAAAGAAATAGGGCACTCTGTGAGCCACTT 1837
Db 1965 TGAGATGTGTTGTCCTTGTAGTTAATGAAAGAAATAGGGCACTCTGTGAGCCACTT 2024
QY 1838 AGGCTTCACTCCTGGCAATTAAGAAATTTTCAAGA 1872
Db 2025 AGGCTTCACTCCTGGCAATTAAGAAATTTTCAAGA 2059

RESULT 6
US-10-144-678A-690
; Sequence 690, Application US/10144678A
; Publication No. US20030157089A1

GENERAL INFORMATION:

APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Jiang, Yugu
APPLICANT: Henderson, Robert A.
APPLICANT: Kalos, Michael D.
APPLICANT: Fanger, Gary R.
APPLICANT: Reiter, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Day, Craig H.
APPLICANT: Vedrick, Thomas S.
APPLICANT: Carter, Darick
APPLICANT: Li, Samuel X.
APPLICANT: Wang, Aljun
APPLICANT: Skeiky, Yasir A. W.
APPLICANT: Hepler, William T.
APPLICANT: Hurst, John
APPLICANT: McNeill, Patricia D.
APPLICANT: Houghton, Raymond L.
APPLICANT: Vinals y de Bassols, Carlota
APPLICANT: Foy, Teresa M.
APPLICANT: Watanabe, Yoshihiro
APPLICANT: Deng, Ta
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.42YC28
CURRENT APPLICATION NUMBER: US/10/144,678A
CURRENT FILING DATE: 2002-08-12
NUMBER OF SEQ ID NOS: 1033
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 690
LENGTH: 3923
TYPE: DNA
ORGANISM: Homo sapiens
US-10-144-678A-690

Query Match 73.0%; Score 1367; DB 12; Length 3923;
Best Local Similarity 99.5%; Pred. No. 0;
Matches 1767; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 98 GGTGGAATATAAGAAAGCGTGTGACTTTACATCTAGAGCCACACATCTGCTGAATGG 157
Db 285 GGTGGAATATAAGAAAGCGTGTGACTTTACATCTAGAGCCACACATCTGCTGAATGG 344
QY 158 AGATATATTAACATCACTAGAAACACCAAGATGACATATTAATGCTTAAGTAGTACATGT 217
Db 345 AGATATATTAACATCACTAGAAACACCAAGATGACATATTAATGCTTAAGTAGTACATGT 404
QY 218 TTTTGACATTTTCCAGCCCTTTAAATATCCACACACAGAGAACACAAAAAGAAAGC 277
Db 405 TTTTGACATTTTCCAGCCCTTTAAATATCCACACACAGAGAACACAAAAAGAAAGC 464
QY 278 AGAGATCCCTGGGAATATGCCCCGCCATCTTGGTGATCCATGAGCCTCGCCCTGT 337
Db 465 AGAGATCCCTGGGAATATGCCCCGCCATCTTGGTGATCCATGAGATGAGCCCTCGCT 524
QY 338 GCGTGTCCCGCTTGTAGAGGAAGACATTTAGAAATGAATGATGTCTTCTTAAAGA 397
Db 525 GCGTGTCCCGCTTGTAGAGGAAGACATTTAGAAATGAATGATGTCTTCTTAAAGA 584
QY 398 TGGCAGAAAAACAGATCCTGTGTGATATTTTGAACGGGATTAACAGATTTGAAT 457
Db 585 TGGCAGAAAAACAGATCCTGTGTGATATTTTGAACGGGATTAACAGATTTGAAT 644
QY 458 GAAGTCACAAAGTGAAGCATTTACCATTTAGAGAGAAAAACAGCAGAAATCTTGATGGCTT 517
Db 645 GAAGTCACAAAGTGAAGCATTTACCAATGAGAGAAAAACAGCAGAAATCTTGATGGCTT 704
QY 518 CACAAGACATGCAACAAACAAATGAAATGATCTGATGACATGAGCAGCCAAAGCTGGGG 577
Db 705 CACAAGACATGCAACAAACAAATGAAATGATCTGATGACATGAGCAGCCAAAGCTGGGG 764
QY 578 AGGAGATTAACACAGGGGAGAGGGTACAGATTTGCGCCCTGCTTAACCTGCGTTC 637
Db 765 AGGAGATTAACACAGGGGAGAGGGTACAGATTTGCGCCCTGCTTAACCTGCGTTC 824
QY 638 ATTAACCAATATCTTATATTTCTTAACCTCAAAACAAAGCGTGTATATCTGATCTC 697
Db 825 ATTAACCAATATCTTATATTTCTTAACCTCAAAACAAAGCGTGTATATCTGATCTC 884
QY 825 TACGGTCTCTTGGGCCCAACATCTCTCATATATCCAGCCACACTATTTTATATTT 757
Db 885 TACGGTCTCTTGGGCCCAACATCTCTCATATATCCAGCCACACTATTTTATATTT 944
QY 758 AGTCCAGATCTGATCTGTGACCTTTCTACCTGTAGAATTAACATTAATCTATTTGTTTC 817
Db 945 AGTCCAGATCTGATCTGTGACCTTTCTACCTGTAGAATTAACATTAATCTATTTGTTTC 1004
QY 818 AAAGACCCCTGCTGTGCTGCTATATGATGACGACGTTTCTTAAGAGCTGCTG 877
Db 1005 AAAGACCCCTGCTGTGCTGCTATATGATGACGACGTTTCTTAAGAGCTGCTG 1064
QY 878 GCCCAGGGGATCTGGAACAGGCTGGGAAGCATCTCAAGATCTTCCAGGGTATACTTGA 937
Db 1065 GCCCAGGGGATCTGGAACAGGCTGGGAAGCATCTCAAGATCTTCCAGGGTATACTTGA 1124
QY 938 CTAGCAGACAGCATGATTAAGGAGTGAATTAATCAACATCAATCTCACTGCT 997
Db 1125 CTAGCAGACAGCATGATTAAGGAGTGAATTAATCAACATCAATCTCACTGCT 1184
QY 998 TTGGCCATACGAAATTAATTTCCCACTTTTGGCCCATCTCAAGACCTCAAAATGTCA 1057
Db 1185 TTGGCCATACGAAATTAATTTCCCACTTTTGGCCCATCTCAAGACCTCAAAATGTCA 1244
QY 1058 TTCCATTAATACAGAGATTAATTTTATTAACCTGGAAGATTAATGATGATG 1117
Db 1245 TTCCATTAATACAGAGATTAATTTTATTAACCTGGAAGATTAATGATGATG 1304
QY 1118 CAGCTATGGAATTAATTAATTAATTTTTCAGTGCAAAAGATGATGATGCTTGA 1177
Db 1305 CAGCTATGGAATTAATTAATTAATTTTTCAGTGCAAAAGATGATGATGCTTGA 1364

1178 TCCCTCCCTGTTGATTTTTCAGATATAAGTTAAATGCTTACCTGTACTG 1237
1365 TCCCTCCCTGTTGATTTTTCAGATATAAGTTAAATGCTTACCTGTACTG 1424
1238 AGGCTGATATACAGACGCTCTCCCATGCTTCACCTTATCTGTGATCACCATTAC 1237
1425 AGGCTGATATACAGACGCTCTCCCATGCTTCACCTTATCTGTGATCACCATTAC 1484
1298 CCGTCCCATATACAGACGCTCTCCCATGCTTCACCTTATCTGTGATCACCATTAC 1357
1485 CCGTCCCATATACAGACGCTCTCCCATGCTTCACCTTATCTGTGATCACCATTAC 1544
1358 ATTTTCCTTCTGCTGAGAGAGCTCTGCTCTCTTAATCTAGATGATGAAGTT 1417
1545 ATTTTCCTTCTGCTGAGAGAGCTCTGCTCTCTTAATCTAGATGATGAAGTT 1604
1418 TTGATATAGTGTACTATCTTACTTATCTGATGAGAGAGAGAGAGAGAGAGAGAG 1477
1605 TTGATATAGTGTACTATCTTACTTATCTGATGAGAGAGAGAGAGAGAGAGAGAG 1664
1478 CATGAGACAGCAATATCTTAAAGTGTATTTGATTTATAGAGTTAGATTAATATGAA 1537
1665 CATGAGACAGCAATATCTTAAAGTGTATTTGATTTATAGAGTTAGATTAATATGAA 1724
1538 ATGCAAGAKCCACAGAGAGAGATGTTATGAGGACAGCTTTGAGGAGATGGAAGA 1597
1725 ATTCAGAGAGCCACAGAGAGAGATGTTATGAGGACAGCTTTGAGGAGATGGAAGA 1784
1598 AAGGAGAGAGAGAGAGAGATGTTATGAGGAGAGAGAGAGAGAGAGAGAGAGAGAG 1657
1785 AAGGAGAGAGAGAGAGAGATGTTATGAGGAGAGAGAGAGAGAGAGAGAGAGAGAG 1844
1658 TATCCAAACAAGCTTTTTCACAGAAATGATGAGAGAGAGAGAGAGAGAGAGAGAGAG 1717
1845 TATCCAAACAAGCTTTTTCACAGAAATGATGAGAGAGAGAGAGAGAGAGAGAGAGAG 1904
1718 ATTTTCATGATGATGAGAGAGATGTTATGAGGAGAGAGAGAGAGAGAGAGAGAGAG 1777
1905 ATTTTCATGATGATGAGAGAGATGTTATGAGGAGAGAGAGAGAGAGAGAGAGAGAG 1964
1778 TGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1837
1965 TGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2024
1838 AGGCTTACTCTGAGCAATTAAGATTTTACAAAGA 1872
2025 AGGCTTACTCTGAGCAATTAAGATTTTACAAAGA 2059

RESULT 7
US-10-012-896-690
Sequence 690, Application US/10012896
Publication No. US20020183251A1
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Jiang, Yugu
APPLICANT: Kalos, Michael D.
APPLICANT: Retter, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Day, Craig H.
APPLICANT: Vedrick, Thomas S.
APPLICANT: Carter, Darick
APPLICANT: Li, Samuel X.
APPLICANT: Wang, Aijun
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Hepler, William T.
APPLICANT: Henderson, Robert A.
APPLICANT: Hural, John
APPLICANT: McNeill, Patricia D.
APPLICANT: Houghton, Raymond L.

APPLICANT: Vinals de Baesols, Carlota
APPLICANT: Foy, Teresa
APPLICANT: Fanger, Gary R.
APPLICANT: Mantanabe, Yoshihiro
APPLICANT: Meagher, Madeleine Joy
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
FILE REFERENCE: 210121.427C27
CURRENT APPLICATION NUMBER: US/10/012.896
CURRENT FILING DATE: 2001-12-10
NUMBER OF SEQ ID NOS: 1011
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO: 690
LENGTH: 3923
TYPE: DNA
ORGANISM: Homo sapiens
US-10-012-896-690

Query Match 73.0%; Score 1367; DB 13; Length 3923;
Best Local Similarity 99.5%; Pred. No. 0;
Matches 1767; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

98 GGTGAGAAATTAAGAAAGGCTGCTGATCTTACATCTGAGGCCACACATCTGCTGAATGG 157
285 GGTGAGAAATTAAGAAAGGCTGCTGATCTTACATCTGAGGCCACACATCTGCTGAATGG 344
158 AGATTAATTAATCATCATCAG 217
345 AGATTAATTAATCATCATCAG 404
218 TTTTGCACATTTCCAGCCCTTTAATATATCCACACACAGAGAGAGAGAGAGAGAGAGAGAG 277
405 TTTTGCACATTTCCAGCCCTTTAATATATCCACACACAGAGAGAGAGAGAGAGAGAGAGAG 464
278 AGAGATCCCTGGAG 337
465 AGAGATCCCTGGAG 524
338 GCGTGGTCCCGCTTGTGAGGAG 397
525 GCGTGGTCCCGCTTGTGAGGAG 564
398 TGGGAG 457
585 TGGGAG 644
458 GAAGTCAACAAGTGAAGATTAACCAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 517
645 GAAGTCAACAAGTGAAGATTAACCAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 704
518 CACAAGACATGACAACAACAACAACAACAACAACAACAACAACAACAACAACAACAACAACA 577
705 CACAAGACATGACAACAACAACAACAACAACAACAACAACAACAACAACAACAACAACAACA 764
578 AGAGATTAACAG 637
765 AGAGATTAACAG 824
638 ATAACCAATATCATTTCTATTTCTTAACCCCTCAACAACAACAACAACAACAACAACAACA 697
825 ATAACCAATATCATTTCTATTTCTTAACCCCTCAACAACAACAACAACAACAACAACAACA 884
698 TAGGTTCTTCTGAGGCCCAACATTTCTCATATATCCAGGACACATCTTATTAATATTT 757
885 TAGGTTCTTCTGAGGCCCAACATTTCTCATATATCCAGGACACATCTTATTAATATTT 944
758 AGTTCCAGATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 817
945 AGTTCCAGATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1004
818 AAAGACCCCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 877
1005 AAAGACCCCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1064

```
QY 878 GCCCAGGGGATCTGTAAGAGCTGGAGACATCTCAAGATCTTTCCAGGGTTATACCTTA 937
    |||||||
Db 1065 GCCCAGGGGATCTGTAAGAGCTGGAGACATCTCAAGATCTTTCCAGGGTTATACCTTA 1124
QY 938 CTAGACACACACGATGATTAACGAGATGAATTAATCTAATCAATCATCTCAGTGTCT 997
    |||||||
Db 1125 CTAGACACACACGATGATTAACGAGATGAATTAATCTAATCAATCATCTCAGTGTCT 1184
QY 998 TTGCCCATCTGAATTTATTTCCACTTTTGTGCCCCATTCGACAGACCTCAAAATGCA 1057
    |||||||
Db 1185 TTGCCCATCTGAATTTATTTCCACTTTTGTGCCCCATTCGACAGACCTCAAAATGCA 1244
QY 1058 TTCCATTAATATCAAGATTAACCTTTTTCCTGAGAGATTCGAATGTTACAG 1117
    |||||||
Db 1245 TTCCATTAATATCAAGATTAACCTTTTTCCTGAGAGATTCGAATGTTACAG 1304
QY 1118 CAGCTATGGAATTTAATTAATTAATTTGTTTCCAGTGCAGAAAGATGACTAAGTCTTTA 1177
    |||||||
Db 1305 CAGCTATGGAATTTAATTAATTAATTTGTTTCCAGTGCAGAAAGATGACTAAGTCTTTA 1364
QY 1178 TCCCTCCCTTGTGTTGATTTTTCAGATATAAGTTAAATGCTTACCTTGTACTG 1237
    |||||||
Db 1365 TCCCTCCCTTGTGTTGATTTTTCAGATATAAGTTAAATGCTTACCTTGTACTG 1424
QY 1238 AGGCTATATACAGACACCTCTCCCATCCCTCAGCCTTATCTGATCAGCATCAAC 1297
    |||||||
Db 1425 AGGCTATATACAGACACCTCTCTCCCATCCCTCAGCCTTATCTGATCAGCATCAAC 1484
QY 1298 CCGTCCCATATY SACTTAACAAATCTACTTGTATTCCTGTAACATGTGAGNCATAC 1357
    |||||||
Db 1485 CCGTCCCATATCACTTAACAAATCTACTTGTATTCCTGTAACATGTGAGNCATAC 1544
QY 1358 ATTTCTCTTCTGCTGGAAGCTTCTCTGTCTTAANTCTGAATGATGTAAGTT 1417
    |||||||
Db 1545 ATTTCTCTTCTGCTGGAAGCTTCTCTGTCTTAANTCTGAATGATGTAAGTT 1604
QY 1418 TTGAATTAAGTACTATCTTACTTATGCAAAAGAGGACATATGATTCATCATCA 1477
    |||||||
Db 1605 TTGAATTAAGTACTATCTTACTTATGCAAAAGAGGACATATGATTCATCATCA 1664
QY 1478 CATGAGACAGCAAAATCTAATAAGTGTATTTGATTTATAGAAGTTAGATTAATATGTA 1537
    |||||||
Db 1665 CATGAGACAGCAAAATCTAATAAGTGTATTTGATTTATAGAAGTTAGATTAATATGTA 1724
QY 1538 ATGCAAGKCCACAGAGGGAATGTTATGGGCGACGTTGTAAGCCTGGATGTGAAGA 1597
    |||||||
Db 1725 ATGCAAGKCCACAGAGGGAATGTTATGGGCGACGTTGTAAGCCTGGATGTGAAGA 1784
QY 1598 AAGGAGGGAACCTATAGTATCTATATATATATCTTCTCTATCTCTATCACA 1657
    |||||||
Db 1785 AAGGAGGGAACCTATAGTATCTATATATATATCTTCTCTATCTCTATCACA 1844
QY 1658 TATCCAAACAGCTTTTACAGAAATTCATGAGTGAATTCGCCAAAGTAACTTATCC 1717
    |||||||
Db 1845 TATCCAAACAGCTTTTACAGAAATTCATGAGTGAATTCGCCAAAGTAACTTATCC 1904
QY 1718 ATTTCATGCTGAGTGCCTTTAGAAATTTTGGCAATCATACTGCTACTTATCTCACTT 1777
    |||||||
Db 1905 ATTTCATGCTGAGTGCCTTTAGAAATTTTGGCAATCATACTGCTACTTATCTCACTT 1964
QY 1778 TGAGATGTGTTGCTGCTGTTAGTTAATGAAAGAAATAGGGGACCTGTGAGCCACTT 1837
    |||||||
Db 1965 TGAGATGTGTTGCTGCTGTTAGTTAATGAAAGAAATAGGGGACCTGTGAGCCACTT 2024
QY 1838 AGGCTTCACTCTGTGCAATTAAGAATTTACAAGA 1872
    |||||||
Db 2025 AGGCTTCACTCTGTGCAATTAAGAATTTACAAGA 2059
```

RESULT 8
US-10-205-823-316
; Sequence 316, Application US/10205823

```
/ Publication No. US20030108963A1
/ GENERAL INFORMATION:
/ APPLICANT: Schlegel, Robert
/ APPLICANT: Monahan, John E.
/ APPLICANT: Endege, Wilson O.
/ APPLICANT: Gannavarapu, Manjula
/ APPLICANT: Gorbacheva, Bella
/ APPLICANT: Hoersch, Sebastian
/ APPLICANT: Kamatkar, Shubhangi
/ APPLICANT: Monsey, Angela M.
/ APPLICANT: Galt, Karen
/ APPLICANT: Zhao, Xumel
/ APPLICANT: Anderson, Dustin
/ TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
/ METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
/ THERAPY OF PROSTATE CANCER
/ TITLE OF INVENTION: THERAPY OF PROSTATE CANCER
/ FILE REFERENCE: MRI-044
/ CURRENT APPLICATION NUMBER: US/10/205,823
/ CURRENT FILING DATE: 2002-07-25
/ PRIOR APPLICATION NUMBER: 60/307,982
/ PRIOR FILING DATE: 2001-07-25
/ PRIOR APPLICATION NUMBER: 60/314,356
/ PRIOR FILING DATE: 2001-08-22
/ PRIOR APPLICATION NUMBER: 60/325,020
/ PRIOR FILING DATE: 2001-09-25
/ PRIOR APPLICATION NUMBER: 60/341,746
/ PRIOR FILING DATE: 2001-12-12
/ PRIOR APPLICATION NUMBER: 60/362,158
/ PRIOR FILING DATE: 2002-03-05
/ NUMBER OF SEQ ID NOS: 455
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 316
/ LENGTH: 3923
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ US-10-205-823-316

Query Match 73.0% Score 1367; DB 14; Length 3923;
Best Local Similarity 99.5% Pred. No. 0;
Matches 1167; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 98 GGTGGAATTAAGAAGCTGCTGACTTATACATCTGAGGCCACATCTGCTGAATGG 157
    |||||||
Db 285 GGTGGAATTAAGAAGCTGCTGACTTATACATCTGAGGCCACATCTGCTGAATGG 344
QY 158 AGATTAATTAACATCTAGAAAACAGCAAGATGACATTAATGTCTAAGTAGTGCATGT 217
    |||||||
Db 345 AGATTAATTAACATCTAGAAAACAGCAAGATGACATTAATGTCTAAGTAGTGCATGT 404
QY 218 TTTTGCACATTTCCAGCCCCCTTTAATATCCACACACAGGAACCAAAAAGAAAGAC 277
    |||||||
Db 405 TTTTGCACATTTCCAGCCCCCTTTAATATCCACACACAGGAACCAAAAAGAAAGAC 464
QY 278 AGAGATCCCTGGGGAAGAAATGCCCGCCCATCTTGGGTCATGATGAGCCTCGCCCTGT 337
    |||||||
Db 465 AGAGATCCCTGGGGAAGAAATGCCCGCCCATCTTGGGTCATGATGAGCCTCGCCCTGT 524
QY 338 GCGTGTCCCGCTTGTGAGGGAAGACATTTAGAAAATGAATGATGTCTTCTTAAAGA 397
    |||||||
Db 525 GCGTGTCCCGCTTGTGAGGGAAGACATTTAGAAAATGAATGATGTCTTCTTAAAGA 584
QY 398 TGGGAGAGAAAACAGATCCTGTGTGATATTTATTAAGCGGATTTACAGATTTGAAT 457
    |||||||
Db 585 TGGGAGAGAAAACAGATCCTGTGTGATATTTATTAAGCGGATTTACAGATTTGAAT 644
QY 458 GAAGTCACAAAGTGAAGTATACCATGAGAGAAACAGAGAGAAATCTTGATGGCTT 517
    |||||||
Db 645 GAAGTCACAAAGTGAAGTATACCATGAGAGAAACAGAGAGAAATCTTGATGGCTT 704
QY 518 CACAAGACATGCACAAAACAAATGGAATTAAGTATGATGATGATGAGCAGCAAGCTGGGG 577
    |||||||
Db 705 CACAAGACATGCACAAAACAAATGGAATTAAGTATGATGATGATGAGCAGCAAGCTGGGG 764
```


Db 1530 TGCCTGTCCTCCCTGTGTGAGGAGACATTAAGAAATGATTTGATGTTCTTAAGG 1471
QY 397 ATGGCAGAGAAACAGATCTGTTGGATTTATTTGAGGGATTCAGATTTGAA 456
Db 1470 ATGGCAGAGAAACAGATCTGTTGGATTTATTTGAGGGATTCAGATTTGAA 1411
QY 457 TGAAGTCACAAAGATGAGATTTACATGAGAGAAACAGAGAGAAATCTTGATGCT 516
Db 1410 TGAAGTCACAAAGATGAGATTTACATGAGAGAAACAGAGAGAAATCTTGATGCT 1351
QY 517 TCACAAGACATGCAACAAACAAATGGAATGATGATGATGAGAGAGAGAGAGAGAG 576
Db 1350 TCACAAGACATGCAACAAACAAATGGAATGATGATGATGAGAGAGAGAGAGAG 1291
QY 577 GAGGAGATTAACAGAGAGAGAGAGAGATTTGAGAGAGAGAGAGAGAGAGAGAGAG 636
Db 1290 GAGGAGATTAACAGAGAGAGAGAGAGATTTGAGAGAGAGAGAGAGAGAGAGAGAG 1231
QY 637 CATACCAAAATCATTTATTTCTTAACCTCAAAACAAAGCTGTTGTAATTCGATCT 696
Db 1230 CATACCAAAATCATTTATTTCTTAACCTCAAAACAAAGCTGTTGTAATTCGATCT 1171
QY 697 CTACGCTTCCTTCTGAGGAGAGAGATTTCTCAATATTCAGAGAGAGAGAGAGAG 756
Db 1170 CTACGCTTCCTTCTGAGGAGAGAGATTTCTCAATATTCAGAGAGAGAGAGAGAG 1111
QY 757 TAGTTCCTCAGATCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 816
Db 1110 TAGTTCCTCAGATCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1051
QY 817 CAAGAAGCTTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 876
Db 1050 CAAGAAGCTTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 991
QY 877 GGCAGAGAGAGATCTGTGAACAGAGCTGGAAGCATCTCAAGATCTTCCAGGTTATCT 936
Db 990 GGCAGAGAGAGATCTGTGAACAGAGCTGGAAGCATCTCAAGATCTTCCAGGTTATCT 931
QY 937 ACTACACACAGACATGATGATGATGATGATGATGATGATGATGATGATGATGAT 996
Db 930 ACTACACACAGACATGATGATGATGATGATGATGATGATGATGATGATGATGAT 871
QY 997 TTTGGCCATGAGAAATTCATTTCCACTTTTGTGCCATCTCAAGAGAGAGAGAGAG 1056
Db 870 TTTGGCCATGAGAAATTCATTTCCACTTTTGTGCCATCTCAAGAGAGAGAGAGAG 811
QY 1057 ATTCATTAATATTCACAGAGATTAATTTTATTTTAACTGGAAGATTCATGTTACAT 1116
Db 810 ATTCATTAATATTCACAGAGATTAATTTTATTTTAACTGGAAGATTCATGTTACAT 751
QY 1117 GGAGCTATGGAATTAATTAATTAATTTTGTTCAGTGAAGAGAGAGAGAGAGAG 1176
Db 750 GGAGCTATGGAATTAATTAATTAATTTTGTTCAGTGAAGAGAGAGAGAGAGAGAG 691
QY 1177 ATCCCTCCCTTTGTTGATTTTTCAGTGAAGAGAGAGAGAGAGAGAGAGAGAG 1236
Db 690 ATCCCTCCCTTTGTTGATTTTTCAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAG 631
QY 1237 GAGGCTGTATACAGC 1251
Db 630 GAGGCTGTATACAGC 616

RESULT 10

US-09-780-669-470/c
; Sequence 470, Application US/09780669
; Patent No. US20020051977A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, David C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yugu

; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C24
; CURRENT APPLICATION NUMBER: US/09/780,669
; NUMBER OF SEQ ID NOS: 943
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 470
; LENGTH: 2426
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-780-669-470

Query Match 61.7%; Score 1155; DB 9; Length 2426;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1155; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 97 AGGTGAGAAATTAAGAAAGCTGCTGATTTACATCTGAGGAGAGAGAGAGAGAGAG 156
Db 1770 AGGTGAGAAATTAAGAAAGCTGCTGATTTACATCTGAGGAGAGAGAGAGAGAG 1711
QY 157 GAGATTAATTAACATCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 216
Db 1710 GAGATTAATTAACATCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1651
QY 217 TTTTGGACATTTCCAGGCTTTTAAATATTCACACACAGAGAGAGAGAGAGAGAG 276
Db 1650 TTTTGGACATTTCCAGGCTTTTAAATATTCACACACAGAGAGAGAGAGAGAGAG 1591
QY 277 CAGAGATCCCTGGAGAAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 336
Db 1590 CAGAGATCCCTGGAGAAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1531
QY 337 TGCCTGATCCCTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 396
Db 1530 TGCCTGATCCCTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1471
QY 397 ATGGCAGAGAAACAGATCTGTTGATTTATTTTGAAGAGAGAGAGAGAGAGAGAG 456
Db 1470 ATGGCAGAGAAACAGATCTGTTGATTTATTTTGAAGAGAGAGAGAGAGAGAGAG 1411
QY 457 TGAAGTCACAAAGATGAGATTTACATGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 516
Db 1410 TGAAGTCACAAAGATGAGATTTACATGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1351
QY 517 TCACAAGACATGCAACAAACAAATGGAATGATGATGATGAGAGAGAGAGAGAGAG 576
Db 1350 TCACAAGACATGCAACAAACAAATGGAATGATGATGATGAGAGAGAGAGAGAGAG 1291
QY 577 GAGGAGATTAACAGAGAGAGAGAGAGATTTGAGAGAGAGAGAGAGAGAGAGAGAG 636
Db 1290 GAGGAGATTAACAGAGAGAGAGAGAGATTTGAGAGAGAGAGAGAGAGAGAGAGAG 1231
QY 637 CATACCAAAATCATTTATTTCTTAACCTCAAAACAAAGCTGTTGTAATTCGATCT 696
Db 1230 CATACCAAAATCATTTATTTCTTAACCTCAAAACAAAGCTGTTGTAATTCGATCT 1171
QY 697 CTACGCTTCCTTCTGAGGAGAGAGATTTCTCAATATTCAGAGAGAGAGAGAGAG 756

Db 1170 CTAGCGTTCTCTGGGCCCCACATCTCCATATATCCACGACACATCTTAAATTT 1111
 QY 757 TAGTCCAGATCTGTACTGTGACCTTTTACACTGTAGATATACATCTACTATTGT 816
 Db 1110 TAGTCCAGATCTGTACTGTGACCTTTTACACTGTAGATATACATCTACTATTGT 1051
 QY 817 CAAGACCCCTGCTGTTGCTGCTTAATATGTAGCTGACTTTTCTTAAGAGAGTGTCT 876
 Db 1050 CAAGACCCCTGCTGTTGCTGCTTAATATGTAGCTGACTTTTCTTAAGAGAGTGTCT 991
 QY 877 GGGCCAGGGATCTGTGAACAGGCTGGGAAGCATCTCAATCTTTCCAGGTTATCTT 936
 Db 990 GGGCCAGGGATCTGTGAACAGGCTGGGAAGCATCTCAATCTTTCCAGGTTATCTT 931
 QY 937 ACTAGCACAGCATGTATCTTACGAGTGAATATATCAACATCATCTCAAGTCTC 996
 Db 930 ACTAGCACAGCATGTATCTTACGAGTGAATATATCAACATCATCTCAAGTCTC 871
 QY 997 TTGGCCCATCTGAATTTCAATTTCCACTTTTGTGCCATTTCTCAAGACCTCAAAATGTC 1056
 Db 870 TTGGCCCATCTGAATTTCAATTTCCACTTTTGTGCCATTTCTCAAGACCTCAAAATGTC 811
 QY 1057 ATTCCATTATATCACAGGATTAATCTTTTAACTGTGAAGAAATTCATGTATCAT 1116
 Db 810 ATTCCATTATATATCACAGGATTAATCTTTTAACTGTGAAGAAATTCATGTATCAT 751
 QY 1117 GCAGCTATGGGAATTTAATACATATTTTTCAGTCAATAAAGTTAAATGCTTACTTACT 1176
 Db 750 GCAGCTATGGGAATTTAATACATATTTTTCAGTCAATAAAGTTAAATGCTTACTTACT 691
 QY 1177 ATCCCTCCCTTTGTTGATTTTTTTCAGATATAAAGTTAAATGCTTACTTACT 1236
 Db 690 ATCCCTCCCTTTGTTGATTTTTTTCAGATATAAAGTTAAATGCTTACTTACT 631
 QY 1237 GAGGCTGTATACAGC 1251
 Db 630 GAGGCTGTATACAGC 616

RESULT 11

US-09-822-470/c
 ; Sequence 470, Application US/09822827
 ; Patent No. US2002008160A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Xu, Jiangchun
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
 ; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
 ; FILE REFERENCE: 210121.534C1
 ; CURRENT APPLICATION NUMBER: US/09/822, 827
 ; CURRENT FILING DATE: 2001-03-28
 ; NUMBER OF SEQ ID NOS: 982
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 470
 ; LENGTH: 2426
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-09-822-827-470

Query Match 61.7%; Score 1155; DB 9; Length 2426;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1155; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 97 AGGTGAAATTAAGAAAGGCTGCTGACTTTACACTGTGAGGCCACACATCTGCTGAATG 156
 Db 1770 AGGTGAAATTAAGAAAGGCTGCTGACTTTACACTGTGAGGCCACACATCTGCTGAATG 1711
 QY 157 GAGATAATTAACACTAGTAAACAGCAGATGACATATATATGTCTAAGTAGATG 216
 Db 1710 GAGATAATTAACACTAGTAAACAGCAGATGACATATATATGTCTAAGTAGATG 1651
 QY 217 TTTTGGACATTTCCAGCCCTTTAAATATCCACACACAGGAGACAAAGGAAGCA 276

Db 1650 TTTTGGACATTTCCAGCCCTTTAAATATCCACACACAGGAGACAAAGGAAGCA 1591
 QY 277 CAGAGATCCCTGGGAGAAATGCCGCGCCATCTTGGTGCATGATGAGCTCGCCCTG 336
 Db 1590 CAGAGATCCCTGGGAGAAATGCCGCGCCATCTTGGTGCATGATGAGCTCGCCCTG 1531
 QY 337 TGCCTGCTCCGCTTGTGAGGGAAGACATTTAGAAAATGAATTGATGTCTTAAAG 396
 Db 1530 TGCCTGCTCCGCTTGTGAGGGAAGACATTTAGAAAATGAATTGATGTCTTAAAG 1471
 QY 397 ATGGGCGAGAAACAGATCCCTGTTGTGATATTTATTTGAACGGGATTTACAGTTTAAA 456
 Db 1470 ATGGGCGAGAAACAGATCCCTGTTGTGATATTTATTTGAACGGGATTTACAGTTTAAA 1411
 QY 457 TGAAGTCACAAAGAGACATTTACCAATGAGAGGAAAACAGACGAAATCTTGATGCT 516
 Db 1410 TGAAGTCACAAAGAGACATTTACCAATGAGAGGAAAACAGACGAAATCTTGATGCT 1351
 QY 517 TCACAGACATGCAACAAACAAATGGAATACGTGTGATGACATGAGGACCCAAAGCTGGG 576
 Db 1350 TCACAGACATGCAACAAACAAATGGAATACGTGTGATGACATGAGGACCCAAAGCTGGG 1291
 QY 577 GAGGATTAACACAGGGGAGAGGCTCAGGATTCCTGCTGCTTAACGTGGCTT 636
 Db 1290 GAGGATTAACACAGGGGAGAGGCTCAGGATTCCTGCTGCTTAACGTGGCTT 1231
 QY 637 CATTAACCAATCATTTCTATTTCTAACCTCAAAACAGAGCTGTTAAATCTGATCT 696
 Db 1230 CATTAACCAATCATTTCTATTTCTAACCTCAAAACAGAGCTGTTAAATCTGATCT 1171
 QY 697 CTACGGTCTCTGCGGCCCAACATTTCTCAATATTCACGACACATCTTTTAATAT 756
 Db 1170 CTACGGTCTCTGCGGCCCAACATTTCTCAATATTCACGACACATCTTTTAATAT 1111
 QY 757 TAGTCCAGATCTGTACTGTGACCTTTTACACTGTAGATATACATTTACTTTTGT 816
 Db 1110 TAGTCCAGATCTGTACTGTGACCTTTTACACTGTAGATATACATTTACTTTTGT 1051
 QY 817 CAAGACCCCTGCTGTTGCTGCTTAATATGTAGCTGACTTTTCTTAAGAGAGTGTCT 876
 Db 1050 CAAGACCCCTGCTGTTGCTGCTTAATATGTAGCTGACTTTTCTTAAGAGAGTGTCT 691
 QY 877 GGGCCAGGGATCTGTGAACAGGCTGGGAAGCATCTCAATCTTTCCAGGTTATCTT 936
 Db 990 GGGCCAGGGATCTGTGAACAGGCTGGGAAGCATCTCAATCTTTCCAGGTTATCTT 931
 QY 937 ACTAGCACAGCATGTATCTTACGAGTGAATATATCAACATCATCTCAAGTCTC 996
 Db 930 ACTAGCACAGCATGTATCTTACGAGTGAATATATCAACATCATCTCAAGTCTC 871
 QY 997 TTGGCCCATCTGAATTTCAATTTCCACTTTTGTGCCATTTCTCAAGACCTCAAAATGTC 1056
 Db 870 TTGGCCCATCTGAATTTCAATTTCCACTTTTGTGCCATTTCTCAAGACCTCAAAATGTC 811
 QY 1057 ATTCCATTATATCACAGGATTAATCTTTTAACTGTGAAGAAATTCATGTATCAT 1116
 Db 810 ATTCCATTATATATCACAGGATTAATCTTTTAACTGTGAAGAAATTCATGTATCAT 751
 QY 1117 GCAGCTATGGGAATTTAATACATATTTTTCAGTCAATAAAGTTAAATGCTTACTTACT 1176
 Db 750 GCAGCTATGGGAATTTAATACATATTTTTCAGTCAATAAAGTTAAATGCTTACTTACT 691
 QY 1177 ATCCCTCCCTTTGTTGATTTTTTTCAGATATAAAGTTAAATGCTTACTTACT 1236
 Db 690 ATCCCTCCCTTTGTTGATTTTTTTCAGATATAAAGTTAAATGCTTACTTACT 631

RESULT 12
 US-09-895-793-470/c

```
; Sequence 470, Application US/09895793
; Publication No. US20020192763A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yugu
; APPLICANT: Kalos, Michael D.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedrick, Thomas S.
; APPLICANT: Carter, Darriek
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Vinals de Bassols, Carlota
; APPLICANT: Foy, Teresa
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.534C2
; CURRENT FILING DATE: 2001-06-29
; NUMBER OF SEQ ID NOS: 982
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO: 470
; LENGTH: 2426
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-895-793-470

Query Match          61.7%; Score 1155; DB 10; Length 2426;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1155; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 97 AGGTGAGAAATTAAGAAAGCTGCTGACTTTTACATCTGAGGCACACATCTGCTGAATG 156
DB 1770 AGGTGAGAAATTAAGAAAGCTGCTGACTTTTACATCTGAGGCACACATCTGCTGAATG 1711
QY 157 GAGATTAATTAACATCTAGTAAACAGCAAGATGACATTAATTAATGCTTAAGTAGACATG 216
DB 1710 GAGATTAATTAACATCTAGTAAACAGCAAGATGACATTAATTAATGCTTAAGTAGACATG 1651
QY 217 TTTTGGACATTTCCAGCCCTTTAATATCCACACACAGCAAGCAACAAAGGAACGA 276
DB 1650 TTTTGGACATTTCCAGCCCTTTAATATCCACACACAGCAAGCAACAAAGGAACGA 1591
QY 277 CAGAGATCCCTGGGAGAAATGCCGCCCATCTTGGGTATCGATGAGCCTGCCCTG 336
DB 1590 CAGAGATCCCTGGGAGAAATGCCGCCCATCTTGGGTATCGATGAGCCTGCCCTG 1531
QY 337 TGCGTGTCCGCTTGTGAGGGAAGACATTAAGAAATGAATGATGCTTCTTAAGG 396
DB 1530 TGCGTGTCCGCTTGTGAGGGAAGACATTAAGAAATGAATGATGCTTCTTAAGG 1471
QY 397 ATGGGACAGAAACAGATCTGTGTGATATTTTATTTGAACGGGATTAACAGATTGAAA 456
DB 1470 ATGGGACAGAAACAGATCTGTGTGATATTTTATTTGAACGGGATTAACAGATTGAAA 1411
QY 457 TGAAGTCAACAAGTGAAGATTAACATGAGAGGAAACAGACGAGAAATCTTGTAGCT 516
DB 1410 TGAAGTCAACAAGTGAAGATTAACATGAGAGGAAACAGACGAGAAATCTTGTAGCT 1351
QY 517 TCACAAGCATGCAACAACAATGAAATGAAATCTGTGATGACATGAGGCAAGCCAGCTGGG 576
DB 1350 TCACAAGCATGCAACAACAATGAAATGAAATCTGTGATGACATGAGGCAAGCCAGCTGGG 1291
```

```
QY 577 GAGGAGATTAACCAAGGGGAGAGGGTACAGGATTTCGCCCTGCTCAAACTGNGCGTT 636
DB 1290 GAGGAGATTAACCAAGGGGAGAGGGTACAGGATTTCGCCCTGCTCAAACTGNGCGTT 1231
QY 637 CATAACCAAAATCATTTATATTTCTAACCTCAAAACAAAGCTGTTGAATATGANTCT 696
DB 1230 CATAACCAAAATCATTTATATTTCTAACCTCAAAACAAAGCTGTTGAATATGANTCT 1171
QY 697 CTACGGTTCCTTCTGGGCCCCAATCTTCATATATCCAGCCACATCTATTTTAATAT 756
DB 1170 CTACGGTTCCTTCTGGGCCCCAATCTTCATATATCCAGCCACATCTATTTTAATAT 1111
QY 757 TAGTCCAGATCTGATGAGACCTTTCTACAGTGAATGAATTAACATTAACATTTGTT 816
DB 1110 TAGTCCAGATCTGATGAGACCTTTCTACAGTGAATGAATTAACATTAACATTTGTT 1051
QY 817 CAAGAACCCTTCGTGCTGCTGAATATATGATGAGTGTCTTCTTAAGAGTGTCT 876
DB 1050 CAAGAACCCTTCGTGCTGCTGAATATATGATGAGTGTCTTCTTAAGAGTGTCT 991
QY 877 GGCCAGGGGATCTGTGAACAGGCTGGGAAGCATCTCAAGATCTTCCAGGTTATCTT 936
DB 990 GGCCAGGGGATCTGTGAACAGGCTGGGAAGCATCTCAAGATCTTCCAGGTTATCTT 931
QY 937 ACTAGCACAGCATGATCATTAAGAGATGATTTCTTAATCAATCATCTCAAGTGTCT 996
DB 930 ACTAGCACAGCATGATCATTAAGAGATGATTTCTTAATCAATCATCTCAAGTGTCT 871
QY 997 TTTGCCATATGAAATTCATTTCCACATTTTGTGCCCCATCTCAAGACCTCAAAATGTC 1056
DB 870 TTTGCCATATGAAATTCATTTCCACATTTTGTGCCCCATCTCAAGACCTCAAAATGTC 811
QY 1057 ATTCATTAATATACACAGATTAACCTTTTTTTTAACTGGAAGAAATTCATGTTACAT 1116
DB 810 ATTCATTAATATACACAGATTAACCTTTTTTTTAACTGGAAGAAATTCATGTTACAT 751
QY 1117 GCAGCTATGGGAATTAATTAATTAATTTGTTTCCAGTGCAGAAAGATGACTAAGCTTT 1176
DB 750 GCAGCTATGGGAATTAATTAATTAATTTGTTTCCAGTGCAGAAAGATGACTAAGCTTT 691
QY 1177 ATCCCTCCCTTTGTTGATTTTCTTCCAGTATTAAGTTAAATGCTTAGCCTGTACT 1236
DB 690 ATCCCTCCCTTTGTTGATTTTCTTCCAGTATTAAGTTAAATGCTTAGCCTGTACT 631
QY 1237 GAGGCTGTATACAGC 1251
DB 630 GAGGCTGTATACAGC 616

RESULT 13
US-09-895-814-470/c
; Sequence 470, Application US/09895814
; Publication No. US20020193296A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yugu
; APPLICANT: Kalos, Michael D.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedrick, Thomas S.
; APPLICANT: Carter, Darriek
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
```



```

: APPLICANT: Houghton, Raymond L.
: APPLICANT: Vinals de Bassols, Carlota
: APPLICANT: Foy, Teresa
: APPLICANT: Fanger, Gary R.
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
: FILE REFERENCE: 210121.427C26
: CURRENT APPLICATION NUMBER: US/09/895,814
: CURRENT FILING DATE: 2001-06-29
: NUMBER OF SEQ ID NOS: 990
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 470
: LENGTH: 2426
: TYPE: DNA
: ORGANISM: Homo sapiens
US-09-895-814-470

```

```

Query Match      61.7%; Score 1155; DB 10; Length 2426;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1155; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 97 AGGTGAGAAATGAAGAGCGCTGACTTTACATCTGAGGCCACACATCTGCTGAATG 156
DB 1770 AGGTGAGAAATGAAGAGCGCTGACTTTACATCTGAGGCCACACATCTGCTGAATG 1711
QY 157 GAGATTAATTAACATCTAGTAAGACAGAGATGCAATATATGTCTAAGTATGATG 216
DB 1710 GAGATTAATTAACATCTAGTAAGACAGAGATGCAATATATGTCTAAGTATGATG 1651
QY 217 TTTTTCGACATTTCCACCCCTTTAAATATCCACACACAGAGAACACAAAGGAAGCA 276
DB 1650 TTTTTCGACATTTCCACCCCTTTAAATATCCACACACAGAGAACACAAAGGAAGCA 1591
QY 277 CAGAGATCCCTGGGAGAAATGCGCGCCGACATCTGGGTATGATGAGCTCGCCCTG 336
DB 1590 CAGAGATCCCTGGGAGAAATGCGCGCCGACATCTGGGTATGATGAGCTCGCCCTG 1531
QY 337 TGCCTGTCCTGCTGTGTGAGGAGAGACATTAAGAAATGATGTGCTTAAAGG 396
DB 1530 TGCCTGTCCTGCTGTGTGAGGAGAGACATTAAGAAATGATGTGCTTAAAGG 1471
QY 397 ATGGCGCAGAAACAGATCCTGTTGTGATATTTATTTGAACGGGATTAAGATTGAAA 456
DB 1470 ATGGCGCAGAAACAGATCCTGTTGTGATATTTATTTGAACGGGATTAAGATTGAAA 1411
QY 457 TGAAGTCACAAAGTGAACATTTACCAATGAGAGAGAAACAGACGAGAAATCTTGATGCT 516
DB 1410 TGAAGTCACAAAGTGAACATTTACCAATGAGAGAGAAACAGACGAGAAATCTTGATGCT 1351
QY 517 TCACAGACATGCAACAAACAAATGGAATACGTGTGATGACATGAGCAGCAGCTGGG 576
DB 1350 TCACAGACATGCAACAAACAAATGGAATACGTGTGATGACATGAGCAGCAGCTGGG 1291
QY 577 GAGGAGTAACCAACGGGCGAGAGGATGATGCTGCTGCTTAACCTGCTGCTT 636
DB 1290 GAGGAGTAACCAACGGGCGAGAGGATGATGCTGCTGCTTAAACCTGCTGCTT 1231
QY 637 CATACCAATCAATTCATATTTCTAATCCTCAAAACAAAGCTGTGTATATCTGATCT 696
DB 1230 CATACCAATCAATTCATATTTCTAATCCTCAAAACAAAGCTGTGTATATCTGATCT 1171
QY 697 CTACGCTCTCTGCGCCCAACATCTCTCATATATCCACAGCAGCAGCTATTTTAATAT 756
DB 1170 CTACGCTCTCTGCGCCCAACATCTCTCATATATCCACAGCAGCAGCTATTTTAATAT 1111
QY 757 TACTTCCCAATCTGATCTGATCTTGTACACTGTAGAAATACATTAATCTATTTGTT 816
DB 1110 TACTTCCCAATCTGATCTGATCTTGTACACTGTAGAAATACATTAATCTATTTGTT 1051
QY 817 CAAGAGACCTCTGCTGTGCTGCTAATATATGATGATGATGATGATGATGATGATG 876
DB 1050 CAAGAGACCTCTGCTGTGCTGCTAATATATGATGATGATGATGATGATGATGATG 991

```

```

QY 877 GGCCAGGAGATCTGTGAACAGGCTGGGAAAGCATCTCAAGATCTTCCAGGGTATACTT 936
DB 990 GGCCAGGAGATCTGTGAACAGGCTGGGAAAGCATCTCAAGATCTTCCAGGGTATACTT 931
QY 937 ACTAGCACACAGCATGATGATCTTACGAGTGAATATATATCAACATCAATCCAGTGC 996
DB 930 ACTAGCACACAGCATGATGATCTTACGAGTGAATATATCAACATCAATCCAGTGC 871
QY 997 TTTGCCATCTGTAATTCATTTTCCACTTTTGGCCCATTTCAAGACCTCAAAAGTGC 1056
DB 870 TTTGCCATCTGTAATTCATTTTCCACTTTTGGCCCATTTCAAGACCTCAAAAGTGC 811
QY 1057 ATTCATTAATATACAGAGATTAATCTTTTAACTGGAAGAAATCAATGATTAAT 1116
DB 810 ATTCATTAATATACAGAGATTAATCTTTTAACTGGAAGAAATCAATGATTAAT 751
QY 1117 GCACATATGGAATTTATATATTTTGTTCACAGTGCAGAAAGATGATGATGATG 1176
DB 750 GCACATATGGAATTTATATATTTTGTTCACAGTGCAGAAAGATGATGATGATG 691
QY 1177 ATCCCTCCCTTTGTTGATTTTTCAGATATTAAGTTAAATGCTTAGCCTGACT 1236
DB 690 ATCCCTCCCTTTGTTGATTTTTCAGATATTAAGTTAAATGCTTAGCCTGACT 631
QY 1237 GAGGCTGTATACAGC 1251
DB 630 GAGGCTGTATACAGC 616

```

```

RESULT 14
US-10-144-678A-470/c
: Sequence 470, Application US/10144678A
: Publication No. US20030157089A1
: GENERAL INFORMATION:

```

```

: APPLICANT: Xu, Jiangchun
: APPLICANT: Dillon, David C.
: APPLICANT: Mitcham, Jennifer L.
: APPLICANT: Harlocker, Susan L.
: APPLICANT: Jiang, Yugu
: APPLICANT: Henderson, Robert A.
: APPLICANT: Kalos, Michael D.
: APPLICANT: Fanger, Gary R.
: APPLICANT: Retter, Marc W.
: APPLICANT: Stolk, John A.
: APPLICANT: Day, Craig H.
: APPLICANT: Vedvick, Thomas S.
: APPLICANT: Carter, Darrick
: APPLICANT: Li, Samuel X.
: APPLICANT: Wang, Aljun
: APPLICANT: Skeiky, Yasir A. W.
: APPLICANT: Hepler, William T.
: APPLICANT: Hurst, John
: APPLICANT: McNeill, Patricia D.
: APPLICANT: Houghton, Raymond L.
: APPLICANT: Vinals y de Bassols, Carlota
: APPLICANT: Foy, Teresa M.
: APPLICANT: Matanabe, Yoshihiro
: APPLICANT: Deng, Ta
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
: FILE REFERENCE: 210121.427C28
: CURRENT APPLICATION NUMBER: US/10/144,678A
: CURRENT FILING DATE: 2002-08-12
: NUMBER OF SEQ ID NOS: 1033
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 470
: LENGTH: 2426
: TYPE: DNA
: ORGANISM: Homo sapiens
US-10-144-678A-470

```

```

Query Match      61.7%; Score 1155; DB 12; Length 2426;
Best Local Similarity 100.0%; Pred. No. 0;

```


Matches 1155; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				
QY	97	AGGTGAGAAATTAAGAAAGGCTGCTGCTTACTTATCATCTGTAGGCGCACACATCTGCTAAATG	156	
DB	1770	AGGTGAGAAATTAAGAAAGGCTGCTGCTTACTTATCATCTGTAGGCGCACACATCTGCTAAATG	1711	
QY	157	GAGATTAATTAATCACTAGTAAGAAACAGCAAGATGACATATATATGCTAAGTAGTACATG	216	
DB	1710	GAGATTAATTAATCACTAGTAAGAAACAGCAAGATGACATATATATGCTAAGTAGTACATG	1651	
QY	217	TTTTTGACATTTTCCAGCCCTTTAATATTCACACACACAGGAAGCAACAAAGGAGCA	276	
DB	1650	TTTTTGACATTTTCCAGCCCTTTAATATTCACACACAGGAAGCAACAAAGGAGCA	1591	
QY	277	CAGAGATCCCGGGGAAATGCCCGGCCATCTGGGTATGATGATAGGCTGCCCTG	336	
DB	1590	CAGAGATCCCGGGGAAATGCCCGGCCATCTGGGTATGATGATAGGCTGCCCTG	1531	
QY	337	TGCTGTGCTCCGCTTGAGGGAAGGACATTAAGAAATGAATGATGCTTCTTAAAGG	396	
DB	1530	TGCTGTGCTCCGCTTGAGGGAAGGACATTAAGAAATGAATGATGCTTCTTAAAGG	1471	
QY	397	ATGGGCAAGAAACAGATCCTGCTGTGATATTTATTTGAACGGGATTACAGATTTGAAA	456	
DB	1470	ATGGGCAAGAAACAGATCCTGCTGTGATATTTATTTGAACGGGATTACAGATTTGAAA	1411	
QY	457	TGAAGTCACAAAGAGGAGCATTAACATAGAGGAAACAGAGAAATCTGTATGCT	516	
DB	1410	TGAAGTCACAAAGAGGAGCATTAACATAGAGGAAACAGAGAAATCTGTATGCT	1351	
QY	517	TCACAAGACATGCAACAACAATAATGAACTGTGATGATGAGCAGCCAAAGCTGG	576	
DB	1350	TCACAAGACATGCAACAACAATAATGAACTGTGATGATGAGCAGCCAAAGCTGG	1291	
QY	577	GAGGATTAACACAGGGGCGAGAGGCTCAGATTTGCGCCCTGCTTAACTGTGCTT	636	
DB	1290	GAGGATTAACACAGGGGCGAGAGGCTCAGATTTGCGCCCTGCTTAACTGTGCTT	1231	
QY	637	CATAACCAAAATCATTTCTATTTCTAACCTCAAAACAAGCTGTGTAATCTGATCT	696	
DB	1230	CATAACCAAAATCATTTCTATTTCTAACCTCAAAACAAGCTGTGTAATCTGATCT	1171	
QY	697	CTAGGTTCTCTTGCGGCCCAACATTTCTCATATATTCAGCCACACATCTTTTAAAT	756	
DB	1170	CTAGGTTCTCTTGCGGCCCAACATTTCTCATATATTCAGCCACACATCTTTTAAAT	1111	
QY	757	TAGTTCACAGATCTGTACTGTGACCTTTCTACACTGTGAAATACATTTACTTTGTT	816	
DB	1110	TAGTTCACAGATCTGTACTGTGACCTTTCTACACTGTGAAATACATTTACTTTGTT	1051	
QY	817	CAAGAGACCTTCGTGCTGCTCAATATATAGTGAAGTCTTTTCTTAAGAGTCTCT	876	
DB	1050	CAAGAGACCTTCGTGCTGCTCAATATATAGTGAAGTCTTTTCTTAAGAGTCTCT	991	
QY	877	GGCCAGGGGATCTGTGAACAGGCTGGAGACATCTCAAGATCTTCCAGGGTTTACTT	936	
DB	990	GGCCAGGGGATCTGTGAACAGGCTGGAGACATCTCAAGATCTTCCAGGGTTTACTT	931	
QY	937	ACTAGACACAGCATGATCATTTAGGAGTGAATATATCATACATCATCTCAGTGTG	996	
DB	930	ACTAGACACAGCATGATCATTTAGGAGTGAATATATCATACATCATCTCAGTGTG	871	
QY	997	TTTGCCCATCTAGTAATTCATTTCCACTTTTGTGCCATTTCTCAAGACCTCAAAATGTC	1056	
DB	870	TTTGCCCATCTAGTAATTCATTTCCACTTTTGTGCCATTTCTCAAGACCTCAAAATGTC	811	
QY	1057	ATTCATTAATATCACAGGATTAATCTTTTAACTGGAAGAAATTCATTTTACT	1116	
DB	810	ATTCATTAATATCACAGGATTAATCTTTTAACTGGAAGAAATTCATTTTACT	751	
QY	1117	GCAGCTATGGAATTTAATACATATTTTGTTCACATGCAAAAGATGACTAAGTCTTT	1176	
DB	750	GCAGCTATGGAATTTAATACATATTTTGTTCACATGCAAAAGATGACTAAGTCTTT	691	

QY	1177	ATCCCTCCCTTTGTGATTTTTCACATATAAGTTAAATGCTTAGCCTTACT	1236	
DB	690	ATCCCTCCCTTTGTGATTTTTCACATATAAGTTAAATGCTTAGCCTTACT	631	
QY	1237	GAGGCTGTATCAGC	1251	
DB	630	GAGGCTGTATCAGC	616	
RESULT 15				
US-10-012-896-470/c				
Sequence 470, Application US/10012896				
Publication No. US20020183251A1				
GENERAL INFORMATION:				
APPLICANT: Xu, Jiaqun				
APPLICANT: Dillon, David C.				
APPLICANT: Mitcham, Jennifer L.				
APPLICANT: Harlocker, Susan L.				
APPLICANT: Jiang, Yugu				
APPLICANT: Kalos, Michael D.				
APPLICANT: Retter, Marc W.				
APPLICANT: Stolk, John A.				
APPLICANT: Day, Craig H.				
APPLICANT: Vedvick, Thomas S.				
APPLICANT: Carter, Darlick				
APPLICANT: Li, Samuel X.				
APPLICANT: Wang, Aijun				
APPLICANT: Skeiky, Yasir A.W.				
APPLICANT: Hepler, William T.				
APPLICANT: Henderson, Robert A.				
APPLICANT: Hural, John				
APPLICANT: McNeill, Patricia D.				
APPLICANT: Houghton, Raymond L.				
APPLICANT: Vinals de Bassols, Carlota				
APPLICANT: Foy, Teresa				
APPLICANT: Fanger, Gary R.				
APPLICANT: Mantanabe, Yoshihiro				
APPLICANT: Meagher, Madeleine Joy				
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND				
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER				
FILE REFERENCE: 210121.427C27				
CURRENT APPLICATION NUMBER: US/10/012,896				
CURRENT FILING DATE: 2001-12-10				
NUMBER OF SEQ ID NOS: 1011				
SOFTWARE: FastSeq for Windows Version 3.0				
SEQ ID NO 470				
LENGTH: 2426				
TYPE: DNA				
ORGANISM: Homo sapiens				
US-10-012-896-470				
Query Match				
Best Local Similarity 61.7%; Score 1155; DB 13; Length 2426;				
Matches 1155; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				
QY	97	AGGTGAGAAATTAAGAAAGGCTGCTGCTTACTTATCATCTGTAGGCGCACACATCTGCTAAATG	156	
DB	1770	AGGTGAGAAATTAAGAAAGGCTGCTGCTTACTTATCATCTGTAGGCGCACACATCTGCTAAATG	1711	
QY	157	GAGATTAATTAATCACTAGTAAGAAACAGCAAGATGACATATATATGCTAAGTAGTACATG	216	
DB	1710	GAGATTAATTAATCACTAGTAAGAAACAGCAAGATGACATATATATGCTAAGTAGTACATG	1651	
QY	217	TTTTTGACATTTTCCAGCCCTTTAATATTCACACACAGGAAGCAACAAAGGAGCA	276	
DB	1650	TTTTTGACATTTTCCAGCCCTTTAATATTCACACACAGGAAGCAACAAAGGAGCA	1591	
QY	277	CAGAGATCCCGGGGAAATGCCCGGCCATCTGGGTATGATGATAGGCTGCCCTG	336	
DB	1590	CAGAGATCCCGGGGAAATGCCCGGCCATCTGGGTATGATGATAGGCTGCCCTG	1531	
QY	337	TGCTGTGCTCCGCTTGAGGGAAGGACATTAAGAAATGAATGATGCTTCTTAAAGG	396	

Db 1530 TGGCTGGTCCCGCTTGAGGGAAGGACATTAGAAAATGAATGATGTGTTCTTAAGG 1471
QY 397 ATGGGACAGAAAACAGATCCTGTTGAGATATTATTGTAACGGGATTACAGATTGAAA 456
Db 1470 ATGGGACAGAAAACAGATCCTGTTGAGATATTATTGTAACGGGATTACAGATTGAAA 1411
QY 457 TGAAGTCACAAGTAGAGCATTACCAATGAGAGAAAACAGACGAGAAAATCTTGATGGCT 516
Db 1410 TGAAGTCACAAGTAGAGCATTACCAATGAGAGAAAACAGACGAGAAAATCTTGATGGCT 1351
QY 517 TCACAAGACATGCAACAACAAAATGGAATACGTGTGATGACATGAGGACGCCAAGCTGGG 576
Db 1350 TCACAAGACATGCAACAACAAAATGGAATACGTGTGATGACATGAGGACGCCAAGCTGGG 1291
QY 577 GAGGATATACCCACGGGGGCGAGAGGTCAGATTTCTGGCCCTGCTGCTTAACGTGGCTT 636
Db 1290 GAGGATATACCCACGGGGGCGAGAGGTCAGATTTCTGGCCCTGCTGCTTAACGTGGCTT 1231
QY 637 CATACCAAAATCATTTCAATTTCTAACCCCTCAAAACAAAGCTGTTGTAATATCTGATCT 696
Db 1230 CATACCAAAATCATTTCAATTTCTAACCCCTCAAAACAAAGCTGTTGTAATATCTGATCT 1171
QY 697 CTACGGTTCCTTGTGGGCCCAACATTCCTCATATATCCAGCCACACTCATTTTAAATAT 756
Db 1170 CTACGGTTCCTTGTGGGCCCAACATTCCTCATATATCCAGCCACACTCATTTTAAATAT 1111
QY 757 TAGTTCCAGATCTGATGATGACCTTTCTACACTGTAGAAATACATTAATCTTGTGT 816
Db 1110 TAGTTCCAGATCTGATGATGACCTTTCTACACTGTAGAAATACATTAATCTTGTGT 1051
QY 817 CAAGAACCCTTCGTGCTGCTGCTTAATATATGATGATGATGATGATGATGATGATGAT 876
Db 1050 CAAGAACCCTTCGTGCTGCTGCTTAATATATGATGATGATGATGATGATGATGATGAT 991
QY 877 GGGCCAGGGGATCTGTAACAGGCTGGGAAGCATCTCAGATCTTTCAGGGTTATACCT 936
Db 990 GGGCCAGGGGATCTGTAACAGGCTGGGAAGCATCTCAGATCTTTCAGGGTTATACCT 931
QY 937 ACTAGCACACAGATGATCATTTACGAGATGATTAATCTAATCAACATCATCTCAGTGC 996
Db 930 ACTAGCACACAGATGATCATTTACGAGATGATTAATCTAATCAACATCATCTCAGTGC 871
QY 997 TTTGCCATACGAAATTCATTTCCACTTTTGTGCCATTCACAGACCTCAAAAATGTC 1056
Db 870 TTTGCCATACGAAATTCATTTCCACTTTTGTGCCATTCACAGACCTCAAAAATGTC 811
QY 1057 ATTCCATTAATATCACAGATTAATCTTTTAACTGGAAGATTCATGTTACAT 1116
Db 810 ATTCCATTAATATCACAGATTAATCTTTTAACTGGAAGATTCATGTTACAT 751
QY 1117 GCAGCTATGGGATTAATTAATATTTGTTTCCAGTGAAGATGATGATGATGATGATGAT 1176
Db 750 GCAGCTATGGGATTAATTAATATTTGTTTCCAGTGAAGATGATGATGATGATGATGAT 691
QY 1177 ATCCCTCCCTTGTGTTGATTTTTTCCAGTGAAGATTAAGTTAAATGCTTAGCTGTACT 1236
Db 690 ATCCCTCCCTTGTGTTGATTTTTTCCAGTGAAGTTAAATGCTTAGCTGTACT 631
QY 1237 GAGGCTGTATACGC 1251
Db 630 GAGGCTGTATACGC 616

Search completed: September 27, 2003, 12:16:08
Job time : 436.819 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 26, 2003, 21:39:38 : Search time 3928.47 seconds
(without alignments)
11581.589 Million cell updates/sec

Title: US-09-402-713A-3

Perfect score: 1872
Sequence: 1 agaagctgcacacagaataa.....caataagaattaccagaaga 1872

Scoring table: OLIGO_NUC

Gapop 60.0 , Gapext 60.0

Searched: 22781392 seqs, 1215238056 residues

Word size : 0

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estinu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hic:*
9: gb_est1:*
10: gb_est2:*
11: gb_hic:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: em_gss_hum:*
18: em_gss_inv:*
19: em_gss_pln:*
20: em_gss_vrt:*
21: em_gss_fun:*
22: em_gss_mam:*
23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_rod:*
26: em_gss_phg:*
27: em_gss_vrt1:*
28: gb_gss1:*
29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	367	19.6	402	9	AA578773
2	238	12.7	290	10	BF373619
3	222	11.9	654	28	AO319247
4	214	11.4	226	10	BF858371

C	5	214	11.4	394	28	AO206972	AO206972 HS_3238_B
C	6	213	11.4	332	10	BF858286	BF858286 RC5-FT019
C	7	198	10.6	282	10	BF373581	BF373581 MR0-FT017
C	8	167	8.9	167	10	BF373406	BF373406 IL2-FT015
C	9	147	7.9	856	9	A1557225	A1557225 PT2.1-15
C	10	124	6.6	441	10	BF858890	BF858890 RC5-FT019
C	11	100	5.3	572	13	BQ292550	BQ292550 PM0-AN008
C	12	86	4.6	657	9	A1557495	A1557495 PT2.1-7 H
C	13	43	2.3	451	28	AO246715	AO246715 HS_2059_B
C	14	26	1.4	305	14	RO1974	RO1974 yeb5f01.r1
C	15	26	1.4	371	14	T79384	T79384 yd74g09.r1
C	16	26	1.4	438	14	R24922	R24922 yb38g05.r1
C	17	26	1.4	435	10	BE763909	BE763909 RC4-NT005
C	18	26	1.4	437	10	BE763867	BE763867 RC4-NT005
C	19	26	1.4	448	14	T83051	T83051 yd43d10.r1
C	20	26	1.4	594	12	BM761346	BM761346 K-EST0042
C	21	26	1.4	613	10	AM969419	AM969419 EST81496
C	22	26	1.4	644	12	BM843410	BM843410 K-EST0121
C	23	26	1.4	647	12	BI604102	BI604102 603244033
C	24	26	1.4	691	12	BM761207	BM761207 K-EST0041
C	25	26	1.4	726	9	AI084676	AI084676 0278h07.x
C	26	26	1.4	766	13	B0623156	B0623156 UI-H-FT1-
C	27	26	1.4	823	10	BG715096	BG715096 602676034
C	28	26	1.4	840	9	AL545416	AL545416 AL545416
C	29	26	1.4	847	9	AL530074	AL530074 AL530074
C	30	26	1.4	876	12	BM453922	BM453922 AGENCOURT
C	31	26	1.4	931	12	BM047350	BM047350 603628473
C	32	26	1.4	938	13	BQ226375	BQ226375 AGENCOURT
C	33	26	1.4	943	9	AL540648	AL540648 AL540648
C	34	26	1.4	950	13	BX433585	BX433585 BX433585
C	35	26	1.4	961	13	BU174024	BU174024 AGENCOURT
C	36	26	1.4	984	12	BI517827	BI517827 603042086
C	37	26	1.4	1021	12	BM924430	BM924430 AGENCOURT
C	38	26	1.4	1043	12	BM919376	BM919376 AGENCOURT
C	39	26	1.4	1059	12	BM546894	BM546894 AGENCOURT
C	40	26	1.4	1201	9	AL517341	AL517341 AL517341
C	41	26	1.4	1201	9	AL530467	AL530467 AL530467
C	42	26	1.4	1201	13	BX361048	BX361048 BX361048
C	43	26	1.4	1414	11	BC015146	BC015146 Homo sapi
C	44	25	1.3	472	28	A2194043	A2194043 SP_1025_B
C	45	23	1.2	510	10	BE239955	BE239955 EST404004

ALIGNMENTS

RESULT 1
LOCUS AA578773
DEFINITION nh24a04.s1 NCI_CGAP_Prl Homo sapiens CDNA clone IMAGE:953262, mRNA sequence.
ACCESSION AA578773
VERSION AA578773.1 GI:2356957
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 402)
AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
JOURNAL Unpublished
CONTACT: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: W. Marston Linehan, M.D., Rodrigo Chuagui, M.D.
Michael Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: David B. Krizman, Ph.D.
CDNA Library Arrayed by: Genome Systems Inc., Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html

Insert Length: 565 Std Error: 0.00
Seq primer: -40m13 fwd. EY from Amersham
High quality sequence stop: 373.
Location/Qualifiers

FEATURES
source

1. 402
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:953262"
/sex="Male"
/dev_stage="45 years old"
/lab_host="DH10B"
/clone_id="NCI_CGAP_Prl"
/note="Vector: PAMp10; Site_1: NotI; Site_2: EcoRI; 1st strand cDNA was primed with oligo(dT)17 on 50 ng of DNase-treated, total cellular RNA obtained from 5,000-10,000 microdissected, histologically normal prostate epithelial cells. Double-stranded cDNA was ligated to EcoRI adaptors, 5 cycles of PCR applied to the cDNA with an adaptor-specific primer, and the resulting PCR product subcloned into PAMp10 by the UDG-cloning method (Life Technologies). Average insert size is 600 bp. NOTE: Not directionally cloned. This library was constructed by David Krizman."

BASE COUNT 128 a 86 c 84 g 104 t
ORIGIN

Query Match 19.6%; Score 367; DB 9; Length 402;
Best Local Similarity 100.0%; Pred. No. 2.3e-146;
Matches 367; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 430 TATTGACGGGATTACAGATTGAAATGATGACAAAGTGCATTACCATGAGAGG 489
|||||
DB 36 TATTGACGGGATTACAGATTGAAATGATGACAAAGTGCATTACCATGAGAGG 95
QY 490 AAAACAGACGAGAAAATCTGATGGCTTCACAGACATGCAACAAAGAAATGGAATCT 549
|||||
DB 96 AAAACAGACGAGAAAATCTGATGGCTTCACAGACATGCAACAAAGAAATGGAATCT 155
QY 550 GTGATGACATGAGGACGACCAAGCTGGGAGAGAGATTAACACAGGGGACAGAGGATG 609
|||||
DB 156 GTGATGACATGAGGACGACCAAGCTGGGAGAGAGATTAACACAGGGGACAGAGGATG 215
QY 610 CTGGCCCTGCTGCTTAACAGTGGCTTCATTAACCAATTCATTTCTTAACCTCA 669
|||||
DB 216 CTGGCCCTGCTGCTTAACAGTGGCTTCATTAACCAATTCATTTCTTAACCTCA 275
QY 670 AAACAAAGCTGTGTAATATCTGATCTCTACGGTCTCTGGGCCCAACATCTCCATA 729
|||||
DB 276 AAACAAAGCTGTGTAATATCTGATCTCTACGGTCTCTGGGCCCAACATCTCCATA 335
QY 730 TATCCAGCCACACTCAATTTTAAATTTAGTCCACAGATCTGACTGACCTTTTACA 789
|||||
DB 336 TATCCAGCCACACTCAATTTTAAATTTAGTCCACAGATCTGACTGACCTTTTACA 395
QY 790 CTGTAGA 796
|||||
DB 396 CTGTAGA 402

RESULT 2
BF373619

LOCUS BF373619 290 bp mRNA linear EST 24-NOV-2000
DEFINITION MK0-FT0175-310800-106-h09 FT0175 Homo sapiens cDNA, mRNA sequence.
ACCESSION BF373619
VERSION BF373619.1 GI:11335644

KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 290)
AUTHORS Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,

TITLE Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE 20202663
PubMed 10737800

COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
Fax: +55-11-2704922
Tel: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?fl=MR06t2-MR0-FT0175-310800-106-h09&f3=2000-08-31&t4=1)
Seq primer: puc 18 forward
High quality sequence stop: 290.
Location/Qualifiers

FEATURES
source

1. 290
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_id="FT0175"
/note="Organ: prostate_tumor; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the puc 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

BASE COUNT 78 a 73 c 53 g 86 t
ORIGIN

Query Match 12.7%; Score 238; DB 10; Length 290;
Best Local Similarity 100.0%; Pred. No. 5.3e-91;
Matches 238; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 575 GGGAGGAGTAACACGCGGCGACAGAGGTCTGCGCTGCTCTAAACTGCGG 634
|||||
DB 21 GGGAGGAGTAACACGCGGCGACAGAGGTCTGCGCTGCTCTAAACTGCGG 80
QY 635 TTGATAACCAATTCATTTCAATTTTCTAACCCCTCAAAAACAAGCTGTTGAATATCTGAT 694
|||||
DB 81 TTGATAACCAATTCATTTCAATTTTCTAACCCCTCAAAAACAAGCTGTTGAATATCTGAT 140
QY 695 CTCTAGCGTCTCTTGGGGCCCAACATCTCCCATATTCACGACACATCTTTTATA 754
|||||
DB 141 CTCTAGCGTCTCTTGGGGCCCAACATCTCCCATATTCACGACACATCTTTTATA 200
QY 755 TTGAGTCCGAGATCTGACTGACCTTCTACAGCTGTAATAATCAATTAATCTATT 812
|||||
DB 201 TTGAGTCCGAGATCTGACTGACCTTCTACAGCTGTAATAATCAATTAATCTATT 258

RESULT 3
AQ319247/c

LOCUS AQ319247 654 bp DNA linear GSS 06-MAY-1999
DEFINITION RC111-108L4 JV RPCR-11 Homo sapiens genomic clone RPCR-11-108L4,
genomic survey sequence.
ACCESSION AQ319247
VERSION AQ319247.1 GI:4052212

KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 654)
AUTHORS Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;

REFERENCE 1 (bases 1 to 654)
AUTHORS Adams M.D., Rounsley S.D., Zhao S., Bass S., Linher K., Golden K., Berry K., Granger D., Suh E., Wible C., de Jong P. and Venter J.C.
TITLE Use of human BAC End Sequences for Sequence-Ready Map Building
JOURNAL Unpublished
COMMENT Contact: Shaying Zhao, William Nierman, Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850
Tel: 301 838 0200
Fax: 301 838 0208
Email: hbeetlgr.org

Clones are derived from the human BAC library RPCI-11. For BAC library availability, please contact Pieter de Jong (pieteredejong.med.buitalo.edu). Clones may be purchased from BACPAC Resources (<http://bacpac.med.buitalo.edu/ordering>) or from Research Genetics (inforesgen.com). BAC end search page: http://www.tigr.org/tdb/hungen/bac_end_search/bac_end_search.html
Seq primer: 77
Class: BAC ends.

FEATURES
source
Location/Qualifiers

1..654
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="GDB:7541355"
/db_xref="taxon:9606"
/clone="RPCI-11-108L4"
/sex="Male"
/cell_type="Lymphocytes"
/clone_1lb="RPCI-11"
/note="Vector: pBAC3.6; Site_1: EcoRI; Site_2: EcoRI;
RPC11 Human Male BAC Library"

BASE COUNT 213 a 100 c 139 g 202 t
ORIGIN

Query Match 11.9%; Score 222; DB 28; Length 654;
Best Local Similarity 100.0%; Pred. No. 3.4e-84;

Matches 222; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1030 TGGCCATTCGCAAGACCTCAAAATGTCATTCATTAAATCAAGATTACTTTT 1089
DB 654 TGCCCATTCGCAAGACCTCAAAATGTCATTCATTAAATCAAGATTACTTTT 595
QY 1090 TTAACCTGGAGAAATTCATGTACATGACGCTAGGGAATTAATTCATATTTT 1149
DB 594 TTAACCTGGAGAAATTCATGTACATGACGCTAGGGAATTAATTCATATTTT 535
QY 1150 TCCAGTGAAGATGACTAAGCTTATCCCTCCCTTTGTTGATTTTTCAGTA 1209
DB 534 TCCAGTGAAGATGACTAAGCTTATCCCTCCCTTTGTTGATTTTTCAGTA 475
QY 1210 TAAAGTTAAATGCTTACCTGTACTAGGCTGTATACAG 1251
DB 474 TAAAGTTAAATGCTTACCTGTACTAGGCTGTATACAG 433

RESULT 4
BF858371/c

LOCUS BF858371 226 bp mRNA linear EST 16-JAN-2001
DEFINITION RC5-FT0193-211100-012-E11 FT0193 Homo sapiens cDNA, mRNA sequence.
ACCESSION BF858371
VERSION BF858371.1 GI:12246115
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 226)
AUTHORS Mammalia; Eutheria; Primates; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Eutheria; Primates; Catarrhini; Homiidae; Homo.
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bala, G.S., Simpson, D.H., Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare

TITLE 'M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.
JOURNAL Shotgun sequencing of the human transcriptome with ORF expressed
MEDLINE sequence tags
PUBMED Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
10737800
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(<http://www.ludwig.org.br/scripts/gethtml2.pl?cl=RC5&cl2=RC5-FT0193-211100-012-E11&cl3=2000-11-21&cl4=1>)
Seq primer: puc 18 forward
High quality sequence stop: 226.

FEATURES
source
Location/Qualifiers

1..226
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_1lb="FT0193"
/note="Organ: prostate-tumor; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESSES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the puc 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

BASE COUNT 79 a 29 c 59 g 59 t
ORIGIN

Query Match 11.4%; Score 214; DB 10; Length 226;
Best Local Similarity 100.0%; Pred. No. 1.1e-80;

Matches 214; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 622 CCTAAGTGTGGTTCATACCAATTCATATTTCTATACCCCAAAAGAGCT 681
DB 226 CCTAAGTGTGGTTCATACCAATTCATATTTCTATACCCCAAAAGAGCT 167
QY 682 TGTAAATATGATCTCTACGCTTCTCTGGGCCCAACATTCATATATCCAGCACA 741
DB 166 TGTAAATATGATCTCTACGCTTCTCTGGGCCCAACATTCATATATCCAGCACA 107
QY 742 CTCATTTTAAATTTAGTTCGCCAGATCTGACCTTTTCTACACTGTAGAAATAC 801
DB 106 CTCATTTTAAATTTAGTTCGCCAGATCTGACCTTTTCTACACTGTAGAAATAC 47
QY 802 ATTACCAATTTGTCAAGACCTTCGTTGTC 835
DB 46 ATTACCAATTTGTCAAGACCTTCGTTGTC 13

RESULT 5.
AQ206972/c

LOCUS AQ206972 394 bp DNA linear GSS 17-SEP-1998
DEFINITION HS_3238_B1.G11_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3238 Col=21 Row=N, genomic survey
ACCESSION AQ206972
VERSION AQ206972.1 GI:3617542
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 394)
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

AUTHORS	TITLE	JOURNAL	MEDLINE	PUBMED	COMMENT	FEATURES	BASE COUNT	ORIGIN
Mahairas,C.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T., Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and Hood L.	Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome	Proc. Natl. Acad. Sci. U.S.A.	96 (17), 9739-9744 (1999)	10449764	Contact: Mahairas GG, Wallace JC, Hood L High Throughput Sequencing Center University of Washington 401 Queen Anne Avenue North, Seattle, WA 98109, USA Tel: (206) 616-3618 Fax: (206) 616-3887 Email: jwallace@u.washington.edu Sequence Tagged Connector Plate: 3238 row: N column: 21 Class: BAC ends High quality sequence stop: 394.	134 a 62 c 93 g 103 t 2 others		
	Location/Qualifiers							
	1..394							
	/organism="Homo sapiens"							
	/mol.type="genomic DNA"							
	/db.xref="taxon:9606"							
	/clone="Plate=3238 Col=21 Row=N"							
	/sex="male"							
	/clone.lib="CIR Approved Human Genomic Sperm Library D"							
	/note="Organ: sperm; Vector: pBel0BAC11; BAC Clones in E-Coli DH10B"							
Query Match	11.4%	Score 214;	DB 28;	Length 394;				
Best Local Similarity	99.4%;	Pred. No. 1e-80;						
Matches 314;	Conservative 0;	Mismatches 2;	Indels 0;	Gaps 0;				
OY	718	ACATTTCGCATATATCCAGCCACACTATTTTATATATTAGTCCCATCTGACTGT	777					
DB	361	ACATTTCGCATATATCCAGCCACACTATTTTATATTAGTCCCATCTGACTGT	322					
OY	778	GACCTTCTACACTGTAGAAATACATTTACTATTTGTTCAAAGACCCTTGCTGTGCTG	837					
DB	321	GACCTTCTACACTGTAGAAATACATTTACTATTTGTTCAAAGACCCTTGCTGTGCTG	262					
OY	838	CCTAATATATGATGCTGACGTGTTTTCCTATAGAGATGTTGGCCAGGGGATCTGTGAACA	897					
DB	261	CCTAATATATGATGCTGACGTGTTTTCCTATAGAGATGTTGGCCAGGGGATCTGTGAACA	202					
OY	898	GCGTGGAGAGATCTCAAGATCTTCCAGGGGTATTTACTTACTAGACACAGCATGATCAT	957					
DB	201	GCGTGGAGAGATCTCAAGATCTTCCAGGGGTATTTACTTACTAGACACAGCATGATCAT	142					
OY	958	TACGAGATGAATATCTAATCAATCAATCATCTCAAGTGTCTTTGCCCATATCTGAATTCAT	1017					
DB	141	TACGAGATGAATATCTAATCAATCAATCATCTCAAGTGTCTTTGCCCATATCTGAATTCAT	82					
OY	1018	TTCCCACTTTTGCC 1033						
DB	81	TTCCCACTTTTGCTGC 66						
RESULT 6	BF858286	332 bp	mRNA	linear	EST 16-JAN-2001			
LOCUS	BF858286							
DEFINITION	RC3-FT0193-201100-012-D06-FT0193		Homo sapiens CDNA,	mRNA sequence.				
ACCESSION	BF858286							
VERSION	BF858286.1	GI:12246030						
KEYWORDS	EST.							
SOURCE	Homo sapiens (human)							
ORGANISM	Homo sapiens							
REFERENCE	1 (bases 1 to 332)							

AUTHORS		TITLE		JOURNAL MEDLINE PUBLISHED		COMMENT	
<p>Dias Neto, E., Garcia Correa, R., Veijola, S., Almeida, S., Bionesi, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bata, G.S., Simpson, D.H., Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brenlan, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.</p>		<p>Shotgun sequencing of the human transcriptome with ORF expressed sequence tags</p>		<p>Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)</p>		<p>Contact: Simpson A.J.G. Laboratory of Cancer Genetics Ludwig Institute for Cancer Research Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil Tel: +55-11-2704922 Fax: +55-11-2707001 Email: asimpson@ludwig.org.br This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?lcr=RC56t2-RC5-FR0193-201100-012-DB66t3=2000-11-2066t4=1) Seq primer: puc 18 forward High quality sequence stop: 332.</p>	
FEATURES		source		location/Qualifiers			
		1..332		/organism="Homo sapiens"			
				/mol_type="mRNA"			
				/db_xref="taxon:9606"			
				/dev_stage="Adult"			
				/clone_lib="FR0193"			
				/note="Organ: prostate; tumor; Vector: puc18; site_1: SmaI; site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - ludwig institute for Cancer Research) profiles into the puc 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."			
BASE COUNT		90 a		84 c		64 g	
ORIGIN						94 t	
Query Match		11.4%		Score 213;		DB 10; Length 332;	
Best Local Similarity		100.0%		Pred. No. 2.7e-80;			
Matches 213; Conservative		0;		Mismatches 0;		Indels 0; Gaps 0;	
Oy	576 GGAGGAGTAAACACGAGGAGGTCAGAGGATCTGGCCCTGACTAACTGTCGT	635					
Db	61 GGAGGAGTAAACACGAGGAGGTCAGAGGATCTGGCCCTGACTAACTGTCGT	120					
Oy	636 .TCATTAACCAATTCATTTTCATATTTTCTAACCCCTCAAAACAAGCTGTTGTAATATCTGATC	695					
Db	121 TCATTAACCAATTCATTTTCATATTTTCTAACCCCTCAAAACAAGCTGTTGTAATATCTGATC	180					
Oy	696 TCTACGGTCTCTGGGGCCCAACATCTCATATTCACGACGACACTCAATTTTATAT	755					
Db	181 TCTACGGTCTCTGGGGCCCAACATTCATATTCACGACGACACTCAATTTTATAT	240					
Oy	756 TTAGTCCACGATCTGACTGTGACCTTTCAC	788					
Db	241 TTAGTCCACGATCTGACTGTGACCTTTCAC	273					
RESULT 7							
BF373581/c							
LOCUS		282 bp		mRNA		linear	
DEFINITION		MR0-FR0175-210800-101-d05 FR0175 Homo sapiens cDNA, mRNA sequence.					
ACCESSION		BF373581					
VERSION		BF373581.1 GI:11335606					
KEYWORDS		EST.					
SOURCE		Homo sapiens (human)					
ORGANISM		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					

REFERENCE 1 (bases 1 to 282)
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.P., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bala, G.S., Simpson, D.H., Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.
TITLE Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE 20202663
PUBMED 10737800
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?rl=MR0&t2=MR0-FT0175-210800-101-d05&t3=2000-08-21&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 35
High quality sequence stop: 282.
Location/Qualifiers
1..282
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="FT0175"
/note="Organ: prostate_tumor; Vector: puc18; Site:1: Sma1; Site:2: Sma1; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the puc 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
BASE COUNT 85 a 51 c 70 g 76 t
ORIGIN
Query Match 10.6%; Score 198; DB 10; Length 282;
Best Local Similarity 100.0%; Pred. No. 7.6e-74;
Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 588 CACGGGCGAGAGGTCAGGATTCGGCCCTGCTCAATCAAGCGCTTCAATCAACCAAT 647
Db 262 CACGGGCGAGAGGTCAGGATTCGGCCCTGCTCAATCAAGCGCTTCAATCAACCAAT 203
Oy 648 CATTTCATATTTCTAACCCCAAAACAAAGCTGTGTATATCTGATCTCAAGGTTCT 707
Db 202 CATTTCATATTTCTAACCCCAAAACAAAGCTGTGTATATCTGATCTCAAGGTTCT 143
Oy 708 TCTGGGCCCAATTTCTCATATATCCAGCACACTATTTTAAATATTAGTCCAGA 767
Db 142 TCTGGGCCCAATTTCTCATATATCCAGCACACTATTTTAAATATTAGTCCAGA 83
Oy 768 TCTGTAAGTGAACCTTTT 785
Db 82 TCTGTAAGTGAACCTTTT 65

RESULT 8
BE373406 167 bp mRNA linear EST 24-NOV-2000
LOCUS BE373406
DEFINITION IL2-FT0159-070800-120-H01 FT0159 Homo sapiens cDNA, mRNA sequence.
ACCESSION BE373406.1 GI:11335431
VERSION
KEYWORDS EST.

SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 167)
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.P., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bala, G.S., Simpson, D.H., Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.
TITLE Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE 20202663
PUBMED 10737800
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?rl=IL2&t2=IL2-FT0159-070800-120-H01&t3=2000-08-07&t4=1)
Seq primer: puc 18 forward
High quality sequence stop: 167.
Location/Qualifiers
1..167
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="FT0159"
/note="Organ: prostate_tumor; Vector: puc18; Site:1: Sma1; Site:2: Sma1; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the puc 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
BASE COUNT 47 a 38 c 49 g 33 t
ORIGIN
Query Match 8.9%; Score 167; DB 10; Length 167;
Best Local Similarity 100.0%; Pred. No. 1.6e-60;
Matches 167; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 254 CACAGGAACACAAAGAGACAGAGATCCCTGGAGAAATGCCGCGCCATCTTG 313
Db 1 CACAGGAACACAAAGAGACAGAGATCCCTGGAGAAATGCCGCGCCATCTTG 60
Oy 314 GGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 373
Db 61 GGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 120
Oy 374 TGAATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 420
Db 121 TGAATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 167

RESULT 9
A1557225 856 bp mRNA linear EST 09-AUG-1999
LOCUS A1557225
DEFINITION PT2.1.15_B05.r tumor2 Homo sapiens cDNA 3', mRNA sequence.
ACCESSION A1557225
VERSION A1557225.1 GI:4489588
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 856)
Huang,G.M., Ng,W.L., Farkas,J., He,L., Liang,H.A., Gordon,D., Yu,J. and Hood,L.
Prostate cancer expression profiling by cDNA sequencing analysis
Genomics 59 (2), 178-186 (1999)
99338982
JOURNAL MEDLINE
PUBMED 10409429
COMMENT Contact: Guyang Matthew Huang
Leroy Hood
University of Washington
Department of Molecular Biotechnology, Box 357730, University of Washington, Seattle, WA 98195
Tel: 5106280100
Fax: 5106280108
Email: huangm@yahoo.com.
Location/Qualifiers
1. 856
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone_1lb="tumor2"
/note="Organ: Prostate; Vector: pBluescript; Directional cDNA library was constructed using lambda ZP II kit (Stratagene). mRNA was extracted from a frozen prostate tumor tissue (Mayo Clinics)."
BASE COUNT 237 a 191 c 180 g 214 t 34 others
ORIGIN

Query Match 7.9%; Score 147; DB 9; Length 856;
Best Local Similarity 100.0%; Pred. No. 4.9e-52;
Matches 147; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1399 TCTAGATGATGTAAGTTTGAATAGTGCATCTTACTTCATGCAAGAGGACA 1458
|||||
Db 251 TCTAGATGATGTAAGTTTGAATAGTGCATCTTACTTCATGCAAGAGGACA 310

QY 1459 CATATGAGATTCATCATCATGAGACAGCAAACTAAAGTGAATTGATTATAGA 1518
|||||
Db 311 CATATGAGATTCATCATCATGAGACAGCAAACTAAAGTGAATTGATTATAGA 370

QY 1519 GTTTAGATAATATATGAAATGCAAGA 1545
|||||
Db 371 GTTTAGATAATATATGAAATGCAAGA 397

RESULT 10
BF858890 441 bp mRNA linear EST 16-JAN-2001
DEFINITION RC5-FT0194-071200-023-G11 FT0194 Homo sapiens cDNA, mRNA sequence.
ACCESSION BF858890
VERSION BF858890.1 GI:12246634
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 441)
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare ,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.
Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
JOURNAL MEDLINE
PUBMED 20202663
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research

Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?l=RC5&ct=RC5-FT0194-071200-023-G11&t3=2000-12-07&t4=1)
Seq primer: puc 18 forward
High quality sequence stop: 3
Location/Qualifiers
1. 441
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_1lb="FT0194"
/note="Organ: prostate-tumor; Vector: puc18; Site:1; SmaI; Site:2; SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196/716 - Ludwig Institute for Cancer Research) profiles into the puc 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
BASE COUNT 142 a 67 c 97 g 135 t
ORIGIN

Query Match 6.6%; Score 124; DB 10; Length 441;
Best Local Similarity 100.0%; Pred. No. 4e-42;
Matches 124; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1128 AATTTAATCATATTTTGTTCACAGTGAAGATGATGATGCTTTATCCCTCCCT 1187
|||||
Db 441 AATTTAATCATATTTTGTTCACAGTGAAGATGATGATGCTTTATCCCTCCCT 382

QY 1188 TTGTTGATTTTTCACATTAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAA 1247
|||||
Db 381 TTGTTGATTTTTCACATTAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAA 322

QY 1248 CAGC 1251
|||||
Db 321 CAGC 318

RESULT 11
BQ292550 572 bp mRNA linear EST 15-MAY-2002
DEFINITION PM0-AN0087-240501-019-a06 AN0087 Homo sapiens cDNA, mRNA sequence.
ACCESSION BQ292550
VERSION BQ292550.1 GI:20801500
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 572)
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare ,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.
Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
JOURNAL MEDLINE
PUBMED 20202663
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,

Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=PM0<2=PM0-AN0087-240501-019-a06<3=2001-05-24<4=1)
Seq primer: puc 18 forward
High quality sequence stop: 572.

FEATURES

source

1..572
Location/Qualifiers

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/dev_stage="Adult"

/clone_lib="AN0087"

/note="Organ: amnion_normal; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the puc 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

BASE COUNT

150 a 90 c 169 g 163 t

ORIGIN

Query Match 5.3%; Score 100; DB 13; Length 572;

Best Local Similarity 100.0%; Pred. No. 7.6e-32;

Matches 100; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy

1 AGAAGCTGGCATCGAAGAAACAGAGGAGATTTGTGGTGCAGCCGAGGAGACAG 60

116 AGAAGCTGGCATCGAAGAAACAGAGGAGATTTGTGGTGCAGCCGAGGAGACAG 175

Db

61 GAAGATCTGCATGGTGGAGAGACCTGATGATACAGAGT 100

176 GAAGATCTGCATGGTGGAGAGACCTGATGATACAGAGT 215

RESULT 12

A1557495

LOCUS A1557495 657 bp mRNA linear EST 09-AUG-1999

DEFINITION PT2.1.7.H12.r tumor2 Homo sapiens CDNA 3', mRNA sequence.

ACCESSION A1557495

VERSION A1557495.1 GI:4489858

KEYWORDS

EST.

SOURCE

Homo sapiens

ORGANISM

Homo sapiens

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

COMMENT

CONTACT: Guyang Matthew Huang

Leroy Hood

Department of Washington

Biotechnology, Box 357730, University of

Washington, Seattle, WA 98195

Tel: 5106280100

Fax: 5106280108

Email: huanggm@yahoo.com.

Location/Qualifiers

1..657

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone_lib="tumor2"

/note="Organ: Prostate; Vector: pbluescript; Directional

CDNA library was constructed using Lambda ZP II kit (Stratagene). mRNA was extracted from a frozen prostate tumor tissue (Mayo Clinics)."

BASE COUNT

179 a 112 c 153 g 166 t 47 others

ORIGIN

Query Match 4.6%; Score 86; DB 9; Length 657;
Best Local Similarity 100.0%; Pred. No. 7.6e-26;
Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy

13 CAGAAAACAGAGGAGGAGATTTGTGGTGCAGCCGAGGAGACAGAGATCTGCAT 72

14 CAGAAAACAGAGGAGGAGATTTGTGGTGCAGCCGAGGAGACAGAGATCTGCAT 73

73 GGTGGAGAGACCTGATCATACAGAG 98

74 GGTGGAGAGACCTGATCATACAGAG 99

RESULT 13

A0246715

LOCUS A0246715 451 bp DNA linear GSS 06-OCT-1998

DEFINITION HS_2059_B2_E08_T7 CIT Approved Human Genomic Sperm Library D Homo

sapiens genomic clone plate=2059 Col=16 Row=J, genomic survey

ACCESSION

A0246715

VERSION

A0246715.1

KEYWORDS

GSS.

SOURCE

Homo sapiens

ORGANISM

Homo sapiens

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

COMMENT

CONTACT: Mahalras GG, Wallace JC, Hood L

High Throughput Sequencing Center

University of Washington

401 Queen Anne Avenue North, Seattle, WA 98109, USA

Tel: (206) 616-3618

Fax: (206) 616-3887

Email: jwallace@u.washington.edu

Sequence Tagged Connector

Plate: 2059 row: J column: 16

Class: BAC ends

High quality sequence stop: 451.

Location/Qualifiers

1..451

/organism="Homo sapiens"

/mol_type="genomic DNA"

/db_xref="taxon:9606"

/clone_plate=2059 Col=16 Row=J"

/sex="male"

/note="Organ: sperm; Vector: pellobAC11; BAC Clones in

E-Coli DH10B"

BASE COUNT

133 a 101 c 86 g 130 t 1 others

ORIGIN

Query Match 2.3%; Score 43; DB 28; Length 451;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;

Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy

1745 TTGGCAATCACTACTGTCACCTATCTCAACTTGGAGATGCT 1787

26 TTGGCAATCACTACTGTCACCTATCTCAACTTGGAGATGCT 68

RESULT	14
LOCUS	R01974 305 bp mRNA linear EST 31-MAR-1995 ye5f0l.r1 Soares fetal liver spleen INFLS Homo sapiens CDNA clone IMAGE:124537 5', mRNA sequence.
ACCESSION	R01974
VERSION	R01974.1 GI:751710
KEYWORDS	EST.
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 305) Hillier,L., Clark,N., Dubnque,T., Elliston,K., Hawkins,M., Holman ,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J... Ritkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston ,R., Williamson,A., Woldmann,P. and Wilson,R. The WashU-Merck EST Project Unpublished
TITLE	Contact: Wilson RK Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel.: 314 286 1800 Fax: 314 286 1810 Email: est@watson.wustl.edu Insert Size: 864
JOURNAL	High quality sequence stops: 200 Source: IMAGE Consortium, LNL This clone is available royalty-free through LNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Seq Length: 864 Std Error: 0.00 Insert primer: M13Rp1
FEATURES	High quality sequence stop: 200. location/Qualifiers 1..305 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="GDB:477082" /db_xref="taxon:9606" /clone="IMAGE:124537" /sex="male" /dev_stage="20 week-post conception fetus" /lab_host="DH10B (ampicillin resistant)" /clone_lib="Soares fetal liver spleen INFLS" /note="Organ: Liver and Spleen; Vector: pT73D (Pharmacia) with a modified polylinker; Site_1: Pac I; Site_2: Eco RI; 1st strand cDNA was primed with a Pac I - oligo(dT) primer [5' AACTGGAGATTTAATTAAAGAATCTTTTCTTTTTC 3'] , double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Pac I and cloned into the Pac I and Eco RI sites of the modified pT73 vector. Library went through one round of normalization. Library constructed by Bento Soares and M.Fatima Bonaldo."
BASE COUNT	76 a 68 c 69 g 86 t 6 others
ORIGIN	
Query Match	1.4%; Score 26; DB 14; Length 305;
Best Local Similarity	100.0%; Pred. No. 4.7;
Matches	26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY	977 TCAACATCATCCTCAGTGCTTTGCC 1002 Db 20 TCACATCATCCATCGTGTCTTGC 45
RESULT	15
LOCUS	T79384 371 bp mRNA linear EST 15-MAR-1995 y6t4g09.r1 Soares fetal liver spleen INFLS Homo sapiens CDNA clone IMAGE:114016 5', mRNA sequence.
ACCESSION	T79384
VERSION	T79384.1 GI:697893
KEYWORDS	EST.

SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens
REFERENCE	Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Emteleostomi; Mammalia; Metazoa; Primates; Catarrhini; Hominoidea; Homo.
AUTHORS	1 (bases 1 to 371) Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman ,M., Hultman,M., Kuababa,T., Le,M., Lennon,G., Marra,M., Parsons,J. Rifkin,L., Rolfling,T., Soares,M., Tan,F., Trevaskis,E., Waterston ,R., Williamson,A., Wohldmann,P. and Wilson,R.
TITLE	The WashU-Merck EST Project
JOURNAL	Unpublished
COMMENT	Other_ESTs: yd474g09.s1 Contact: Wilson RK Washington University School of Medicine 444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email: est@wustl.wustl.edu Insert Size: 1236 High quality sequence stops: 275 Source: IMAGE Consortium, LNL This clone is available royalty-free through LNL ; contact the IMAGE Consortium (info@image.lnl.gov) for further information. Insert Length: 1236 Std Error: 0.00 Seq primer: M13RP1 High quality sequence stop: 275. Location/Qualifiers 1..371 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="GDB:469633" /db_xref="taxon:9606" /clone="IMAGE:114016" /sex="male" /dev_stage="20 week-post conception fetus" /lab_host="DH10B (ampicillin resistant)" /note="Organ: Liver and Spleen. Vector: pTZ19D (Pharmacia) with a modified polylinker. Site_1: Pac I; Site_2: Eco RI 1st strand cDNA was primed with a Pac I - oligo(dT) primer 15' AACGTGAAGAATTAATAACACTCTTTTTTTTTTTTTTTTTT 3', double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Pac I and cloned into the Pac I and Eco RI sites of the modified pTZ19 vector. Library went through one round of normalization. Library constructed by Bento Soares and M.Fatima Bonaldo."
BASE COUNT	105 a 81 c 70 g 113 t 2 others
ORIGIN	
Query Match	1.4%; Score 26; DB 14; Length 371;
Best Local Similarity	100.0%; Pred. No. 4.5;
Matches	26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DQ	977 TCAACATCATCCTCAGTCGCTTTGGC 1002
Db	127 TCACATCATCCTCAGTCGCTTTGCC 152

Search completed: September 27, 2003, 11:35:44
Job time : 3929.47 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 26, 2003, 21:01:08 ; Search time 2984.11 Seconds
(without alignments)
11241.524 Million cell updates/sec

Title: US-09-402-713A-4

Perfect score: 820

Sequence: 1 agaagctgcacgcagaaaaa.....cattactcatttgcacaa 820

Scoring table: OLIGO_NUC

Gapop 60.0 , Gapext 60.0

Searched: 2888711 seqs, 20454813386 residues

Word size : 0

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_cm:*
5: gb_ov:*
6: gb_ph:*
7: gb_pl:*
8: gb_pr:*
9: gb_ro:*
10: gb_sy:*
11: gb_un:*
12: gb_vl:*
13: gb_vl:*
14: gb_vl:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_cm:*
21: em_or:*
22: em_ov:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sts:*
28: em_un:*
29: em_vl:*
30: em_htg_hum:*
31: em_htg_inv:*
32: em_htg_other:*
33: em_htg_mus:*
34: em_htg_din:*
35: em_htg_fod:*
36: em_htg_mam:*
37: em_htg_vrl:*
38: em_sy:*
39: em_htgo_hum:*
40: em_htgo_mus:*
41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	820	100.0	820	6	BD082484 PCA3, PCA
2	820	100.0	1872	6	BD082483 PCA3, PCA
3	812	99.0	812	6	AR261039 Sequence
4	812	99.0	812	6	AR278570 Sequence
5	812	99.0	812	6	AX106207 Sequence
6	812	99.0	812	6	AX106590 Sequence
7	812	99.0	812	6	AX140981 Sequence
8	812	99.0	812	6	AX200841 Sequence
9	812	99.0	812	6	AX267497 Sequence
10	812	99.0	812	6	AR261037 Sequence
11	812	99.0	812	6	AR278568 Sequence
12	812	99.0	812	6	AX106205 Sequence
13	812	99.0	812	6	AX106688 Sequence
14	812	99.0	812	6	AX140979 Sequence
15	812	99.0	812	6	AX200839 Sequence
16	812	99.0	812	6	AX267495 Sequence
17	812	99.0	812	6	AR261038 Sequence
18	812	99.0	812	6	AR278569 Sequence
19	812	99.0	812	6	AX106206 Sequence
20	812	99.0	812	6	AX106689 Sequence
21	812	99.0	812	6	AX140980 Sequence
22	812	99.0	812	6	AX200840 Sequence
23	812	99.0	812	6	AX267496 Sequence
24	812	99.0	812	6	AR261036 Sequence
25	812	99.0	812	6	AR278567 Sequence
26	812	99.0	812	6	AX106204 Sequence
27	812	99.0	812	6	AX106687 Sequence
28	812	99.0	812	6	AX140978 Sequence
29	812	99.0	812	6	AX200838 Sequence
30	812	99.0	812	6	AX267494 Sequence
31	812	99.0	812	6	BD082482 PCA3, PCA
32	812	99.0	812	6	BD082485 PCA3, PCA
33	812	99.0	812	6	AR261166 Sequence
34	812	99.0	812	6	AR278697 Sequence
35	812	99.0	812	6	AX200988 Sequence
36	812	99.0	812	6	AX267716 Sequence
37	812	99.0	812	6	AF103907 Sequence
38	812	99.0	812	6	AF103908 Sequence
39	812	99.0	812	6	AL359314 Human DNA
40	812	99.0	812	6	BD078456 101 human
41	812	99.0	812	6	AX018075 Sequence
42	812	99.0	812	6	BD134961 Human nuc
43	812	99.0	812	6	BD030513 Sequence
44	812	99.0	812	6	AR237401 Sequence
45	812	99.0	812	6	AR260894 Sequence

ALIGNMENTS

RESULT 1
LOCUS BD082484 820 bp DNA
DEFINITION PCA3, PCA3 genes, and methods of use.
ACCESSION BD082484
VERSION BD082484.1 GI:22628094
KEYWORDS JP 2001522240-A/3.
SOURCE
ORGANISM
Mastadenovirus
Mastadenovirus
1 (bases 1 to 820)
REFERENCE
AUTHORS Bussemakers,M.J.G.
TITLE PCA3, PCA3 genes, and methods of use
JOURNAL Patent: JP 2001522240-A 3 13-NOV-2001;
DIAGNOCURE INC

```

COMMENT
PN JP 2001522240-A/3
PD 13-NOV-2001
PR 09-APR-1998 JP 1998542194
PI 10-APR-1997 US 60/041836
PC MARION J G BUSSEMAKERS
PC C12N15/00, C12N15/12, C12N5/12, C12N1/21, C07K14/47, C07K16/18, PC
C1201/68,
PC G01N33/577, A61K39/395, A01K67/027
CC Strandedness: Double;
CC Topology: Linear;
FEATURES
source Location/Qualifiers
1..820
/mol_type="genomic DNA"
/db_xref="taxon:10509"
BASE COUNT 262 a 169 c 191 g 198 t
ORIGIN
Query Match 100.0%; Score 820; DB 6; Length 820;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 820; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGAAGCTGGCATCGAAAAACACAGGGAGATTGTTGCTGCTGACGCCGAGGAGACCAG 60
DB 1 AGAAGCTGGCATCGAAAAACAGAGGGAGATTGTTGCTGCTGACGCCGAGGAGACCAG 60
QY 61 GAAGATCTGGTGGGAAAGGACCTGATGATACAGAGGTGAGAAATTAAGAAGGCTGCT 120
DB 61 GAAGATCTGGTGGGAAAGGACCTGATGATACAGAGGTGAGAAATTAAGAAGGCTGCT 120
QY 121 GACTTTACCATCTGAGGCCACACATCTGCTGAATGAGATTAATTAATCATCATAAGAAC 180
DB 121 GACTTTACCATCTGAGGCCACACATCTGCTGAATGAGATTAATTAATCATCATAAGAAC 180
QY 181 AGCAAGTGAACAATATATATGCTTAAAGTAGACATCTTTTGGCATTTCACAGCCCTTT 240
DB 181 AGCAAGTGAACAATATATATGCTTAAAGTAGACATCTTTTGGCATTTCACAGCCCTTT 240
QY 181 AGCAAGTGAACAATATATATGCTTAAAGTAGACATCTTTTGGCATTTCACAGCCCTTT 240
DB 181 AGCAAGTGAACAATATATATGCTTAAAGTAGACATCTTTTGGCATTTCACAGCCCTTT 240
QY 241 AAATATCCACACACACAGGAAGCACAAGGAAGGACAGAGATCCCTGGGAGAAATGCC 300
DB 241 AAATATCCACACACACAGGAAGCACAAGGAAGGACAGAGATCCCTGGGAGAAATGCC 300
QY 301 GCGCCCATCTGGGTCATGATGAGCCCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360
DB 301 GCGCCCATCTGGGTCATGATGAGCCCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360
QY 361 GGACATTAGAAAATGAATGATGCTCTTAAAGTAGAGTGGGCAAGAAACAGATCTGTT 420
DB 361 GGACATTAGAAAATGAATGATGCTCTTAAAGTAGAGTGGGCAAGAAACAGATCTGTT 420
QY 421 GTGATATTTTATTTGAAGGGGATTTACAGATTTGAATGAAGTCAAAAGTGAGCATTAAC 480
DB 421 GTGATATTTTATTTGAAGGGGATTTACAGATTTGAATGAAGTCAAAAGTGAGCATTAAC 480
QY 481 AATGAGAGGAAACAGACGAGAAATCTTGATGGCTTACAGACATGCAACAAACAAA 540
DB 481 AATGAGAGGAAACAGACGAGAAATCTTGATGGCTTACAGACATGCAACAAACAAA 540
QY 481 AATGAGAGGAAACAGACGAGAAATCTTGATGGCTTACAGACATGCAACAAACAAA 540
DB 481 AATGAGAGGAAACAGACGAGAAATCTTGATGGCTTACAGACATGCAACAAACAAA 540
QY 541 TGGATATCTGATGATGATGAGGAGCAGCTGGGAGAGATTAACACAGGGGCAAGG 600
DB 541 TGGATATCTGATGATGATGAGGAGCAGCTGGGAGAGATTAACACAGGGGCAAGG 600
QY 601 GTGAGATTTGCGCCCTGCTGCTTAACTGCTGCTTAACTGCTGCTGCTGCTGCTGCTGCT 660
DB 601 GTGAGATTTGCGCCCTGCTGCTTAACTGCTGCTTAACTGCTGCTGCTGCTGCTGCTGCT 660
QY 661 TAAACCTCAAAACAAAGCTGTTGATATATCTGATCTAGAGTCTTCTTGAGGCCAACA 720
DB 661 TAAACCTCAAAACAAAGCTGTTGATATATCTGATCTAGAGTCTTCTTGAGGCCAACA 720
QY 721 TTCTCCATATATCCAGCACATCTTTTAAATATTTAGTCCAGATCTGTACTGTGAC 780
DB 721 TTCTCCATATATCCAGCACATCTTTTAAATATTTAGTCCAGATCTGTACTGTGAC 780

RESULT 2
LOCUS BD082483 1872 bp DNA linear PAT 27-AUG-2002
DEFINITION PCA3, PCA3 genes, and methods of use.
ACCESSION BD082483
VERSION BD082483.1 GI:22628093
KEYWORDS JP 2001522240-A/2.
SOURCE Mastadenovirus
ORGANISM Mastadenovirus
REFERENCE 1 (bases 1 to 1872)
AUTHORS Bussemakers, M.J.G.
TITLE PCA3, PCA3 genes, and methods of use
JOURNAL Patient: JP 2001522240-A 2 13-NOV-2001;
DIAGNOCURE INC
COMMENT
PN JP 2001522240-A/2
PD 13-NOV-2001
PR 09-APR-1998 JP 1998542194
PI 10-APR-1997 US 60/041836
PC MARION J G BUSSEMAKERS
PC C12N15/00, C12N15/12, C12N5/12, C12N1/21, C07K14/47, C07K16/18, PC
C1201/68,
PC G01N33/577, A61K39/395, A01K67/027
CC Strandedness: Double;
CC Topology: Linear;
FEATURES
source Location/Qualifiers
1..1872
/mol_type="genomic DNA"
/db_xref="taxon:10509"
BASE COUNT 567 a 389 c 369 g 539 t 8 others
ORIGIN
Query Match 100.0%; Score 820; DB 6; Length 1872;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 820; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGAAGCTGGCATCGAAAAACACAGGGAGATTGTTGCTGCTGACGCCGAGGAGACCAG 60
DB 1 AGAAGCTGGCATCGAAAAACACAGGGAGATTGTTGCTGCTGACGCCGAGGAGACCAG 60
QY 61 GAAGATCTGGTGGGAAAGGACCTGATGATACAGAGGTGAGAAATTAAGAAGGCTGCT 120
DB 61 GAAGATCTGGTGGGAAAGGACCTGATGATACAGAGGTGAGAAATTAAGAAGGCTGCT 120
QY 121 GACTTTACCATCTGAGGCCACACATCTGCTGAATGAGATTAATTAATCATCATAAGAAC 180
DB 121 GACTTTACCATCTGAGGCCACACATCTGCTGAATGAGATTAATTAATCATCATAAGAAC 180
QY 121 GACTTTACCATCTGAGGCCACACATCTGCTGAATGAGATTAATTAATCATCATAAGAAC 180
DB 121 GACTTTACCATCTGAGGCCACACATCTGCTGAATGAGATTAATTAATCATCATAAGAAC 180
QY 181 AGCAAGTGAACAATATATATGCTTAAAGTAGACATCTTTTGGCATTTCACAGCCCTTT 240
DB 181 AGCAAGTGAACAATATATATGCTTAAAGTAGACATCTTTTGGCATTTCACAGCCCTTT 240
QY 241 AAATATCCACACACACAGGAAGCACAAGGAAGGACAGAGATCCCTGGGAGAAATGCC 300
DB 241 AAATATCCACACACACAGGAAGCACAAGGAAGGACAGAGATCCCTGGGAGAAATGCC 300
QY 301 GCGCCCATCTGGGTCATGATGAGCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360
DB 301 GCGCCCATCTGGGTCATGATGAGCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360
QY 361 GGACATTAGAAAATGAATGATGCTCTTAAAGTAGAGTGGGCAAGAAACAGATCTGTT 420
DB 361 GGACATTAGAAAATGAATGATGCTCTTAAAGTAGAGTGGGCAAGAAACAGATCTGTT 420

```

QY 421 GTGATATTTATTTGACGGGATTACAGATTTGAAATGACAGTACACAAAGTACAGATTTAC 480
DB 421 GTGATATTTATTTGAAACGGGATTACAGATTTGAAATGACAGTACACAAAGTACAGATTTAC 480
QY 481 AATGAGAGAAACAGACAGAGAAATCTTGATGGCTTACACAGATATCCACAAACAAA 540
DB 481 AATGAGAGAAACAGACAGAGAAATCTTGATGGCTTACACAGATATCCACAAACAAA 540
QY 541 TGGATATCTGATGATGACATGAGGCGACCAAGCTGGGGAGAGATACACAGGGGAGAG 600
DB 541 TGGATATCTGATGATGACATGAGGCGACCAAGCTGGGGAGAGATACACAGGGGAGAG 600
QY 601 GTACAGATTTGCGCCCTGCTGCTTAACCTGCTGCTTACCAATCATTTTCATTTTC 660
DB 601 GTACAGATTTGCGCCCTGCTGCTTAACCTGCTGCTTACCAATCATTTTCATTTTC 660
QY 661 TAACCTCAAAACAAAGCTGTTGATATCTGATCTGACGGTCTCTGCGCCCAACA 720
DB 661 TAACCTCAAAACAAAGCTGTTGATATCTGATCTGACGGTCTCTGCGCCCAACA 720
QY 721 TTCTCATATATCCAGCCACACTCTTTTATATTTAGTCCAGATCTGATCTGAC 780
DB 721 TTCTCATATATCCAGCCACACTCTTTTATATTTAGTCCAGATCTGATCTGAC 780
QY 781 CTCTCTACACTGATGATATACATTTACTATTTTGTTCAA 820
DB 781 CTCTCTACACTGATGATATACATTTACTATTTTGTTCAA 820

RESULT 3
LOCUS AR261039 812 bp DNA linear PAT 29-JAN-2003
DEFINITION Sequence 471 from patent US 6321716.
ACCESSION AR261039
VERSION AR261039.1 GI:28071802
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 812)
AUTHORS Mashiki,Z. and Harada,J.
TITLE Negative pressure control apparatus for engine mounted in vehicle
JOURNAL Patent: US 6321716-A 471 27-NOV-2001;
FEATURES Location/Qualifiers
source 1. 812
BASE COUNT 198 a 189 c 169 g 256 t
ORIGIN

Query Match 99.0%; Score 812; DB 6; Length 812;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 812; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 CTGGCATCAGAAAAACAGAGGGAGATTGTGTGCTGCAGCCGAGGAGACCAAGAGA 65
DB 812 CTGGCATCAGAAAAACAGAGGGAGATTGTGTGCTGCAGCCGAGGAGACCAAGAGA 753
QY 66 TCTGATGTTGGGAAGGACCTGATGATACAGAGGTGAATAAAGAGCTGCTGACTT 125
DB 752 TCTGATGTTGGGAAGGACCTGATGATACAGAGGTGAATAAAGAGCTGCTGACTT 693
QY 126 TACCATCTGAGGCCACACATCTGCTGAATGAGATTAATTAATCATCAGTAAACAGCA 185
DB 632 TACCATCTGAGGCCACACATCTGCTGAATGAGATTAATTAATCATCAGTAAACAGCA 633
QY 186 GATGCAATATATATGTTCTAAGTAGTACATGTTTTTGCACATTTTCAGCCCTTAAATA 245
DB 632 GATGCAATATATATGTTCTAAGTAGTACATGTTTTTGCACATTTTCAGCCCTTAAATA 573
QY 246 TCCACACACACAGAGCAACAAAGAGACAGAGATCCCTGGGAGAAATCCCGGCGG 305
DB 572 TCCACACACACAGAGCAACAAAGAGACAGAGATCCCTGGGAGAAATCCCGGCGG 513

QY 306 CCATCTGGGTCATCATGATGAGCTCGCCCTGTGCTGTCCTGCGCTTGAGGAGAGACA 365
DB 512 CCATCTGGGTCATCATGATGAGCTCGCCCTGTGCTGTCCTGCGCTTGAGGAGAGACA 453
QY 366 TTGAGAAATGATTTATGTTGCTTAAAGATGGGCGAGAAACAGATCCCTGTTGTGA 425
DB 452 TTGAGAAATGATTTATGTTGCTTAAAGATGGGCGAGAAACAGATCCCTGTTGTGA 393
QY 426 TATTTATTTGAAAGGGATTTACAGATTTTGAATGAAGTACACAAAGTACATTAACATGA 485
DB 332 TATTTATTTGAAAGGGATTTACAGATTTTGAATGAAGTACACAAAGTACATTAACATGA 333
QY 486 GAGGAAACAGACAGAGAAATCTTGATGCTTACACAGATCAACAAACAAATGGA 545
DB 332 GAGGAAACAGACAGAGAAATCTTGATGCTTACACAGATCAACAAACAAATGGA 273
QY 546 TACTGTGATGATGATGAGCGACCAAGCTGGGAGAGATTAACACAGGGGAGAGGCTAG 605
DB 272 TACTGTGATGATGATGAGCGACCAAGCTGGGAGAGATTAACACAGGGGAGAGGCTAG 213
QY 606 GATTCGGCCCTGCTGCTTAACCTGCTGCTTACCAACCAATCATTTTCATTTTCAC 665
DB 212 GATTCGGCCCTGCTGCTTAACCTGCTGCTTACCAACCAATCATTTTCATTTTCAC 153
QY 666 CTCAAACAAACAGCTGTTGATATATCTGATCTGACGGTCTCTGCGCCCAACATTC 725
DB 152 CTCAAACAAACAGCTGTTGATATATCTGATCTGACGGTCTCTGCGCCCAACATTC 93
QY 726 CATATATTCAGCCACACTCATTTTAAATATTTAGTCCAGATCTGATCTGACCTTTC 785
DB 92 CATATATTCAGCCACACTCATTTTAAATATTTAGTCCAGATCTGATCTGACCTTTC 33
QY 786 TACACTGTAGATATACATTTACTATTTTGTTC 817
DB 32 TACACTGTAGATATACATTTACTATTTTGTTC 1

RESULT 4
LOCUS AR278570/c 812 bp DNA linear PAT 10-APR-2003
DEFINITION Sequence 471 from patent US 6512094.
ACCESSION AR278570
VERSION AR278570.1 GI:29712816
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 812)
AUTHORS Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,X.,
Kalos,M.D., Fanger,G.R., Retter,M.W., Stolk,J.A., Day,C.H.,
Vedrick,T.S., Carter,D., Li,S.X., Wang,A., Skelky,Y.A.W.,
Hepler,W.T. and Henderson,R.A.
TITLE Compositions and methods for the therapy and diagnosis of prostate
cancer
JOURNAL Patent: US 6512094-A 471 28-JAN-2003;
FEATURES Location/Qualifiers
source 1. 812
BASE COUNT 198 a 189 c 169 g 256 t
ORIGIN

Query Match 99.0%; Score 812; DB 6; Length 812;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 812; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 CTGGCATCAGAAAAACAGAGGGAGATTGTGTGCTGCAGCCGAGGAGACCAAGAGA 65
DB 812 CTGGCATCAGAAAAACAGAGGGAGATTGTGTGCTGCAGCCGAGGAGACCAAGAGA 753
QY 66 TCTGATGTTGGGAAGGACCTGATGATACAGAGGTGAATAAAGAGCTGCTGACTT 125
DB 752 TCTGATGTTGGGAAGGACCTGATGATACAGAGGTGAATAAAGAGCTGCTGACTT 693

QY 126 TACATCTGAGCCACACATCTGCTGAATGAGAGATTAATTAACATCACTAGAAACACGAA 185
|||||
Db 692 TACCATCTGAGGCCACACATCTGCTGAATGAGAGATTAATTAACATCACTAGAAACACGAA 633
QY 186 GATGACATTAATTAATGCTAGTAGTGACATGTTTTCACATTTCCAGCCCTTTAATA 245
|||||
Db 632 GATGACATTAATTAATGCTAGTAGTGACATGTTTTCACATTTCCAGCCCTTTAATA 573
QY 246 TCCACACACACAGAGAACACAAAAGAGACAGAGATCCCTGGGAAATGCCCCGCG 305
|||||
Db 572 TCCACACACACAGAGAACACAAAAGAGACAGAGATCCCTGGGAAATGCCCCGCG 513
QY 306 CCATCTTGGGTATCATGAGCCTCCGCTGTGCTGCTGCTGCTGCTGAGGAGAGACA 365
|||||
Db 512 CCATCTTGGGTATCATGAGCCTCCGCTGTGCTGCTGCTGCTGAGGAGAGACA 453
QY 366 TTGAAATGAATTAATGATGCTGCTTAAGAGATGGGAGAAACAGATCCTGTTGGA 425
|||||
Db 452 TTGAAATGAATTAATGATGCTGCTTAAGAGATGGGAGAAACAGATCCTGTTGGA 393
QY 426 TATTTATTTGAAGGGATTAACAGATTTGAATGAAGTCAACAAAGTGACATTTACCAATGA 485
|||||
Db 392 TATTTATTTGAAGGGATTAACAGATTTGAATGAAGTCAACAAAGTGACATTTACCAATGA 333
QY 486 GAGGAAACACAGAGAGAAATCTTGATGCGTTCACAAAGACATGCAACAAATGGA 545
|||||
Db 332 GAGGAAACACAGAGAGAAATCTTGATGCGTTCACAAAGACATGCAACAAATGGA 273
QY 546 TACTGTGATGACATGAGGACGACCAAGCTGGGAGAGATTAACCAAGGGGAGAGGTCAG 605
|||||
Db 272 TACTGTGATGACATGAGGACGACCAAGCTGGGAGAGATTAACCAAGGGGAGAGGTCAG 213
QY 606 GATTCTGGCCCTGCTGCTAAACTGTGCTCATTAACCAATCTTTCATATTTCTAAC 665
|||||
Db 212 GATTCTGGCCCTGCTGCTAAACTGTGCTCATTAACCAATCTTTCATATTTCTAAC 153
QY 666 CTGAAAACAAAGCTGTTGTAATCTGATCTTACGGTCTCTTGCGGCCAACATCTC 725
|||||
Db 152 CTGAAAACAAAGCTGTTGTAATCTGATCTTACGGTCTCTTGCGGCCAACATCTC 93
QY 726 CATATATCCAGCCACACTCAATTTTATATTTAGTCCAGATCTGACTGTGACCTTTC 785
|||||
Db 92 CATATATCCAGCCACACTCAATTTTATATTTAGTCCAGATCTGACTGTGACCTTTC 33
QY 786 TACACTGTAGAAATTAACATTAATCTCAATTTTGTTC 817
|||||
Db 32 TACACTGTAGAAATTAACATTAATCTCAATTTTGTTC 1

RESULT 5
AX106207/c 812 bp DNA linear PAT 30-Apr-2001
LOCUS Sequence 345 from Patent WO0125273.
DEFINITION AX106207
ACCESSION AX106207
VERSION AX106207.1 GI:13921896
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
AUTHORS Skelly, Y.A., Xu, J., Cheever, M.A. and Reed, S.G.
TITLES Compositions and methods for wtl specific immunotherapy
JOURNAL Patent: WO 0125273-A 345 12-Apr-2001;
CORIXA CORPORATION (US)
FEATURES
source location/Qualifiers
1. 812
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

BASE COUNT 198 a 189 c 169 g 256 t
ORIGIN

Query Match 99.0%; Score 812; DB 6; Length 812;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 812; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 CTGCAATCAGAAAACAGAGGGGATTTGTGTGCTGACGCCAGAGAACAGGAAAGA 65
|||||
Db 812 CTGCAATCAGAAAACAGAGGGGATTTGTGTGCTGACGCCAGAGAACAGGAAAGA 753
QY 66 TCTCATGTGGGAGAGACCTGATGATACAGAGGTGAGAAATAGAAAGGCTGCTGACTT 125
|||||
Db 752 TCTCATGTGGGAGAGACCTGATGATACAGAGGTGAGAAATAGAAAGGCTGCTGACTT 693
QY 126 TACATCTGAGCCACACATCTGCTGAATGAGATTAATTAACATCACTAGAAACAGCAA 185
|||||
Db 692 TACATCTGAGCCACACATCTGCTGAATGAGATTAATTAACATCACTAGAAACAGCAA 633
QY 186 GATGACATTAATTAATGCTAGTAGTGACATGTTTTCACATTTCCAGCCCTTTAATA 245
|||||
Db 632 GATGACATTAATTAATGCTAGTAGTGACATGTTTTCACATTTCCAGCCCTTTAATA 573
QY 246 TCCACACACACAGAGAACACAAAAGAGACAGAGATCCCTGGGAAATGCCCCGCG 305
|||||
Db 572 TCCACACACACAGAGAACACAAAAGAGACAGAGATCCCTGGGAAATGCCCCGCG 513
QY 306 CCATCTTGGGTATCATGAGCCTCCGCTGTGCTGCTGCTGCTGAGGAGAGACA 365
|||||
Db 512 CCATCTTGGGTATCATGAGCCTCCGCTGTGCTGCTGCTGCTGAGGAGAGACA 453
QY 366 TTGAAATGAATTAATGATGCTGCTTAAGAGATGGGAGAAACAGATCCTGTTGGA 425
|||||
Db 452 TTGAAATGAATTAATGATGCTGCTTAAGAGATGGGAGAAACAGATCCTGTTGGA 393
QY 426 TATTTATTTGAAGGGATTAACAGATTTGAATGAAGTCAACAAAGTGACATTTACCAATGA 485
|||||
Db 392 TATTTATTTGAAGGGATTAACAGATTTGAATGAAGTCAACAAAGTGACATTTACCAATGA 333
QY 486 GAGGAAACACAGAGAGAAATCTTGATGCGTTCACAAAGACATGCAACAAATGGA 545
|||||
Db 332 GAGGAAACACAGAGAGAAATCTTGATGCGTTCACAAAGACATGCAACAAATGGA 273
QY 546 TACTGTGATGACATGAGGACGACCAAGCTGGGAGAGATTAACCAAGGGGAGAGGTCAG 605
|||||
Db 272 TACTGTGATGACATGAGGACGACCAAGCTGGGAGAGATTAACCAAGGGGAGAGGTCAG 213
QY 726 CATATATCCAGCCACACTCAATTTTATATTTAGTCCAGATCTGACTGTGACCTTTC 785
|||||
Db 92 CATATATCCAGCCACACTCAATTTTATATTTAGTCCAGATCTGACTGTGACCTTTC 33
QY 786 TACACTGTAGAAATTAACATTAATCTCAATTTTGTTC 817
|||||
Db 32 TACACTGTAGAAATTAACATTAATCTCAATTTTGTTC 1

RESULT 6
AX106690/c 812 bp DNA linear PAT 30-Apr-2001
LOCUS Sequence 471 from Patent WO0125272.
DEFINITION AX106690
ACCESSION AX106690
VERSION AX106690.1 GI:13922355
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1

AUTHORS Xu, J., Skelky, Y. A., Reed, S. G., and Cheever, M. A.
TITLE Compositions and methods for therapy and diagnosis of prostate cancer
JOURNAL Patent: WO 0125272-A 471 12-APR-2001;
CORIXA CORPORATION (US)

FEATURES
source
1. 812
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

BASE COUNT 198 a 189 c 169 g 256 t
ORIGIN

Query Match 99.0%; Score 812; DB 6; Length 812;

Best Local Similarity 100.0%; Pred. No. 0;
Matches 812; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 CTGGCATCAGAAAAACAGAGGGGAGATTGTGTGGCTGCAGCCGAGGAGACCAAGAGA 65

DB 812 CTGGCATCAGAAAAACAGAGGGGAGATTGTGTGGCTGCAGCCGAGGAGACCAAGAGA 753

QY 66 TCTGCATGTGGGAAGACCTGATGATACAGAGGTGAGAAATAAGAAAGGCTGCTGACTT 125

DB 752 TCTGCATGTGGGAAGACCTGATGATACAGAGGTGAGAAATAAGAAAGGCTGCTGACTT 693

QY 126 TACCATCTGAGGCCACACATCTGCTGAATGAGATTAATTAACATCAGTACAGAAACAGCA 185

DB 692 TACCATCTGAGGCCACACATCTGCTGAATGAGATTAATTAACATCAGTACAGAAACAGCA 633

QY 186 GATGACAATATATATCTTAAGTAGACATGTTTTTGGACATTTCCAGCCCTTTAAATA 245

DB 632 GATGACAATATATATCTTAAGTAGACATGTTTTTGGACATTTCCAGCCCTTTAAATA 573

QY 246 TCCACACACACAGAGAACAAAGAGACACAGAGATCCCTGGGAGAAATCCCGGCGG 305

DB 572 TCCACACACACAGAGAACAAAGAGACACAGAGATCCCTGGGAGAAATCCCGGCGG 513

QY 306 CCATCTGGGTCATGATGAGCCCTGCGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 365

DB 512 CCATCTGGGTCATGATGAGCCCTGCGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 453

QY 366 TTGAGAAATGAATGATGCTTCTTAAAGATGGGAGAGAAACAGATCCTGTTGTGA 425

DB 452 TTGAGAAATGAATGATGCTTCTTAAAGATGGGAGAGAAACAGATCCTGTTGTGA 393

QY 426 TATTTATTTGAACGGGATTTACGATTTGAAATGAAAGTCACAAAGATGAGATTTACCAATGA 485

DB 392 TATTTATTTGAACGGGATTTACGATTTGAAATGAAAGTCACAAAGATGAGATTTACCAATGA 333

QY 486 GAGGAAACAGACGAGAAATCTGTATGCTTACACAGACATGCAACAAACAAATGAGAA 545

DB 332 GAGGAAACAGACGAGAAATCTGTATGCTTACACAGACATGCAACAAACAAATGAGAA 273

QY 546 TACTGTGATGACATGAGGACCAAGCTGGGAGAGATTAACACAGGGGAGAGGGTCTAG 605

DB 272 TACTGTGATGACATGAGGACCAAGCTGGGAGAGATTAACACAGGGGAGAGGGTCTAG 213

QY 606 GATTCGGCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 665

DB 212 GATTCGGCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 153

QY 666 CTCAAAACAAAGCTTTGTAATATCTGATCTAGGTTCTTGGGCGCAACATCTC 725

DB 152 CTCAAAACAAAGCTTTGTAATATCTGATCTAGGTTCTTGGGCGCAACATCTC 93

QY 726 CATATATCCAGCCACATCTATTTTAATATTTAGTCCAGATCTGATCTGATCTGATCTG 785

DB 92 CATATATCCAGCCACATCTATTTTAATATTTAGTCCAGATCTGATCTGATCTGATCTG 33

QY 786 TACACTGTAGATTAACATCTACTATTTGCTC 817

DB 32 TACACTGTAGATTAACATCTACTATTTGCTC 1

RESULT 7

AX140981/c AX140981 812 bp DNA linear PAT 31-MAY-2001

LOCUS Sequence 471 from Patent WO0134802.

DEFINITION AX140981

ACCESSION AX140981

VERSION AX140981.1 GI:14281078

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

source

BASE COUNT

ORIGIN

Query Match

Best Local Similarity

Matches

812; Conservative

0; Mismatches

0; Indels

0; Gaps

0;

QY

DB

QY

DB

QY

DB

QY

DB

QY

DB

QY

DB

QY

DB


```
|||||
Db 212 GATTCTGGCCCTGCTGCTTAAGCTGTGGCTCATPACCAATCATTTTATTTCTAAC 153
QY 666 CTCAAAACAAGAGCTGTTGTAATATCTGATCTCTACAGGTTCTCTGGGCCCAACATTTC 725
Db 152 CTCAAAACAAGAGCTGTTGTAATATCTGATCTCTACAGGTTCTCTGGGCCCAACATTTC 93
QY 726 CATATATCCAGCCACACTCATTTTAAATATTTAGTCCGACATCTGACTGTGACCTTTC 785
Db 92 CATATATCCAGCCACACTCATTTTAAATATTTAGTCCGACATCTGACTGTGACCTTTC 33
QY 786 TACACTGTAGATAATCACTACTCATTTTGTTC 817
Db 32 TACACTGTAGATAATCACTACTCATTTTGTTC 1

RESULT 8
AX200841/c
LOCUS AX200841 812 bp DNA linear PAT 29-AUG-2001
DEFINITION Sequence 471 from Patent WO0151633.
ACCESSION AX200841
VERSION AX200841.1 GI:15390744
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1 Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y.,
Reed,S.G., Kalos,M.D., Fanger,G.R., Day,C.H., Rether,M.W.,
Stolk,J.A., Skeiky,Y.A., Wang,A. and Meagher,M.J.
Compositions and methods for the therapy and diagnosis of prostate
cancer
Patent: WO 0151633-A 471 19-JUL-2001;
JOURNAL CORIXA CORPORATION (US)
FEATURES
source location/Qualifiers
1. 812
/mol_type="genomic DNA"
/db_xref="taxon:9606"
BASE COUNT 198 a 189 c 169 g 256 t
ORIGIN
Query Match 99.0%; Score 812; DB 6; Length 812;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 812; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 CTGCATCAGAAAAACAGAGGGAGATTGTGTGGCTGCAGCCGAGGAGACCAAGAGA 65
Db 812 CTGCATCAGAAAAACAGAGGGAGATTGTGTGGCTGCAGCCGAGGAGACCAAGAGA 753
QY 66 TCTGCATGTGGGAAGACCTGATGATACAGAGCTGAGAAATAAGAAAGCTGCTGACTT 125
Db 752 TCTGCATGTGGGAAGACCTGATGATACAGAGCTGAGAAATAAGAAAGCTGCTGACTT 693
QY 126 TACCATGTGAGGCCACATCTGCTGAATATTTAGTACCTACATAGAAACAGCAA 185
Db 692 TACCATGTGAGGCCACATCTGCTGAATATTTAGTACCTACATAGAAACAGCAA 633
QY 186 GATGACATATTAATGTCTAGTAGTACATGTTTTCACATTTCCAGCCCTTAATA 245
Db 632 GATGACATATTAATGTCTAGTAGTACATGTTTTCACATTTCCAGCCCTTAATA 573
QY 246 TCCACACACAGAGAGACAGAAAAAGAGAGACAGAGATCCCTGGAGAAATGCCGCG 305
Db 572 TCCACACACAGAGAGACAGAAAAAGAGAGACAGAGATCCCTGGAGAAATGCCGCG 513
QY 306 CCAATCTGGGTCATCATGAGACCTGCGCCCTGTGCTGCTCCGCTTGTGAGGAGACA 365
Db 512 CCAATCTGGGTCATCATGAGACCTGCGCCCTGTGCTGCTCCGCTTGTGAGGAGACA 453
QY 366 TTGAAATGAATGATGTGTCTTAAAGATGGGAGAAACAGATCCTGTGGGA 425
|||||
```

```
Db 452 TTGAAATGAATGATGTGTCTTAAAGATGGGAGAAACAGATCCTGTGGGA 393
QY 426 TATTATTTGAACGGGATTAACAGATTGAATGAAGTCACAAAGTGAACATTAACAATGA 485
Db 392 TATTATTTGAACGGGATTAACAGATTGAATGAAGTCACAAAGTGAACATTAACAATGA 333
QY 486 GAGGAAACAGACAGAAATCTTGAGGCTTCCACAGACATGCAACAAACAAATGAA 545
Db 332 GAGGAAACAGACAGAAATCTTGAGGCTTCCACAGACATGCAACAAACAAATGAA 273
QY 546 TACTGTGATGACATGAGGACCAAGCTGGGAGAGATTAACCCAGGCGAGAGGTGAG 605
Db 272 TACTGTGATGACATGAGGACCAAGCTGGGAGAGATTAACCCAGGCGAGAGGTGAG 213
QY 606 GATTCTGGCCCTGCTGCTTAACATGTCGCTCATACCAATCATTTTCAATTTCTAAC 665
Db 212 GATTCTGGCCCTGCTGCTTAACATGTCGCTCATACCAATCATTTTCTAAC 153
QY 666 CTCAAAACAAGAGCTGTTGTAATATCTGATCTCTACAGGTTCTCTGGGCCCAACATTTC 725
Db 152 CTCAAAACAAGAGCTGTTGTAATATCTGATCTCTACAGGTTCTCTGGGCCCAACATTTC 93
QY 726 CATATATCCAGCCACACTCATTTTAAATATTTAGTCCGACATCTGACTGTGACCTTTC 785
Db 92 CATATATCCAGCCACACTCATTTTAAATATTTAGTCCGACATCTGACTGTGACCTTTC 33
QY 786 TACACTGTAGATAATCACTACTCATTTTGTTC 817
Db 32 TACACTGTAGATAATCACTACTCATTTTGTTC 1

RESULT 9
AX267497/c
LOCUS AX267497 812 bp DNA linear PAT 26-OCT-2001
DEFINITION Sequence 471 from Patent WO0173032.
ACCESSION AX267497
VERSION AX267497.1 GI:16516261
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1 Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y.,
Kalos,M.D., Fanger,G.R., Rether,M.W., Stolk,J.A., Day,C.H.,
Vedlick,T.S., Carter,D., Li,S.X., Wang,A., Skeiky,Y.A., Hepler,M.T.
and Henderson,R.A.
Compositions and methods for the therapy and diagnosis of prostate
cancer
Patent: WO 0173032-A 471 04-OCT-2001;
JOURNAL CORIXA CORPORATION (US)
FEATURES
source location/Qualifiers
1. 812
/mol_type="genomic DNA"
/db_xref="taxon:9606"
BASE COUNT 198 a 189 c 169 g 256 t
ORIGIN
Query Match 99.0%; Score 812; DB 6; Length 812;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 812; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 CTGCATCAGAAAAACAGAGGGAGATTGTGTGGCTGCAGCCGAGGAGACCAAGAGA 65
Db 812 CTGCATCAGAAAAACAGAGGGAGATTGTGTGGCTGCAGCCGAGGAGACCAAGAGA 753
QY 66 TCTGCATGTGGGAAGACCTGATGATACAGAGCTGAGAAATAAGAAAGCTGCTGACTT 125
Db 752 TCTGCATGTGGGAAGACCTGATGATACAGAGCTGAGAAATAAGAAAGCTGCTGACTT 693
QY 126 TACCATGTGAGGCCACATCTGCTGAATATTTAGTACCTACATAGAAACAGCAA 185
|||||
```


Db	692	TACACATCTGGAGCCACACACATCTGCTGAAATGAGATATTAACATCACTAGAACACGAA	633
Qy	186	GATGACAAATATATATGTCTTAAGTAGTAGACATGTTTTGACATTTTCCAGATCCCTTTAATA	245
Db	632	GATGACAAATATAATGTCTTAAGTAGTAGACATGTTTTGACATTTTCCAGATCCCTTTAATA	573
Qy	246	TTCCACACACACAGGAAAGACACAAAAGAAAGACACAGATTCCTGGGAGAAATATGCCGGCCG	305
Db	572	TTCCACACACACAGGAAAGACACAAAAGAAAGACACAGATTCCTGGGAGAAATATGCCGGCCG	513
Qy	306	CCATCTTGGGTCATCAGATGAGACCTTCGCCCTTGGCTTCCGCTTGGAGAGGAAAGACAA	365
Db	512	CCATCTTGGGTCATCAGATGAGACCTTCGCCCTTGGCTTCCGCTTGGAGAGGAAAGACAA	453
Qy	366	TTAGAAAAATGATTTGATGTGTTCTTTAAAGATGGCGAGAAAAACAGATCCTGTGTGGA	425
Db	452	TTAGAAAAATGATTTGATGTGTTCTTTAAAGATGGCGAGAAAAACAGATCCTGTGTGGA	393
Qy	426	TATTTATTTTGAACGGGANTTACAGATTCGAATGAAATGAAATGCAAGAGACATTTACCAATGA	485
Db	392	TATTTATTTTGAACGGGANTTACAGATTCGAATGAAATGAAATGCAAGAGACATTTACCAATGA	333
Qy	486	GAGGAAAAACAGACAGAAAAATCTTGATGGCTTCCACAGACATGCAACAAACAAATGGA	545
Db	332	GAGGAAAAACAGACAGAAAAATCTTGATGGCTTCCACAGACATGCAACAAACAAATGGA	273
Qy	546	TACTGTGATGACATGAGGACAGCCAAAGCTGGGGAGAGATTAACACAGGGGACAGAGGGTCAG	605
Db	272	TACTGTGATGACATGAGGACAGCCAAAGCTGGGGAGAGATTAACACAGGGGACAGAGGGTCAG	213
Qy	606	GATTCCTGGCCCTGCTGCCCTTAACATCTGCGTTCATTAACCAATCATTTATTTTAAAC	665
Db	212	GATTCCTGGCCCTGCTGCCCTTAACATCTGCGTTCATTAACCAATCATTTATTTTAAAC	153
Qy	666	CTCAAAACAAAGCTGTTTAAATATCTGATCTCTACAGTTCCTTGGGCCCAACATTCCTC	725
Db	152	CTCAAAACAAAGCTGTTTAAATATCTGATCTCTACAGTTCCTTGGGCCCAACATTCCTC	93
Qy	726	CATATATCCAGCCACACTCATTTTAAATATTTAAGTTCGCCAGATCTGTACTGTGACCTTTC	785
Db	92	CATATATCCAGCCACACTCATTTTAAATATTTAAGTTCGCCAGATCTGTACTGTGACCTTTC	33
Qy	786	TACACTGTAGATAAATCACTTACTCATTTTGTTC	817
Db	32	TACACTGTAGATAAATCACTTACTCATTTTGTTC	1
RESULT 10			
AR261037/c	AR261037	2229 bp	DNA
LOCUS	Sequence	469	from patent US 6321716.
DEFINITION	AR261037		
VERSION	AR261037.1	GI:28071800	
KEYWORDS			
SOURCE	Unknown.		
ORGANISM	Unknown.		
REFERENCE	Unclassified.		
AUTHORS	1 (bases 1 to 2229)		
TITLE	Mashiki,Z. and Harada,J.		
JOURNAL	Negative pressure control apparatus for engine mounted in vehicle		
FEATURES	Patent: US 6321716-A 469 27-NOV-2001;		
	Location/Qualifiers		
	1..2229		
	/organism="unknown"		
BASE COUNT	654 a	447 c	481 g 647 t
ORIGIN			
Query Match	88.3%;	Score 724;	DB 6; Length 2229;
Best Local Similarity	100.0%;	Pred. No. 0;	
Matches	724;	Conservative 0;	Mismatches 0; Indels 0; Gaps 0;
Qy	97	AGGTGAGAAATAGAAAGCTGTGCTGACTTTTACATCTGAGGCCACACATCTGCTGAATG	156

Db	1776	AGGTGAGCAAAATTAAGAAAGGCTGCTGACTTTTACCATCTGAGGCCACACACTCTGCTGAANAATG	1717
QY	157	GAGATTAATTAACATCACTAGTAAGAACAGCAAGATGACAAATATATATGTCATAAGTAGATG	216
Db	1716	GAGATAATTAACATCACTAGTAAGAACAGCAAGATGACAAATATATATGTCATAAGTAGATG	1657
QY	217	TTTTTGCCACATTTTCCAGGCCCTTTTAATATATCCACACACACACAGGAAGCAACAAAAGGAAGCA	276
Db	1656	TTTTTGCCACATTTTCCAGGCCCTTTTAATATATCCACACACACAGGAAGCAACAAAAGGAAGCA	1597
QY	277	CAGAGATCCCTGGGAGAAATGCCGGCCGCATCTTGGGTATGATGATGAGCCTGCCCTG	336
Db	1596	CAGAGATCCCTGGGAGAAATGCCGGCCGCATCTTGGGTATGATGATGAGCCTGCCCTG	1537
QY	337	TGCCGTGTCCCGCTTGTGAGGGAAGAGCATTAGAAAATGAATGATGTGTTCCTTAAAGG	396
Db	1536	TGCCGTGTCCCGCTTGTGAGGGAAGAGCATTAGAAAATGAATGATGTGTTCCTTAAAGG	1477
QY	397	ATGGGCAAGAAACAGATCCCTGTTGATTTTATTTGAACGGGATTTACGATTTTGAA	456
Db	1476	ATGGGCAAGAAACAGATCCCTGTTGATTTTATTTTGAACGGGATTTACGATTTTGAA	1417
QY	457	TGAAGTCCAAAGTGAGCATTACCAATGAGAGGAAGAACAGACGAGAAATCTTGATGGCT	516
Db	1416	TGAAGTCCAAAGTGAGCATTACCAATGAGAGGAAGAACAGACGAGAAATCTTGATGGCT	1357
QY	517	TCACAGACATGCAACAACAAACAAATGGAATCTGTGATGACATGAGCGAGCCAAGCTGGG	576
Db	1356	TCACAGACATGCAACAACAAACAAATGGAATCTGTGATGACATGAGCGAGCCAAGCTGGG	1297
QY	577	GAGAGATATACCGAGGGGACAGAGGTACAGATTCTGGCCCTGCTGCTTAAACTGTGCTT	636
Db	1296	GAGAGATATACCGAGGGGACAGAGGTACAGATTCTGGCCCTGCTGCTTAAACTGTGCTT	1237
QY	637	CATAACCAAAATCATTTTCATTTTCTTAACCCCAACAAACAAAGCTGTGTAATGTGATCT	696
Db	1236	CATAACCAAAATCATTTTCATTTTCTTAACCCCAACAAACAAAGCTGTGTAATGTGATCT	1177
QY	697	CTAGCGTTCCTTCTGGGGCCCAACATTTCTCATATATATCCAGGCACAGCATCTATTTTAATAT	756
Db	1176	CTAGCGTTCCTTCTGGGGCCCAACATTTCTCATATATATCCAGGCACAGCATCTATTTTAATAT	1117
QY	757	TAGTTCCCAAGATCTGTACTGTGACCTTTCTACACTGTAGAAATACATTTACATTTTGT	816
Db	1116	TAGTTCCCAAGATCTGTACTGTGACCTTTCTACACTGTAGAAATACATTTACATTTTGT	1057
QY	817	CAAA 820	
Db	1056	CAAA 1053	
RESULT 11			
AR278568/c			
LOCUS	AR278568	2229 bp	DNA linear PAT 10-APR-2003
DEFINITION	Sequence 469 from patent US 6512094.		
ACCESSION	AR278568		
VERSION	AR278568.1	GI:29712814	
KEYWORDS	.		
SOURCE	Unknown.		
ORGANISM	Unknown.		
REFERENCE	Unclassified.		
AUTHORS	1 (bases 1 to 2229)		
TITLE	Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y.,		
	Kallios,M.D., Fanger,G.R., Rether,M.W., Stolk,J.A., Day,C.H.,		
	Vedvick,T.S., Carter,D., Li,S.X., Wang,A., Skeiky,Y.A.W.,		
	Hepler,W.T. and Henderson,R.A.		
	Compositions and methods for the therapy and diagnosis of prostate cancer		
JOURNAL FEATURES	Patent: US 6512094-A 469 28-JAN-2003;		
	Location/Qualifiers		
BASE COUNT	654 a	447 c	481 g 647 t
Source 1..2229 /"organism="unknown"			

KEYWORDS	Homo sapiens (human)
SOURCE	Homo sapiens
ORGANISM	Eukaryota; Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi: Mammalia; Eutheria; Primates: Catarrhini; Homiidae; Homo.
REFERENCE	1
AUTHORS	Xu,J., Skelky,Y.A., Reed,S.G. and Cheever,M.A.
TITLE	Compositions and methods for therapy and diagnosis of prostate cancer
JOURNAL	Patent: WO 0125272-A 469 12-APR-2001; CORIXA CORPORATION (US)
FEATURES	Location/Qualifiers
SOURCE	1. 2229
	/organism="Homo sapiens"
	/mol_type="genomic DNA"
	/db_xref="taxon:9606"
BASE COUNT	654 a 447 c 481 g 647 t
ORIGIN	

Query Match	88.3%	Score 724	DB 6	length 2229
Best Local Similarity	100.0%	Pred. NO.	0	
Matches 724	Conservative	0	Mismatches	0
		0	Indels	0
			Gaps	0

QY	97	AGGAGACAATTAAGAAAAGCGCTGACATTTTACCATCTGAGGCGACACATCTGCTGAATG	156
Db	1776	AGGAGACAATTAAGAAAAGCGCTGACATTTTACCATCTGAGGCGACACATCTGCTGAATG	1711
QY	157	GAGATAATTAACATCACTAGAAAGCAGAAGATGACATATATATGCTCTAAGTAGACATG	216
Db	1716	GAGATAATTAACATCACTAGAAAGCAGAAGATGACATATATATGCTCTAAGTAGACATG	165
QY	217	TTTTTGACATTTCCAGCCCTTTTAAATATCCACACACAGAAAGCACAAGAGACGA	276
Db	1656	TTTTTGACATTTCCAGCCCTTTTAAATATCCACACACAGAAAGCACAAGAGAGACGA	1597
QY	277	CAGAGATCCCTGGGAGAAATCCCGGCCCATCTTGGGTATCATGATAGCCTCGCCGTG	336
Db	1596	CAGAGATCCCTGGGAGAAATCCCGGCCCATCTTGGGTATCATGATAGCCTCGCCGTG	1537
QY	337	TGCGTGGTCCCGCTTGAGGAGAAAGCATTAGAAAATGAAATGTATGTTCTTTAAAG	396
Db	1536	TGCGTGGTCCCGCTTGAGGAGAAAGCATTAGAAAATGAAATGTATGTTCTTTAAAG	1477
QY	397	ATGGGCAAGAAAACAGATCCCTGTTGTGATATTATTTGAACGGGATTAACAGATTTGAA	456
Db	1476	ATGGGCAAGAAAACAGATCCCTGTTGTGATATTATTTGAACGGGATTAACAGATTTGAA	1411
QY	457	TGAAGTCAACAAGTGAGCATTAACCAATGAGAGAAAACAGACGAAGAAATCTTGATGGCT	516
Db	1416	TGAAGTCAACAAGTGAGCATTAACCAATGAGAGAAAACAGACGAAGAAATCTTGATGGCT	1357
QY	517	TCACAAGACATGCAACAACAAATAATGGAATCTGTGATGACATGAGCGAGCCCAAGCTGGG	576
Db	1356	TCACAAGACATGCAACAACAAATAATGGAATCTGTGATGACATGAGCGAGCCCAAGCTGGG	1297
QY	577	GAGAGATTAACACAGGGGCAAGGGTGAGGATTTCTGGCCCTGCTCTAAACTGTGCGTT	636
Db	1296	GAGAGATTAACACAGGGGCAAGGGTGAGGATTTCTGGCCCTGCTCTAAACTGTGCGTT	1237
QY	637	CATTAACCAAAATCATTTTCATATTTTAAACCCCAAAAACAAGCTGTTGTAATATCGATCT	696
Db	1236	CATTAACCAAAATCATTTTCATATTTTAAACCCCAAAAACAAGCTGTTGTAATATCGATCT	1177
QY	697	CTAGCGTTCTCTTGGGGCCAACAATCTCATATATCCAGGCACACTCATTTTAAATTT	756
Db	1176	CTAGCGTTCTCTTGGGGCCAACAATCTCATATATCCAGGCACACTCATTTTAAATTT	1111
QY	757	TAGTTCCCAAGTCTGTACTGTGACCTTCTACACTGTGAATTAACATTAATCATTTTGT	816
Db	1116	TAGTTCCCAAGTCTGTACTGTGACCTTCTACACTGTGAATTAACATTAATCATTTTGT	1057
QY	817	CAAA 820	

Db 1056 CAAA 1053

RESULT 14		
AX140979/c		
LOCUS	2229 bp	DNA
AX140979		linear
DEFINITION	Sequence 469 from Patent WO0134802.	PAT 31-MAY-2001
SEQUENCE	8340020	

VERSION AX140979.1 GT:14281076

KEYWORDS	SOURCE
Homo sapiens	(human)

ORGANISM Homo sapiens
Fulcravota: Metazoa: Chordata: Vertebrata: Euteleostomi:

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

AUTHORS Xu, J., Dillon, D.C., Mitcham, J.L., Harlocker, S.L., Jiang, Y.

Reed, S.G., Kalos, M.D., Ketter, M.W., Stolk, J.A., Day, C.H.,
Skeiky, Y.A. and Wang, A.

TITLE Compositions and methods for the therapy and diagnosis of prostate cancer

JOURNAL Patent: WO 0134802-A 469 17-MAY-2001

FEATURES	Location/Qualifiers	CONTAIN	CONTAINED BY
		CONTAIN	CONTAINED BY

source

```
/mol_type="genomic DNA"
```

BASE COUNT	654 a	447 c	481 g	647 t
------------	-------	-------	-------	-------

Query Match	88.3%;	Score 7/24;	DB 6;	Length 2229;
Best Local Similarity	100.08;	Pred NO.	0;	

Matches 724; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

97 AGTGAGAAATAGAAAGGCTGCTGACTTTACCATCTGAGGCCACACATCTGCTGAATG 156

Db 1776 AGGTGAGAAATAGAAAGGCTGCTGACTTTACCATCTGAGGCCACACATCTGCTGAATG 1717

157 GAGTATTACATCACTAGAAACAGCAGATGACATATATATGTCTAGTAGTGACATG 216

DB 1716 CACATTAATTACCAACAACCAATCACCATTAATCAGTCCACATC 1657

2

27

DB 1656 TTTTTCACATTTCCAGCCCTTTAAATATCCACACACAGGAAGCACAATAAGGAACA 159

277 CAGAGATCCCTGGGAGAAATGCCCGGCCCATCTGGGTCATCGATGAGCCTCGCCCTG 336

Db 1596 CAGAGATCCCTGGGAGAATGCCCGGCCATCTGGGTCATCGATGAGCCTCGCCCTG 1537

337 TGCCTGGTCCCGCTTGTGAGGGAAGACATTAGAAATGAATTGATGTCTCCTTAAGG 396

Db 1536 TGCCCTGGTCCGCTTGTGAGGGAAGGACATTAGAAATGATTTGATGTCTCTTAAGG 1477

00' 307 AAAAAAAAAAAAAAAAAAAAAA 456

[illegible]

45 / TGAAGTCACAAAGTGGCAATTACCAATGGAGGAAACAGACGAGAAATCTTGAATGGCT 516

Db 1416 TGAAGTCACAAAGTGAGCATTACCAATGAGAGGAAACAGACGAGAAATCTTGATGGCT 1357

517 TCACAAGACATGCCAACAAACAAATGGAATACTGTGATGACATGAGGCAGCCAAAGCTGGC 576

Db 1356 TCACAAGACATGCACAACAATAATGGAATACTGTGATGACATGAGGCAGCCAAAGCTGGG 1297

577 GAGGAGATTAAACCACGGGGCAGAGGGTCAAGATTCTGGCCCTGCTGCCCTAAACCTGTGCGTT 636

1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75 76 77 78 79 80 81 82 83 84 85 86 87 88 89 90 91 92 93 94 95 96 97 98 99 100 101 102 103 104 105 106 107 108 109 110 111 112 113 114 115 116 117 118 119 120 121 122 123 124 125 126 127 128 129 130 131 132 133 134 135 136 137 138 139 140 141 142 143 144 145 146 147 148 149 150 151 152 153 154 155 156 157 158 159 160 161 162 163 164 165 166 167 168 169 170 171 172 173 174 175 176 177 178 179 180 181 182 183 184 185 186 187 188 189 190 191 192 193 194 195 196 197 198 199 200 201 202 203 204 205 206 207 208 209 210 211 212 213 214 215 216 217 218 219 220 221 222 223 224 225 226 227 228 229 230 231 232 233 234 235 236 237 238 239 240 241 242 243 244 245 246 247 248 249 250 251 252 253 254 255 256 257 258 259 260 261 262 263 264 265 266 267 268 269 270 271 272 273 274 275 276 277 278 279 280 281 282 283 284 285 286 287 288 289 290 291 292 293 294 295 296 297 298 299 300 301 302 303 304 305 306 307 308 309 310 311 312 313 314 315 316 317 318 319 320 321 322 323 324 325 326 327 328 329 330 331 332 333 334 335 336 337 338 339 340 341 342 343 344 345 346 347 348 349 350 351 352 353 354 355 356 357 358 359 360 361 362 363 364 365 366 367 368 369 370 371 372 373 374 375 376 377 378 379 380 381 382 383 384 385 386 387 388 389 390 391 392 393 394 395 396 397 398 399 400 401 402 403 404 405 406 407 408 409 410 411 412 413 414 415 416 417 418 419 420 421 422 423 424 425 426 427 428 429 430 431 432 433 434 435 436 437 438 439 440 441 442 443 444 445 446 447 448 449 450 451 452 453 454 455 456 457 458 459 460 461 462 463 464 465 466 467 468 469 470 471 472 473 474 475 476 477 478 479 480 481 482 483 484 485 486 487 488 489 490 491 492 493 494 495 496 497 498 499 500 501 502 503 504 505 506 507 508 509 510 511 512 513 514 515 516 517 518 519 520 521 522 523 524 525 526 527 528 529 530 531 532 533 534 535 536 537 538 539 540 541 542 543 544 545 546 547 548 549 550 551 552 553 554 555 556 557 558 559 560 561 562 563 564 565 566 567 568 569 570 571 572 573 574 575 576 577 578 579 580 581 582 583 584 585 586 587 588 589 590 591 592 593 594 595 596 597 598 599 600 601 602 603 604 605 606 607 608 609 610 611 612 613 614 615 616 617 618 619 620 621 622 623 624 625 626 627 628 629 630 631 632 633 634 635 636 637 638 639 640 641 642 643 644 645 646 647 648 649 650 651 652 653 654 655 656 657 658 659 660 661 662 663 664 665 666 667 668 669 670 671 672 673 674 675 676 677 678 679 680 681 682 683 684 685 686 687 688 689 690 691 692 693 694 695 696 697 698 699 700 701 702 703 704 705 706 707 708 709 710 711 712 713 714 715 716 717 718 719 720 721 722 723 724 725 726 727 728 729 730 731 732 733 734 735 736 737 738 739 740 741 742 743 744 745 746 747 748 749 750 751 752 753 754 755 756 757 758 759 760 761 762 763 764 765 766 767 768 769 770 771 772 773 774 775 776 777 778 779 780 781 782 783 784 785 786 787 788 789 790 791 792 793 794 795 796 797 798 799 800 801 802 803 804 805 806 807 808 809 810 811 812 813 814 815 816 817 818 819 820 821 822 823 824 825 826 827 828 829 830 831 832 833 834 835 836 837 838 839 840 841 842 843 844 845 846 847 848 849 850 851 852 853 854 855 856 857 858 859 860 861 862 863 864 865 866 867 868 869 870 871 872 873 874 875 876 877 878 879 880 881 882 883 884 885 886 887 888 889 890 891 892 893 894 895 896 897 898 899 900 901 902 903 904 905 906 907 908 909 910 911 912 913 914 915 916 917 918 919 920 921 922 923 924 925 926 927 928 929 930 931 932 933 934 935 936 937 938 939 940 941 942 943 944 945 946 947 948 949 950 951 952 953 954 955 956 957 958 959 960 961 962 963 964 965 966 967 968 969 970 971 972 973 974 975 976 977 978 979 980 981 982 983 984 985 986 987 988 989 990 991 992 993 994 995 996 997 998 999 1000 1001 1002 1003 1004 1005 1006 1007 1008 1009 1010 1011 1012 1013 1014 1015 1016 1017 1018 1019 1020 1021 1022 1023 1024 1025 1026 1027 1028 1029 1030 1031 1032 1033 1034 1035 1036 1037 1038 1039 1040 1

.....

[illegible]

DB 1236 CATACCAATTCATATTCACCCCTCAAAACAAGCTGTGTAAATATCTGATCT 11 /

QY 697 CTACGGTTCCTTGGGCCCCAACATTCATATATCCAGCCACATTCATTTTAAATTT 756
|||||
Db 1176 CTACGGTTCCTTGGGCCCCAACATTCATATATCCAGCCACATTCATTTTAAATTT 1117
QY 757 TAGTCCAGATCTGTACTGTGACCTTCTTACACTGTAGATATACATTTACTTTGTT 816
|||||
Db 1116 TAGTCCAGATCTGTACTGTGACCTTCTTACACTGTAGATATACATTTACTTTGTT 1057
QY 817 CAAA 820
|||||
Db 1056 CAAA 1053

RESULT 15
AX200839/c 2229 bp DNA linear PAT 29-AUG-2001
LOCUS AX200839 Sequence 469 from Patent WO0151633.
DEFINITION AX200839
ACCESSION AX200839
VERSION AX200839.1 GI:15390742
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1
AUTHORS Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y.,
Reed,S.G., Kalos,M.D., Fanger,G.R., Day,C.H., Retter,M.W.,
Stolk,J.A., Skelky,Y.A., Wang,A. and Meagher,M.J.
TITLE Compositions and methods for the therapy and diagnosis of prostate
cancer
JOURNAL Patent: WO 0151633-A 469 19-JUL-2001;
CORIXA CORPORATION (US)
FEATURES
source 1..2229
Location/Qualifiers
BASE COUNT 654 a 447 c 481 g 647 t
ORIGIN

Query Match 88.3%; Score 724; DB 6; Length 2229;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 724; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 97 AGGTGAGAAATTAAGAAAGGCTGCTGACTTACCATCTGAGGCCACACATCTGCTGAATG 156
|||||
Db 1776 AGGTGAGAAATTAAGAAAGGCTGCTGACTTACCATCTGAGGCCACACATCTGCTGAATG 1717
QY 157 GAGATATTTAATCACTACTAGAAACAGCAGATGACATATATATGTCTAAGTAGTGACATG 216
|||||
Db 1716 GAGATATTTAATCACTACTAGAAACAGCAGATGACATATATATGTCTAAGTAGTGACATG 1657
QY 217 TTTTGGACATTTCCAGCCCCCTTTAAATATCCACACACAGAGCAACAAAAGGAAGCA 276
|||||
Db 1656 TTTTGGACATTTCCAGCCCCCTTTAAATATCCACACACAGAGCAACAAAAGGAAGCA 1597
QY 277 CAGAGATCCCTGGGAGAAATCCCGGCCCATCTTGGTCAATGATGAGCTCGCCCTG 336
|||||
Db 1596 CAGAGATCCCTGGGAGAAATCCCGGCCCATCTTGGTCAATGATGAGCTCGCCCTG 1537
QY 337 TGGCTGGTCCCGCTTGTGAGGGAAGGACATTAGAAATGAATTGATGTGTTCTTAAAGG 396
|||||
Db 1536 TGGCTGGTCCCGCTTGTGAGGGAAGGACATTAGAAATGAATTGATGTGTTCTTAAAGG 1477
QY 397 ATGGGCAAGAAACAGATCTCTGTGTGGATATTTATTTGAACGGGATTAAGATTGAAA 456
|||||
Db 1476 ATGGGCAAGAAACAGATCTCTGTGTGGATATTTATTTGAACGGGATTAAGATTGAAA 1417
QY 457 TGAAGTCACAAAGTAGCATTTACCAATGAGAGGAAAAACAGAGGAAATCTTGATGGCT 516
|||||
Db 1416 TGAAGTCACAAAGTAGCATTTACCAATGAGAGGAAAAACAGAGGAAATCTTGATGGCT 1357

QY 517 TCACAGACATGCAACAAACAAATGGAATACTGTGATGACATGAGCCAGCAAGCTGGG 576
|||||
Db 1356 TCACAGACATGCAACAAACAAATGGAATACTGTGATGACATGAGCCAGCAAGCTGGG 1297
QY 577 GAGGAGATTAACCAAGGGGACAGGGGTCAAGGATTCGCGCCCGCTGAACCTGTGGGTT 636
|||||
Db 1296 GAGGAGATTAACCAAGGGGACAGGGGTCAAGGATTCGCGCCCGCTGAACCTGTGGGTT 1237
QY 637 CATACCAAAATCATTTCAATATTTCTAACCCCTCAAAACAAACAGCTGTGTAATATCTGATCT 696
|||||
Db 1236 CATACCAAAATCATTTCAATATTTCTAACCCCTCAAAACAAACAGCTGTGTAATATCTGATCT 1177
QY 697 CTACGGTTCCTTGGGCCCCAACATTCATATATCCAGCCACATTCATTTTAAATTT 756
|||||
Db 1176 CTACGGTTCCTTGGGCCCCAACATTCATATATCCAGCCACATTCATTTTAAATTT 1117
QY 757 TAGTCCAGATCTGTACTGTGACCTTCTTACACTGTAGATATACATTTACTTTGTT 816
|||||
Db 1116 TAGTCCAGATCTGTACTGTGACCTTCTTACACTGTAGATATACATTTACTTTGTT 1057
QY 817 CAAA 820
|||||
Db 1056 CAAA 1053

Search completed: September 27, 2003, 06:45:01
Job time : 2986.11 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 26, 2003, 20:07:52 : Search time 214.891 Seconds
(without alignments)
10300.748 Million cell updates/sec

Title: US-09-402-713a-4

Perfect score: 820
Sequence: 1 agaagctgcacagaaaaa.....cattactcatttgcacaa 820

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 2552756 seqs, 1349719017 residues

Word size : 0

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : N_Geneseq_19Jun03:*

```

1: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1980.DAT:*
2: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT:*
3: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1982.DAT:*
4: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1983.DAT:*
5: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1984.DAT:*
6: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1985.DAT:*
7: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1986.DAT:*
8: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1987.DAT:*
9: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1988.DAT:*
10: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1989.DAT:*
11: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1990.DAT:*
12: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1991.DAT:*
13: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1992.DAT:*
14: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1993.DAT:*
15: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1994.DAT:*
16: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1995.DAT:*
17: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1996.DAT:*
18: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1997.DAT:*
19: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1998.DAT:*
20: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1999.DAT:*
21: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2000.DAT:*
22: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT:*
23: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT:*
24: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT:*
25: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2003.DAT:*

```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	820	100.0	820	19	AAV62429
2	820	100.0	876	24	AAV62428
3	820	100.0	1872	19	AAV62428
4	812	99.0	812	21	AAV62428
5	812	99.0	812	22	AAV62428
6	812	99.0	812	22	AAV62428
7	812	99.0	812	22	AAV62428
8	812	99.0	812	22	AAV62428

Result No.	Score	Query Match	Length	ID	Description
9	812	99.0	812	22	AAV62429
10	812	99.0	812	24	AAV62428
11	812	99.0	812	25	AAV62428
12	812	99.0	812	21	AAV62428
13	812	99.0	812	22	AAV62428
14	812	99.0	812	22	AAV62428
15	812	99.0	812	22	AAV62428
16	812	99.0	812	22	AAV62428
17	812	99.0	812	22	AAV62428
18	812	99.0	812	22	AAV62428
19	812	99.0	812	22	AAV62428
20	812	99.0	812	22	AAV62428
21	812	99.0	812	22	AAV62428
22	812	99.0	812	22	AAV62428
23	812	99.0	812	22	AAV62428
24	812	99.0	812	22	AAV62428
25	812	99.0	812	22	AAV62428
26	812	99.0	812	22	AAV62428
27	812	99.0	812	22	AAV62428
28	812	99.0	812	22	AAV62428
29	812	99.0	812	22	AAV62428
30	812	99.0	812	22	AAV62428
31	812	99.0	812	22	AAV62428
32	812	99.0	812	22	AAV62428
33	812	99.0	812	22	AAV62428
34	812	99.0	812	22	AAV62428
35	812	99.0	812	22	AAV62428
36	812	99.0	812	22	AAV62428
37	812	99.0	812	22	AAV62428
38	812	99.0	812	22	AAV62428
39	812	99.0	812	22	AAV62428
40	812	99.0	812	22	AAV62428
41	812	99.0	812	22	AAV62428
42	812	99.0	812	22	AAV62428
43	812	99.0	812	22	AAV62428
44	812	99.0	812	22	AAV62428
45	812	99.0	812	22	AAV62428

ALIGNMENTS

RESULT 1
AAV62429
ID AAV62429 standard; CDNA; 820 BP.
XX AAV62429;
AC AAV62429;
XX 30-DEC-1998 (first entry)
DE Prostate cancer antigen (PCA3) CDNA splice variant 3.
XX Prostate cancer antigen CDNA splice variant 3.
KW PC; ds.
XX Homo sapiens.
OS Homo sapiens.
PN WO9845420-A1.
XX 15-OCT-1998.
PD 15-OCT-1998.
PF 09-APR-1998; 98WO-CA00346.
XX 09-APR-1998; 98WO-CA00346.
PR 10-APR-1997; 97US-0041836.
XX (DIAG-) DIAGNOCURE INC.
XX Bussemakers MUG;
XX WPI; 1998-568347/48.
XX New nucleic acid encoding prostate cancer antigen 3 - for diagnosis,
XX prevention and treatment of prostatic cancer

XX Claim 4; Pages 77-78; 11pp; English.
PS
XX The present sequence represents the prostate cancer antigen (PCA3)
CC cDNA splice variant 3 sequence comprising of exons 1, 3, and 4a
CC of the PCA3 gene. The PCA3 cDNA splice variant 3 sequence,
CC isolated from a human primary prostatic tumour tissue cDNA library,
CC was found in approximately 15% of the cDNA clones isolated. The
CC invention claims for PCA3 cDNA variants and the proteins they encode.
CC The invention also claims for antibodies against PCA3 protein. The
CC antibodies are claimed to be useful for detecting PCA3 protein in
CC immunosay tests, for diagnosing, assessing and prognosing of
CC prostatic cancer (PC). Antibodies, optionally coupled to a cytotoxin
CC or radioisotope, and nucleic acids antisense to PCA3 cDNA are claimed
CC to be useful for treating PC, while determining elevated levels of
CC PCA3 (as RNA or protein) is useful for detecting a predisposition
CC to development of PC, e.g. in prenatal tests. Detecting PCA3 protein
CC allows differentiation between malignant and benign prostatic disease,
CC and the level of PCA3 expression allows correlation with the grade of
CC tumour. PCA3 protein and its fragments are also claimed to be useful
CC in vaccines for preventing PC; in drug screens for identifying
CC specific (ant)agonists (potentially useful therapeutically) and for
CC studying protein-DNA interactions.
CC
XX
SQ Sequence 820 Bp; 262 A; 169 C; 191 G; 198 T; 0 other;

Query Match 100.0%; Score 820; DB 19; Length 820;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 820; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGAAGCTGGATCGAGAAAACAGAGGAGGAGATTTGTGCTGAGCCGAGGAGACAG 60
DB 1 AGAAGCTGGATCGAGAAAACAGAGGAGGAGATTTGTGCTGAGCCGAGGAGACAG 60
QY 61 GAAGATCTGATGGTGGGAAGGAGCCTGATGATACAGAGTGAGAAATAGAAAGCTGCT 120
DB 61 GAAGATCTGATGGTGGGAAGGAGCCTGATGATACAGAGTGAGAAATAGAAAGCTGCT 120
QY 121 GACTTACCATCTGAGGCCACACATCTGTGAAATGGAGATTAATTAACATCATAAGAAC 180
DB 121 GACTTACCATCTGAGGCCACACATCTGTGAAATGGAGATTAATTAACATCATAAGAAC 180
QY 181 AGCAAGATGACATATATATGTCCTAAGTAGACATGTTTTGGCATTTCCAGCCCTTT 240
DB 181 AGCAAGATGACATATATATGTCCTAAGTAGACATGTTTTGGCATTTCCAGCCCTTT 240
QY 241 AATATCCACACACACAGAGGAGCAAAAGAGACAGAGATCCCTGGGAGAAATGCC 300
DB 241 AATATCCACACACACAGAGGAGCAAAAGAGACAGAGATCCCTGGGAGAAATGCC 300
QY 301 GCGCGCCATCTTGGGTGATCATGATGAGCCCTGCTGCTGCTGCTGCTGCTGAGGAA 360
DB 301 GCGCGCCATCTTGGGTGATCATGATGAGCCCTGCTGCTGCTGCTGCTGCTGAGGAA 360
QY 361 GGACATTAGAAATGAATGATGCTCTTAAGGATGGGAGGAGAAAGAGATCCCTGTT 420
DB 361 GGACATTAGAAATGAATGATGCTCTTAAGGATGGGAGGAGAAAGAGATCCCTGTT 420
QY 421 GTGGATTTATTTTGAACGGGATTACAGATTTGAAATGAAGTCAAAAGTGAGCATTACC 480
DB 421 GTGGATTTATTTTGAACGGGATTACAGATTTGAAATGAAGTCAAAAGTGAGCATTACC 480
QY 481 AATGAGAGAGAAAACAGACGAGAAATCTGATGGCTTCAAGACATGCAACAAACAAA 540
DB 481 AATGAGAGAGAAAACAGACGAGAAATCTGATGGCTTCAAGACATGCAACAAACAAA 540
QY 541 TGGAAATCTGTGATGATGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 600
DB 541 TGGAAATCTGTGATGATGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 600
QY 601 GTGAGATCTGAGCCCTGCTGCTTAAACTGTGCTTATACCAAAATCATTTCTATTTTC 660
DB 601 GTGAGATCTGAGCCCTGCTGCTTAAACTGTGCTTATACCAAAATCATTTCTATTTTC 660

QY 661 TAACCTCAAAACAAAGCTGTGTATATCTGATCTCTACGGTTCCTTGGGCCAACA 720
DB 661 TAACCTCAAAACAAAGCTGTGTATATCTGATCTCTACGGTTCCTTGGGCCAACA 720
QY 721 TTCTCCATATATCCAGCCACACATCTTTTAATATTTAGTTCCAGATCTGTACTGTAC 780
DB 721 TTCTCCATATATCCAGCCACACATCTTTTAATATTTAGTTCCAGATCTGTACTGTAC 780
QY 781 CTTTCTACCTGTAGAAATTAACATTTACTCATTTGTTCAAA 820
DB 781 CTTTCTACCTGTAGAAATTAACATTTACTCATTTGTTCAAA 820

RESULT 2
AAD38815
ID AAD38815 standard; cDNA; 876 Bp.
AC AAD38815;
XX 23-SEP-2002 (first entry)
DT
XX
DE Human PSNA cDNA, Pro123.
XX
XX Human; prostate specific protein; PSP; prostate specific nucleic acid;
KW vaccine; transgenic; prostate cancer; gene therapy; transgenic animal;
KW PSNA; ss.
OS
XX Homo sapiens.
XX
XX W0200224718-A1.
XX
XX 28-MAR-2002.
XX
XX 19-SEP-2001; 2001WO-US29386.
XX
XX 19-SEP-2000; 2000US-233746P.
PR
XX
XX (DIAD-) DIADEXUS INC.
PA
XX
PI Sun Y, Recipon H, Cafferty R, Ali S;
XX
XX WPI; 2002-471216/50.
XX
XX
XX Novel isolated prostate specific polypeptide useful for identifying,
PT diagnosing, monitoring, staging, imaging, and treating prostate cancer
PT and non-cancerous disease states in prostate
PS
XX Claim 1; Page 179; 210pp; English.
XX
XX The invention relates to prostate specific proteins (PSP) and prostate
CC specific nucleic acids (PSNA). Sequences of the invention are useful
CC for identifying, diagnosing, monitoring, staging, imaging and treating
CC prostate cancer and non-cancerous disease states in prostate. They are
CC also useful for producing engineered prostate tissue for treatment and
CC research. The PSNA sequences are used in gene therapy and for producing
CC transgenic animals and cells. The invention is also used as vaccines.
CC
XX
XX The present sequence is human PSNA cDNA.
SQ Sequence 876 Bp; 275 A; 183 C; 207 G; 211 T; 0 other;

Query Match 100.0%; Score 820; DB 24; Length 876;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 820; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGAAGCTGGATCGAGAAAACAGAGGAGGAGATTTGTGCTGAGCCGAGGAGACAG 60
DB 30 AGAAGCTGGATCGAGAAAACAGAGGAGGAGATTTGTGCTGAGCCGAGGAGACAG 89
QY 61 GAAGATCTGATGGTGGGAAGGAGCCTGATGATACAGAGTGAGAAATAGAAAGCTGCT 120
DB 90 GAAGATCTGATGGTGGGAAGGAGCCTGATGATACAGAGTGAGAAATAGAAAGCTGCT 149

QY 121 GACCTTACCATGAGGCCACACATCTGCTGAATGAGATATTAACATCACTAGAAC 180
PI |||||||||||||||||||||||||||||||||||||||||||||||||||||||
DB 150 GACCTTACCATGAGGCCACACATCTGCTGAATGAGATATTAACATCACTAGAAC 209
QY 181 AGCAAGATGACATATATATGCTTAAGTAGTACATGTTTTTGCATTTCCAGCCCTTT 240
PI |||||||||||||||||||||||||||||||||||||||||||||||||||||||
DB 210 AGCAAGATGACATATATATGCTTAAGTAGTACATGTTTTTGCATTTCCAGCCCTTT 269
QY 241 AATATCCACACACAGAGAGACACAAAAGAACACAGATCCTGGAGAAATGCC 300
PI |||||||||||||||||||||||||||||||||||||||||||||||||||||||
DB 270 AATATCCACACACAGAGAGACACAAAAGAACACAGATCCTGGAGAAATGCC 329
QY 301 GGGCCGCATCTTGGGTCATGATGAGCCTCGCCCTGCTGGCTCCCGTTGGAGGAA 360
DB 330 GGGCCGCATCTTGGGTCATGATGAGCCTCGCCCTGCTGGCTCCCGTTGGAGGAA 389
QY 361 GGACATTTAGAAAATGATGATGTTCTTAAAGAGTGGGAGAAAACAGATCCTGTT 420
DB 390 GGACATTTAGAAAATGATGATGTTCTTAAAGAGTGGGAGAAAACAGATCCTGTT 449
QY 421 GTGGATATTTATTTGACGGGATTTACAGATTTGAATGAAGTCACAAAGTGAATACC 480
DB 450 GTGGATATTTATTTGACGGGATTTACAGATTTGAATGAAGTCACAAAGTGAATACC 509
QY 481 AATGAGAGGAAAACAGAGAGAGAAAATCTTGATGCTTCAAGACATGCAACAAACAAA 540
DB 510 AATGAGAGGAAAACAGAGAGAGAAAATCTTGATGCTTCAAGACATGCAACAAACAAA 569
QY 541 TGGAACTCTGATGATGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 600
DB 570 TGGAACTCTGATGATGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 629
QY 601 GTGAGGATCTGGCCCTGCTGCTAAAGCTGAGTCAATACCAATCTTCAATTTTC 660
DB 630 GTGAGGATCTGGCCCTGCTGCTAAAGCTGAGTCAATACCAATCTTCAATTTTC 689
QY 661 TAACCTCAAAAACAAAGCTGTTGTAATCTGATCTCTAGGTTCTTGGGCCCAACA 720
DB 690 TAACCTCAAAAACAAAGCTGTTGTAATCTGATCTCTAGGTTCTTGGGCCCAACA 749
QY 721 TTCTCATATATTCACGCCACACTCATTTTAAATATTAGTCCAGATCTGACTGAC 780
DB 750 TTCTCATATATTCACGCCACACTCATTTTAAATATTAGTCCAGATCTGACTGAC 809
QY 781 CTTTACACCTGAGAAATGAATTAACATTAATCTCTTTTGTCCAAA 820
DB 810 CTTTACACCTGAGAAATGAATTAACATTAATCTCTTTTGTCCAAA 849

RESULT 3
AAV62428
ID AAV62428 standard; cDNA: 1872 BP.
XX
AC AAV62428;
XX
DT 30-DEC-1998 (first entry)
XX
DE Prostate cancer antigen (PCA3) cDNA splice variant 2.
XX
KW Prostate cancer antigen cDNA splice variant 2; PCA3; prostatic cancer;
KM PC; ds.
XX
OS Homo sapiens.
XX
PN WO9845420-A1.
XX
PD 15-OCT-1998.
XX
PF 09-APR-1998; 98MO-CA00346.
XX
PR 10-APR-1997; 97US-0041836.
XX
PA (DIAG-) DIAGNOCURE INC.

XX
XX Bussemakers MUG;
PI
PI
DR WPI; 1998-568347/48.
XX
PT New nucleic acid encoding prostate cancer antigen 3 - for diagnosis,
PT prevention and treatment of prostatic cancer
XX
PS Claim 4; Pages 76-77; 111pp; English.
XX
XX The present sequence represents the prostate cancer antigen (PCA3)
CC cDNA splice variant 2 sequence comprising of exons 1, 3, 4a and
CC 4b of the PCA3 gene. The PCA3 cDNA splice variant 2 sequence,
CC isolated from a human primary prostatic tumor tissue cDNA library,
CC was found in approximately 65% of the cDNA clones isolated. The
CC invention claims for PCA3 cDNA variants and the proteins they encode.
CC The invention also claims for antibodies against PCA3 protein. The
CC antibodies are claimed to be useful for detecting PCA3 protein in
CC immunosassay tests, for diagnosing, assessing and prognosing of
CC prostatic cancer (PC). Antibodies, optionally coupled to a cytotoxin
CC or radioisotope, and nucleic acids antisense to PCA3 cDNA are claimed
CC to be useful for treating PC, while determining elevated levels of
CC PCA3 (as RNA or protein) is useful for detecting a predisposition
CC to development of PC, e.g. in prenatal tests. Detecting PCA3 protein
CC allows differentiation between malignant and benign prostatic disease,
CC and the level of PCA3 expression allows correlation with the grade of
CC tumour. PCA3 protein and its fragments are also claimed to be useful
CC in vaccines for preventing PC; in drug screens for identifying
CC specific (ant)agonists (potentially useful therapeutically) and for
CC studying protein-DNA interactions.
XX
SQ Sequence 1872 BP; 567 A; 389 C; 369 G; 539 T; 8 other;

Query Match 100.0%; Score 820; DB 19; Length 1872;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 820; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGAAGCTGGCATCAGAAAACAGAGGGAGATTTGTGCTGCTGACCCGAGGAGACAG 60
DB 1 AGAAGCTGGCATCAGAAAACAGAGGGAGATTTGTGCTGCTGACCCGAGGAGACAG 60
QY 61 GAAGATCTGCATGCTGGGAGGAGCCTGATGATACAGAGGTGAGAAATGAAGAGCTGCT 120
DB 61 GAAGATCTGCATGCTGGGAGGAGCCTGATGATACAGAGGTGAGAAATGAAGAGCTGCT 120
QY 121 GACTTTACCATCTGAGGCCACACATCTGCTGAATGAGATTAATTAACATCACTAGAAC 180
DB 121 GACTTTACCATCTGAGGCCACACATCTGCTGAATGAGATTAATTAACATCACTAGAAC 180
QY 181 AGCAAGATGACATATATATGCTTAAGTAGTACATGTTTTTGCATTTCCAGCCCTTT 240
DB 181 AGCAAGATGACATATATATGCTTAAGTAGTACATGTTTTTGCATTTCCAGCCCTTT 240
QY 241 AATATCCACACACAGAGAGACACAAAAGAACACAGATCCTGGAGAAATGCC 300
DB 241 AATATCCACACACAGAGAGACACAAAAGAACACAGATCCTGGAGAAATGCC 300
QY 301 GGGCCGCATCTTGGGTCATGATGAGCCTCGCCCTGCTGGCTCCCGTTGGAGGAA 360
DB 301 GGGCCGCATCTTGGGTCATGATGAGCCTCGCCCTGCTGGCTCCCGTTGGAGGAA 360
QY 361 GGACATTTAGAAAATGATGATGTTCTTAAAGAGTGGGAGAAAACAGATCCTGTT 420
DB 361 GGACATTTAGAAAATGATGATGTTCTTAAAGAGTGGGAGAAAACAGATCCTGTT 420
QY 421 GTGGATATTTATTTGACGGGATTTACAGATTTGAATGAAGTCACAAAGTGAATACC 480
DB 421 GTGGATATTTATTTGACGGGATTTACAGATTTGAATGAAGTCACAAAGTGAATACC 480
QY 481 AATGAGAGGAAAACAGAGAGAGAAAATCTTGATGCTTCAAGACATGCAACAAACAAA 540
DB 481 AATGAGAGGAAAACAGAGAGAGAAAATCTTGATGCTTCAAGACATGCAACAAACAAA 540

QY	541	TGGAACTACTGTCATGACATGAGCGACGCAAGCTGGGGAGAGATAAACAACGGGGCAGAGG	6000
Db	541	TGGAACTACTGTCATGACATGAGCGACGCAAGCTGGGGAGAGATAAACAACGGGGCAGAGG	6000
QY	601	GTCAGAGATTCGGCCCTGCTGGCCTTAACGTCGCGTTCATTAACCAATTCATTTATATATTC	6600
Db	601	GTCAGAGATTCGGCCCTGCTGGCCTTAACGTCGCGTTCATTAACCAATTCATTTATATATTC	6600
QY	661	TAAACCTCAAAAAGCTGTTGTATAATCTGATCTCTACGGTTCCTTGGGGCCCAACA	7200
Db	661	TAAACCTCAAAAAGCTGTTGTATAATCTGATCTCTACGGTTCCTTGGGGCCCAACA	7200
QY	721	TTCTCCATATATTCAGCCACACACTCAATTTTAAATTTAACTTCCCAATCTGTATCTGTGAC	7800
Db	721	TTCTCCATATATTCAGCCACACACTCAATTTTAAATTTAACTTCCCAATCTGTATCTGTGAC	7800
QY	781	CTTTCCTACACTGTAGAAATPACATTTATCTCAATTTTGTGTCAAA	8200
Db	781	CTTTCCTACACTGTAGAAATPACATTTATCTCAATTTTGTGTCAAA	8200

RESULT 4
AAA06690/c
ID AAA06690 standard; cDNA; 812 BP.

CC the present invention.
XX
SQ Sequence 812 BP; 198 A; 189 C; 169 G; 256 T; 0 other.

DE Human prostate cDNA sequence #433.
XX
KW Human; prostate cancer; ss; cytosolic; immunostimulant; tumour.
OS Homo sapiens.
XX
PN WO200173032-A2.
XX
PD 04-OCT-2001.
XX
PE 27-MAR-2001; 2001WO-US09919.
XX
PR 27-MAR-2000; 2000US-0536857.
PR 09-MAY-2000; 2000US-0568100.
PR 12-MAY-2000; 2000US-0570737.
PR 13-JUN-2000; 2000US-0593793.
PR 27-JUN-2000; 2000US-0605783.
PR 10-AUG-2000; 2000US-0636215.
PR 29-AUG-2000; 2000US-0651236.
PR 06-SEP-2000; 2000US-0657279.
PR 02-OCT-2000; 2000US-0679426.
PR 10-OCT-2000; 2000US-0685166.
XX
PA (CORI-) CORIXA CORP.
XX
PI Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Kalos MD;
PI Fanger GR, Retter MW, Stolk JA, Day CH, Vedyick TS, Carter D;
PI Li SX, Wang A, Skelky YAM, Hepler WT, Henderson RA;
XX
DR WPI: 2001-639232/73.
XX
PT New human prostate-specific polypeptides and polynucleotides useful for
PT the diagnosis and treatment of cancer, especially prostate cancer -
XX
PS Claim 1: Page 386-387; 579pp; English.
XX
XX The invention relates to isolated prostate-specific
CC polynucleotides, polypeptides, fusion proteins of the polypeptides,
CC antibodies raised against the polypeptides (or antigenic epitopes
CC derived from them) and antigen-presenting cells expressing the
CC polypeptides. The antibodies are useful for detecting the presence of
CC cancer, especially prostate cancer. The polypeptides, polynucleotides and
CC T cells specific for a tumour protein, and for inhibiting the development
CC of cancer especially prostate cancer. Compositions comprising the
CC polynucleotide and/or polypeptide are useful for stimulating an immune
CC response, and for treating cancer. The oligonucleotide is useful for
CC detecting cancer. The present sequence is a prostate specific
CC polynucleotide of the invention.
XX
SQ Sequence 812 BP; 198 A; 189 G; 169 C; 256 T; 0 other;
Query Match 99.0%; Score 812; DB 22; Length 812;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 812; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 6 CTGGCATTCAGAAAAAGAGGGGAGATTGTGCTGCGTGCAGCCGAGAGAGACCAAGAA 65
Db 812 CTGGCATTCAGAAAAAGAGGGGAGATTGTGCTGCGTGCAGCCGAGAGAGACCAAGAA 753
QY 66 TCTGCATGTGGGAAGGACCTGATGTACAGAGGTGAGAAATTAAGAAAGCTGCTACTT 125
Db 752 TCTGCATGTGGGAAGGACCTGATGTACAGAGGTGAGAAATTAAGAAAGCTGCTACTT 693
QY 126 TACCATCTGAGGCCACACATCTGCTGMAATGAGATTAATTAACATCATTAGAAACAGCAA 185
Db 692 TACCATCTGAGGCCACACATCTGCTGMAATGAGATTAATTAACATCATTAGAAACAGCAA 633
QY 186 GATGACAAATATATGCTCTAAGTAGACATGTTTTGGCATTTCAGCCCTTTAAATA 245
Db 632 GATGACAAATATATGCTCTAAGTAGACATGTTTTGGCATTTCAGCCCTTTAAATA 573
QY 246 TCCACACACAGAGAGCAAAAGAGACACAGACATCCCTGGGAGAAATGCCCGCGC 305

Db 572 TCCACACACAGAGAGCAAAAGAGACACAGAGATCCCTGGGAGAAATGCCCGCGC 513
QY 306 CCATCTGGGTCATGATGATAGCCCTGCGCTGCTGCTCCGCTTGTAGAGGAAGACA 365
Db 512 CCATCTGGGTCATGATGATAGCCCTGCGCTGCTGCTCCGCTTGTAGAGGAAGACA 453
QY 366 TTAGAAAATGAATGATGATGCTTAAAGATGAGGACAGAAACGATCCTGTTGTGA 425
Db 452 TTAGAAAATGAATGATGATGCTTAAAGATGAGGACAGAAACGATCCTGTTGTGA 393
QY 426 TATTTATTTGAACGGGATTACAGATTGMAATGAAGTCACAAAGTAGCATTAACAAATGA 485
Db 392 TATTTATTTGAACGGGATTACAGATTGMAATGAAGTCACAAAGTAGCATTAACAAATGA 333
QY 486 GAGGAAAACAGACGAGAAAATCTTGATGCTTCACAGACATGCAACAAACAAATGAA 545
Db 332 GAGGAAAACAGACGAGAAAATCTTGATGCTTCACAGACATGCAACAAACAAATGAA 273
QY 546 TACTGTGATGACATGAGCGCAGCCAGCTGGGGGAGAGATACACGCGGACAGAGGTCA 605
Db 272 TACTGTGATGACATGAGCGCAGCCAGCTGGGGGAGAGATACACGCGGACAGAGGTCA 213
QY 606 GATTCGGCCCTGCTGCTTAACTGCTGCTTAACTAAACCAATCATTTATTTCTAAC 665
Db 212 GATTCGGCCCTGCTGCTTAACTGCTGCTTAACTAAACCAATCATTTATTTCTAAC 153
QY 666 CTCAAAACAAAGCTGTTGAATATCTGATCTCTAGCGTTCTTCTGGGCCCAACATTC 725
Db 152 CTCAAAACAAAGCTGTTGAATATCTGATCTCTAGCGTTCTTCTGGGCCCAACATTC 93
QY 726 CATATATCCAGCACACCTGATTTTAATTTAGTCCAGATCTGTACTGACCTTTC 785
Db 92 CATATATCCAGCACACCTGATTTTAATTTAGTCCAGATCTGTACTGACCTTTC 33
QY 786 TACACTGTAGAAATTAACATTACTATTTGTTTC 817
Db 32 TACACTGTAGAAATTAACATTACTATTTGTTTC 1
RESULT 6
AAH93806/c
ID AAH93806 standard; cDNA: 812 BP.
AC AAH93806;
XX
DT 04-OCT-2001 (first entry)
XX
DE Human prostate-specific cDNA sequence P710P #4.
XX
KW Human; prostate cancer; prostate-specific; diagnosis; vaccine;
KW cytosolic; gene therapy; metastasis; ss.
XX
OS Homo sapiens.
XX
PN WO200151633-A2.
XX
PD 19-JUL-2001.
XX
PF 16-JAN-2001; 2001WO-US01574.
XX
PR 14-JAN-2000; 2000US-0483672.
XX
PA (CORI-) CORIXA CORP.
XX
PI Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Reed SG;
PI Kalos MD, Fanger GR, Day CH, Retter MW, Stolk JA, Skelky YAM;
PI Wang A, Meagher MJ;
XX
DR WPI: 2001-425873/45.
XX
PT New polynucleotide encoding a prostate-specific protein, for
PT diagnosing, monitoring and treating prostate cancer in a patient and

for use in vaccines -
Claim 1; Page 385; 543pp; English.

The present invention describes polynucleotide sequences (I) which encode prostate-specific proteins (II). (I) and (II) have cytostatic activity, and can be used in vaccine production and gene therapy. (I), (II), antibodies to (I), fusion proteins comprising (I), and isolated T cells prepared using (I) or (II) are used to treat cancer in a patient. (I) and the antibodies are also used in the detection of cancer in a patient. The cancer that is diagnosed or treated is particularly prostate cancer. (I) and (II) can be used in vaccines. The antibodies or (I) can be used for monitoring the progression of cancer in a patient. (I) and (II) can also be used to improve diagnostic and therapeutic methods for prostate cancer. They can indicate the level of metastasis as well as the prostate volume. AAH93357 to AAH93944 and AAH01115 to AAH01318 represent polynucleotide and amino acid sequences used in the exemplification of the present invention.

Sequence 812 BP; 198 A; 189 C; 169 G; 256 T; 0 other;

Query Match 99.0%; Score 812; DB 22; Length 812;

Best Local Similarity 100.0%; Pred. No. 0; Matches 812; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 CTGCGATCAGAAAAACAGAGGGGAGATTGTGTGGCTGCACCCGAGGAGACCAAGAGA 65
DB 812 CTGCGATCAGAAAAACAGAGGGGAGATTGTGTGGCTGCACCCGAGGAGACCAAGAGA 753
QY 66 TCTGCATGTGGGAGAGACCTGATGATACAGAGGTGAAGAAATGAAGAGCTGCTGACTT 125
DB 752 TCTGCATGTGGGAGAGACCTGATGATACAGAGGTGAAGAAATGAAGAGCTGCTGACTT 693
QY 126 TACCATGTAGGCCACACATCTGCTGAATGAGATATTAATACATCAGTACAGCA 185
DB 692 TACCATGTAGGCCACACATCTGCTGAATGAGATATTAATACATCAGTACAGCA 633
QY 186 GATGACATATATATGCTAAGTAGTACATGTTTGGACATTTCCAGCCCTTTAATA 245
DB 632 GATGACATATATATGCTAAGTAGTACATGTTTGGACATTTCCAGCCCTTTAATA 573
QY 246 TCCACACACAGGAGACCAAAAGAGAGACAGAGATCCCTGGGAGAAATGCCGCGC 305
DB 572 TCCACACACAGGAGACCAAAAGAGAGACAGAGATCCCTGGGAGAAATGCCGCGC 513
QY 306 CCATCTTGGGTCATCGATGAGCCTCGCCCTGCTGCTGCCCTTGTGAGGAGAGACA 365
DB 512 CCATCTTGGGTCATCGATGAGCCTCGCCCTGCTGCTGCCCTTGTGAGGAGAGACA 453
QY 366 TTAGAAATGATGATGTGTTCTTAAAGATGGGAGAGAAACAGATCCTGTGGA 425
DB 452 TTAGAAATGATGATGTGTTCTTAAAGATGGGAGAGAAACAGATCCTGTGGA 393
QY 426 TATTTATTTGAACGGATTAACAGATTTGAATGAAGTACAAAGTGAAGTATACCAATGA 485
DB 392 TATTTATTTGAACGGATTAACAGATTTGAATGAAGTACAAAGTGAAGTATACCAATGA 333
QY 486 GAGAGAAACAGAGCAAGAAATCTTGATGCGCTTCAACAAGATGCAACAACAAATGGA 545
DB 332 GAGAGAAACAGAGCAAGAAATCTTGATGCGCTTCAACAAGATGCAACAACAAATGGA 273
QY 546 TACGTGATGATGATGAGGAGCCAAAGCTGGGAGAGATTAACACCGGGGAGAGGTCAG 605
DB 272 TACGTGATGATGATGAGGAGCCAAAGCTGGGAGAGATTAACACCGGGGAGAGGTCAG 213
QY 606 GATTCTGGCCCTGCTGCTAAACTGTGCTTCAATACCAATCTTCAATATTTCTAAC 665
DB 212 GATTCTGGCCCTGCTGCTAAACTGTGCTTCAATACCAATCTTCAATATTTCTAAC 153
QY 666 CTCAGAAACAAAGCTGTGTAATATCTGATCTCAAGGTTCTTCTGGGCCCAACATCTTC 725
DB 152 CTCAGAAACAAAGCTGTGTAATATCTGATCTCAAGGTTCTTCTGGGCCCAACATCTTC 93

QY 726 CATATATCCAGCCACACTCATTTTAAATATTTAGTCCAGACTGTGACTGTGACCTTTC 785
DB 92 CATATATCCAGCCACACTCATTTTAAATATTTAGTCCAGACTGTGACTGTGACCTTTC 33
QY 786 TACACTGTAGAAATACATTAATCTTCTGTTTC 817
DB 32 TACACTGTAGAAATACATTAATCTTCTGTTTC 1

RESULT 7

AAH85120/C
ID AAH85120 standard; CDNA; 812 BP.

AC AAH85120;

DT 25-SEP-2001 (first entry)

XX Human prostate-specific cDNA sequence P710P #4.

XX Human; prostate cancer; therapy; diagnosis; cat eye syndrome;

XX chromosome 22q11.2; prostate-specific protein; chromosome 1;

XX prostate specific antigen; PSA; ss.

XX Homo sapiens.

XX WO200134802-A2.

XX 17-MAY-2001.

XX 09-NOV-2000; 2000WO-US30904.

XX 12-NOV-1999; 99US-0439313.

XX 18-NOV-1999; 99US-0443686.

XX (CORI-) CORIXA CORP.

XX Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Reed SG;

XX Kaios MD, Retter KM, Stolk JA, Day CH, Skeiky IAW, Wang A;

XX WPI: 2001-308785/32.

XX Isolated polypeptide comprising at least an immunogenic portion of a

XX prostate-specific protein, useful in the diagnosis and therapy of a

XX prostate cancer -

XX Claim 5; Page 284-285; 325pp; English.

XX The present invention describes an isolated polypeptide (PI) comprising

XX at least an immunogenic portion of a prostate-specific protein, or its

XX variant. Also described are polynucleotides (NI) encoding (PI). (PI) and

XX (NI) have cytostatic activity and can be used in vaccine production.

XX The polypeptides, nucleic acids and antibodies from the present

XX invention are useful in the diagnosis and therapy of prostate cancer.

XX Prostate specific genes P704P, P712P, P774P, P775P and B305D are located

XX in a genomic region on chromosome 22q11.2 known as the Cat Eye syndrome

XX region. Prostate specific antigen (PSA) P5015 was located on

XX chromosome 1. AAH84671 to AAH85143 and AAH99000 to AAH99077 represent

XX polynucleotide and polypeptide sequences used in the exemplification

XX of the present invention.

Sequence 812 BP; 198 A; 189 C; 169 G; 256 T; 0 other;

Query Match 99.0%; Score 812; DB 22; Length 812;

Best Local Similarity 100.0%; Pred. No. 0; Matches 812; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 CTGCGATCAGAAAAACAGAGGGGAGATTGTGTGGCTGCACCCGAGGAGACCAAGAGA 65
DB 812 CTGCGATCAGAAAAACAGAGGGGAGATTGTGTGGCTGCACCCGAGGAGACCAAGAGA 753
QY 66 TCTGCATGTGGGAGAGACCTGATGATACAGAGGTGAAGAAATGAAGAGCTGCTGACTT 125
DB 752 TCTGCATGTGGGAGAGACCTGATGATACAGAGGTGAAGAAATGAAGAGCTGCTGACTT 693

QY 126 TACCATCTGAGGCCACACATCTGTAAGATGAGATTAATTAACATCTAGTAAGACGAA 185
 DB 692 TACCATCTGAGGCCACACATCTGTAAGATGAGATTAATTAACATCTAGTAAGACGAA 633
 QY 186 GATGCAATATATATCTTAAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGAT 245
 DB 632 GATGCAATATATATCTTAAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGAT 573
 QY 246 TCCACACACACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 305
 DB 572 TCCACACACACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 513
 QY 306 CCATCTGGGTCATGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 365
 DB 512 CCATCTGGGTCATGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 453
 QY 366 TTGAGAAATGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 425
 DB 452 TTGAGAAATGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 393
 QY 426 TATTTATTTGAAGGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 485
 DB 392 TATTTATTTGAAGGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 333
 QY 486 GAGGAAACACAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 545
 DB 332 GAGGAAACACAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 273
 QY 546 TACTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 605
 DB 272 TACTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 213
 QY 606 GATTCGTGCGCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 665
 DB 212 GATTCGTGCGCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 153
 QY 666 CTCAAAACAAAGCTGTGTAATATGATGATGATGATGATGATGATGATGATGATGATGATGAT 725
 DB 152 CTCAAAACAAAGCTGTGTAATATGATGATGATGATGATGATGATGATGATGATGATGATGAT 93
 QY 726 CATATATCCAGCCACATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 785
 DB 92 CATATATCCAGCCACATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 33
 QY 786 TACACTGTAGATTAACATTAACATTAACATTAACATTAACATTAACATTAACATTAACAT 817
 DB 32 TACACTGTAGATTAACATTAACATTAACATTAACATTAACATTAACATTAACATTAACAT 1
 RESULT 8
 AAH02871/C
 ID AAH02871 standard: cDNA, 812 BP.
 AC AAH02871;
 DF 14-JUN-2001 (first entry)
 DE Prostate tumour antigen cDNA sequence for P710P #4.
 XX Human; prostate tumour antigen; prostate tumour; therapy; diagnosis;
 KW prostate cancer; immunogenic; cytostatic; vaccine; ss.
 OS Homo sapiens.
 XX WO200125272-A2.
 XX 12-APR-2001.
 PD 04-OCT-2000; 2000MO-US27464.
 PF 04-OCT-1999; 9905-0157455.
 PR
 XX

PA (CORI-) CORIXA CORP.
 XX Xu J, Skelky YAW, Reed SC, Cheever MA;
 XX WPI: 2001-245062/25.
 DR prostate specific protein and its encoding polynucleotide, useful for
 PT the treatment and diagnosis of prostate cancer -
 PT
 XX
 PS Claim 4; Page 267; 276pp; English.
 CC The present invention describes an isolated polypeptide (I) comprising
 CC at least an immunogenic portion of a prostate tumour antigen protein or
 CC its variant. (I) have cytostatic activity and can be used in vaccine
 CC production. (I) prostate tumour antigen polynucleotides, an antigen
 CC presenting cell (APC e.g. a dendritic cell) that expresses (I), and a
 CC pharmaceutical composition containing (I) are useful for inhibiting the
 CC development of cancer in a patient. Antibodies specific for prostate
 CC polynucleotide that encodes a prostate specific protein are useful
 CC for detecting the presence or absence of a cancer or monitoring the
 CC progression the progression of a cancer, especially prostate cancer.
 CC AAH02422 to AAH2872, AAB74798 to AAB74821 and AAB74830 are sequences
 CC used in the exemplification of the present invention.
 XX
 SQ Sequence 812 BP; 198 A; 189 C; 169 G; 256 T; 0 other;
 Query Match 99.0%; Score 812; DB 22; Length 812;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 812; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 6 CTGCATCGAAGAAACAGAGGAGGAGATTTGTGCTGCGAGCCGAGGAGACAGGAGAA 65
 DB 812 CTGCATCGAAGAAACAGAGGAGGAGATTTGTGCTGCGAGCCGAGGAGACAGGAGAA 753
 QY 66 TCTGCATGCTGGAAGAGACCTGATGATACAGAGTGAGAAATAGAAAGCTGCTGACTT 125
 DB 752 TCTGCATGCTGGAAGAGACCTGATGATACAGAGTGAGAAATAGAAAGCTGCTGACTT 693
 QY 126 TACCATCTGAGGCCACACATCTGTAAGATGAGATGAGATGAGATGAGATGAGATGAGAT 185
 DB 692 TACCATCTGAGGCCACACATCTGTAAGATGAGATGAGATGAGATGAGATGAGATGAGAT 633
 QY 186 GATGCAATATATATCTTAAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGAT 245
 DB 632 GATGCAATATATATCTTAAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGAT 573
 QY 246 TCCACACACACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 305
 DB 572 TCCACACACACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 513
 QY 306 CCATCTGGGTCATGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 365
 DB 512 CCATCTGGGTCATGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 453
 QY 366 TTGAGAAATGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 425
 DB 452 TTGAGAAATGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 393
 QY 426 TATTTATTTGAAGGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 485
 DB 392 TATTTATTTGAAGGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 333
 QY 486 GAGGAAACACAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 545
 DB 332 GAGGAAACACAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 273
 QY 546 TACTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 605
 DB 272 TACTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 213
 QY 606 GATTCGTGCGCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 665

DR WPI; 2000-171268/15.
XX New polypeptide useful for treating and diagnosing prostate cancer
PT comprises an immunogenic portion of prostate tumor protein -
XX
PS Claim 1: Page 260-261; 263pp; English.
XX
The present invention describes isolated polypeptides, comprising an
CC immunogenic portion of a prostate tumor protein (PTP). The polypeptides
CC and polynucleotides encoding them have cytostatic activity and can be
CC used in vaccines and in gene therapy. The polypeptides and
CC polynucleotides encoding them, antigen presenting cells which express
CC the polypeptides, antibodies against the polypeptides and vaccines
CC comprising them can be used for inhibiting the development of prostate
CC cancer in a patient. The polypeptides can be used to generate antibodies
CC or anti-idiotypic antibodies for passive immuno therapy. A portion of
CC the polynucleotides encoding the polypeptides can be used as a probe or
CC to modulate the expression of the polypeptides. AA06241 to AA06691 and
CC AY82000 to AY82020 represent sequences used in the exemplification of
CC the present invention.
XX
XX Sequence 2229 BP; 654 A; 447 C; 481 G; 647 T; 0 other;
SQ
Query Match 88.3%; Score 724; DB 21; Length 2229;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 724; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 97 AGGTGGAATAAGAAAGCTGCTGCTTACCATCTGAGGCCACACATCTGCTGAATG 156
DB 1776 AGGTGGAATAAGAAAGCTGCTGCTTACCATCTGAGGCCACACATCTGCTGAATG 1717
QY 157 GAGATATTAACATCACTGAGAAACAGCAAGATGACATATTAATGCTAGTAGTACATG 216
DB 1716 GAGATATTAACATCACTGAGAAACAGCAAGATGACATATTAATGCTAGTAGTACATG 1657
QY 217 TTTTTCACATTTCCAGCCCTTTAATATCCACACACAGGAGACACAAAAGGAAGA 276
DB 1656 TTTTTCACATTTCCAGCCCTTTAATATCCACACACAGGAGACACAAAAGGAAGA 1597
QY 277 CAGAGATCCCTGGGAGAAATGCCCGCCCATCTGGTGCATGATGAGCTGCCCTG 336
DB 1596 CAGAGATCCCTGGGAGAAATGCCCGCCCATCTGGTGCATGATGAGCTGCCCTG 1537
QY 337 TGCTTGTCCTCCGCTTGAAGGAGACATTAAGAAATGATGATGCTTCTTAAGG 396
DB 1536 TGCTTGTCCTCCGCTTGAAGGAGACATTAAGAAATGATGATGCTTCTTAAGG 1477
QY 397 ATGGGCGAGAAAACAGATCCTGTTGATATTTTGAACGGGATTAAGATTTGAA 456
DB 1476 ATGGGCGAGAAAACAGATCCTGTTGATATTTTGAACGGGATTAAGATTTGAA 1417
QY 457 TGAAGTCACAAAGTGCATTTACCAATGAGAGAAAACAGCAAAATCTTGATGCT 516
DB 1416 TGAAGTCACAAAGTGCATTTACCAATGAGAGAAAACAGCAAAATCTTGATGCT 1357
QY 517 TCACAAGACATGCAACAAACAAATGATGATGATGATGATGATGATGATGATGATG 576
DB 1356 TCACAAGACATGCAACAAACAAATGATGATGATGATGATGATGATGATGATGATG 1297
QY 577 GAGGAGATAACCAAGGGGAGAGAGTCAAGATTTGCGCTGCTTAACGTGCTG 636
DB 1296 GAGGAGATAACCAAGGGGAGAGAGTCAAGATTTGCGCTGCTTAACGTGCTG 1237
QY 637 CATACCAAAATCTTTCAATATTTCTAACCCTCAAAACAAAGCTGTTGTAATATCTGATCT 696
DB 1236 CATACCAAAATCTTTCAATATTTCTAACCCTCAAAACAAAGCTGTTGTAATATCTGATCT 1177
QY 697 CTACGGTTCCTTGCGCCCAACATTCATATATACAGCCACACATTTTAATAT 756
DB 1176 CTACGGTTCCTTGCGCCCAACATTCATATATACAGCCACACATTTTAATAT 1117
QY 757 TAGTCCAGATCTGACTGTGACCTTCTACACTGATGAATTAACATTTACTATTTGTT 816
DB 1117 TAGTCCAGATCTGACTGTGACCTTCTACACTGATGAATTAACATTTACTATTTGTT 816

DB 1116 TAGTCCAGATCTGACTGTGACCTTCTACACTGATGAATTAACATTTACTATTTGTT 1057
QY 817 CAAA 820
DB 1056 CAAA 1053
RESULT 13
AAS63897/C
ID AAS63897 standard; cDNA; 2229 BP.
XX
XX AAS63897;
AC
XX
XX 29-JAN-2002 (first entry)
DE Human prostate cDNA sequence #431.
XX
XX Human; prostate cancer; ss; cytostatic; immunostimulant; tumour.
XX
XX Homo sapiens.
OS
XX
XX WO200173032-A2.
PN
XX
PD 04-OCT-2001.
PD
XX
PF 27-MAR-2001; 2001MO-US09919.
XX
PR 27-MAR-2000; 2000US-0536857.
PR 09-MAY-2000; 2000US-0568100.
PR 12-MAY-2000; 2000US-0570737.
PR 13-JUN-2000; 2000US-0593793.
PR 27-JUN-2000; 2000US-0605783.
PR 10-AUG-2000; 2000US-0636215.
PR 29-AUG-2000; 2000US-0651236.
PR 06-SEP-2000; 2000US-0657279.
PR 02-OCT-2000; 2000US-0679426.
PR 10-OCT-2000; 2000US-0685166.
XX
XX (CORI-) CORIXA CORP.
PI Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Kalos MD;
PI Fanger GR, Retter MW, Stolk JA, Day CH, Vedyvick TS, Carter D;
PI Li SX, Wang A, Skelky YAM, Hepler WT, Henderson RA;
XX
XX WPI; 2001-639232/73.
PT New human prostate-specific polypeptides and polynucleotides useful for
PT the diagnosis and treatment of cancer, especially prostate cancer -
XX
XX
PS Claim 1: Page 385; 579pp; English.
XX
XX The invention relates to isolated prostate-specific
XX polynucleotides, polypeptides, fusion proteins of the polypeptides,
XX antibodies raised against the polypeptides (or antigenic epitopes
XX derived from them) and antigen-presenting cells expressing the
XX polypeptides. The antibodies are useful for detecting the presence of
XX cancer, especially prostate cancer. The polypeptides, polynucleotides and
XX the antigen-presenting cells are useful for stimulating and/or expanding
XX T cells specific for a tumour protein, and for inhibiting the development
XX of cancer especially prostate cancer. Compositions comprising the
XX polynucleotide and/or polypeptide are useful for stimulating an immune
XX response, and for treating cancer. The oligonucleotide is useful for
XX detecting cancer. The present sequence is a prostate specific
XX polynucleotide of the invention.
XX
SQ Sequence 2229 BP; 654 A; 447 C; 481 G; 647 T; 0 other;
Query Match 88.3%; Score 724; DB 22; Length 2229;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 724; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 97 AGGTGGAATAAGAAAGCTGCTGCTTACCATCTGAGGCCACACATCTGCTGAATG 156
DB 1117 AGGTGGAATAAGAAAGCTGCTGCTTACCATCTGAGGCCACACATCTGCTGAATG 156

Db 1776 AGGTGAGAAATTAAGAAAGGCTGCTGACTTTTACCATCTGAGGCCACACATCTGCTGAATG 1717
Qy 157 GAGATTAATTAACATCACTAGAAACAGCAGATGACAAATATATGCTTAAGTATGACATG 216
Db 1716 GAGATTAATTAACATCACTAGAAACAGCAGATGACAAATATATGCTTAAGTATGACATG 1657
Qy 217 TTTTGGACATTTCCAGCCCCCTTTAATATATCCACACACACAGAAAGCAAAAGAGACA 276
Db 1656 TTTTGGACATTTCCAGCCCCCTTTAATATATCCACACACACAGAAAGCAAAAGAGACA 1597
Qy 277 CAGAGATCCCTGGGAGAAATGCCGGGCCCATCTGTGGTGCATGATGATGAGCTGCCCTG 336
Db 1596 CAGAGATCCCTGGGAGAAATGCCGGGCCCATCTGTGGTGCATGATGATGAGCTGCCCTG 1537
Qy 337 TGCCGTGCTCCGCTTGTGAGGAGAGACATTAAGAAATGAATGATGTCTCTTAAGG 396
Db 1536 TGCCGTGCTCCGCTTGTGAGGAGAGACATTAAGAAATGAATGATGTCTCTTAAGG 1477
Qy 397 ATGGGCGAGAAACAGATCCTGTGTGGATTTTATTTGAACGGGATTTACAGATTTGAAA 456
Db 1476 ATGGGCGAGAAACAGATCCTGTGTGGATTTTATTTGAACGGGATTTACAGATTTGAAA 1417
Qy 457 TGAAGTCACAAAGTACATTAACATGAGAGGAAACAGAGGAAATGCTTGAATGCT 516
Db 1416 TGAAGTCACAAAGTACATTAACATGAGAGGAAACAGAGGAAATGCTTGAATGCT 1357
Qy 517 TCACAGACATGCAACAAACAAATGGAATGATGTGATGACATGAGCAGCCAAAGCTGG 576
Db 1356 TCACAGACATGCAACAAACAAATGGAATGATGTGATGACATGAGCAGCCAAAGCTGG 1297
Qy 577 GAGAGATTAACACAGGCGGAGAGGCTCAGATTTGCGCCCTGCTCTTAACTGCTGCTT 636
Db 1296 GAGAGATTAACACAGGCGGAGAGGCTCAGATTTGCGCCCTGCTCTTAACTGCTGCTT 1237
Qy 637 CATTAACAAATCATTTATATTTCTAACCCTCAAAACAAAGCTGTGTAATATGATGATCT 696
Db 1236 CATTAACAAATCATTTATATTTCTAACCCTCAAAACAAAGCTGTGTAATATGATGATCT 1177
Qy 697 CTACGGTTCCTTGTGGGCCCAACATCTCATATATATCCAGCCACATCATTTTAATAT 756
Db 1176 CTACGGTTCCTTGTGGGCCCAACATCTCATATATATCCAGCCACATCATTTTAATAT 1117
Qy 757 TAGTCCCAATCTGTACTGTGACCTTTCTACCTGTGAATTAACATTTACTCATTTTGT 816
Db 1116 TAGTCCCAATCTGTACTGTGACCTTTCTACCTGTGAATTAACATTTACTCATTTTGT 1057
Qy 817 CAAA 820
Db 1056 CAAA 1053
RESULT 14
AAH93804/C
ID AAH93804 standard; cdna; 2229 BP.
AC AAH93804;
XX
XX 04-OCT-2001 (first entry)
DE Human prostate-specific cDNA sequence p710p #2.
XX
XX Human; prostate cancer; prostate-specific; diagnosis; vaccine;
KW cytosolic; gene therapy; metastasis; ss.
XX
XX Homo sapiens.
OS
PN W0200151633-A2.
XX
XX 19-JUL-2001.
PD
XX 16-JAN-2001; 2001WO-US01574.
PF
XX 14-JAN-2000; 2000US-0483672.
PR

XX
PA (CORI-) CORIXA CORP.
XX
PI Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Reed SG,
PI Kalos MD, Fanger GR, Day CH, Retter MW, Stolk JA, Skeiky YAW,
PI Wang A, Meagher MJ;
XX
DR WPI: 2001-425873/45.
XX
PT New polynucleotide encoding a prostate-specific protein, for
PT diagnosing, monitoring and treating prostate cancer in a patient and
PT for use in vaccines -
XX
XX
PS Claim 1; Page 383-384; 543pp; English.
XX
CC The present invention describes polynucleotide sequences (I) which encode
CC prostate-specific proteins (II). (I) and (II) have cytosolic activity,
CC and can be used in vaccine production and gene therapy. (I), (II),
CC antibodies to (II), fusion proteins comprising (II), and isolated
CC T cells prepared using (I) or (II) are used to treat cancer in a patient.
CC (I) and the antibodies are also used in the detection of cancer in a
CC patient. The cancer that is diagnosed or treated is particularly
CC prostate cancer. (I) and (II) can be used in vaccines. The antibodies or
CC (I) can be used for monitoring the progression of cancer in a patient.
CC (I) and (II) can also be used to improve diagnostic and therapeutic
CC methods for prostate cancer. They can indicate the level of metastasis
CC as well as the prostate volume. AAH93357 to AAH93944 and AAH01115 to
CC AAH01318 represent polynucleotide and amino acid sequences used in the
CC exemplification of the present invention.
XX
S0 Sequence 2229 BP; 654 A; 447 C; 481 G; 647 T; 0 other:
Query Match 88.3%; Score 724; DB 22; Length 2229;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 724; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 97 AGGTGAGAAATTAAGAAAGGCTGCTGACTTTTACCATCTGAGGCCACACATCTGCTGAATG 156
Db 1776 AGGTGAGAAATTAAGAAAGGCTGCTGACTTTTACCATCTGAGGCCACACATCTGCTGAATG 1717
Qy 157 GAGATTAATTAACATCACTAGAAACAGCAGATGACAAATATATGCTTAAGTATGACATG 216
Db 1716 GAGATTAATTAACATCACTAGAAACAGCAGATGACAAATATATGCTTAAGTATGACATG 1657
Qy 217 TTTTGGACATTTCCAGCCCCCTTTAATATATCCACACACAGAAAGCAAAAGAGACA 276
Db 1656 TTTTGGACATTTCCAGCCCCCTTTAATATATCCACACACAGAAAGCAAAAGAGACA 1597
Qy 277 CAGAGATCCCTGGGAGAAATGCCGGGCCCATCTGTGGTGCATGATGATGAGCTGCCCTG 336
Db 1596 CAGAGATCCCTGGGAGAAATGCCGGGCCCATCTGTGGTGCATGATGATGAGCTGCCCTG 1537
Qy 337 TGCCGTGCTCCGCTTGTGAGGAGAGACATTAAGAAATGAATGATGTCTCTTAAGG 396
Db 1536 TGCCGTGCTCCGCTTGTGAGGAGAGACATTAAGAAATGAATGATGTCTCTTAAGG 1477
Qy 397 ATGGGCGAGAAACAGATCCTGTGTGGATTTTATTTGAACGGGATTTACAGATTTGAAA 456
Db 1476 ATGGGCGAGAAACAGATCCTGTGTGGATTTTATTTGAACGGGATTTACAGATTTGAAA 1417
Qy 457 TGAAGTCACAAAGTACATTAACATGAGAGGAAACAGAGGAAATGCTTGAATGCT 516
Db 1416 TGAAGTCACAAAGTACATTAACATGAGAGGAAACAGAGGAAATGCTTGAATGCT 1357
Qy 517 TCACAGACATGCAACAAACAAATGGAATGATGTGATGACATGAGCAGCCAAAGCTGG 576
Db 1356 TCACAGACATGCAACAAACAAATGGAATGATGTGATGACATGAGCAGCCAAAGCTGG 1297
Qy 577 GAGGAGATTAACACAGGCGGAGAGGCTCAGATTTGCGCCCTGCTCTTAACTGCTGCTT 636
Db 1296 GAGGAGATTAACACAGGCGGAGAGGCTCAGATTTGCGCCCTGCTCTTAACTGCTGCTT 1237
Qy 637 CATTAACAAATCATTTATATTTCTAACCCTCAAAACAAAGCTGTGTAATATGATGATCT 696


```

Db      1236 CATTAACCAATATTCATATTTCTTAACCTCAAAACAAAGCTGTGTAATATCTATCT 1177
QY      697 CTACGGTTCCTTGCGGCCCAACATTCCTCCATATATCCAGCACACTCTATTTTAATAT 756
Db      1176 CTACGGTTCCTTGCGGCCCAACATTCCTCCATATATCCAGCACACTCTATTTTAATAT 1117
QY      757 TAGTCCCAAGATCTGTACTGTGACCTTTCTACACTGTAGATTAACATTTACTCATTTGTT 816
Db      1116 TAGTCCCAAGATCTGTACTGTGACCTTTCTACACTGTAGATTAACATTTACTCATTTGTT 1057
QY      817 CAAA 820
Db      1056 CAAA 1053

RESULT 15
AAH85118/c
ID      AAH85118 standard; cDNA; 2229 BP.
XX
XX      AAH85118;
XX
XX      25-SEP-2001 (first entry)
XX
XX      Human prostate-specific cDNA sequence P710P #2.
DE
XX      Human; prostate cancer; therapy; diagnosis; cat eye syndrome;
KM      chromosome 22q11.2; prostate-specific protein; chromosome 1;
KM      prostate specific antigen; PSA; ss.
XX
XX      Homo sapiens.
OS
XX      MO200134802-A2.
PN
XX      17-MAY-2001.
PD
XX
XX      09-NOV-2000; 2000MO-US30904.
PF
XX      12-NOV-1999; 99US-0439313.
PR
XX      18-NOV-1999; 99US-0443686.
XX
XX      (CORI-) CORIXA CORP.
PA
PI      Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Reed SG;
PI      Kalos MD, Retter MW, Stolk JA, Day CH, Skeiky YAM, Wang A;
DR      WPI; 2001-308785/32.
XX
XX      Isolated polypeptide comprising at least an immunogenic portion of a
PT      prostate-specific protein, useful in the diagnosis and therapy of
PT      prostate cancer -
XX
XX      Claim 5; Page 283-284; 325pp; English.
PS
XX      The present invention describes an isolated polypeptide (P1) comprising
CC      at least an immunogenic portion of a prostate-specific protein, or its
CC      variant. Also described are polynucleotides (N1) encoding (P1). (P1) and
CC      (N1) have cytostatic activity and can be used in vaccine production.
CC      The polypeptides, nucleic acids and antibodies from the present
CC      invention are useful in the diagnosis and therapy of prostate cancer.
CC      Prostate specific genes P704P, P712P, P774P, P775P and B305D are located
CC      in a genomic region on chromosome 22q11.2 known as the Cat Eye Syndrome
CC      region. Prostate specific antigen (PSA) P501S was located on
CC      chromosome 1. AAH84671 to AAH85143 and AAG99000 to AAG99077 represent
CC      polynucleotide and polypeptide sequences used in the exemplification
CC      of the present invention.
XX
XX      Sequence 2229 BP; 654 A; 447 C; 481 G; 647 T; 0 other:
SQ

```

```

Query Match      88.3%; Score 724; DB 22; Length 2229;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 724; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      97 AGGTGAATAATAGAAAGGCTGCTGACTTTACCATCTGAGGCCACATCTGCTGAATG 156
Db      1776 AGGTGAGAAATAGAAAGGCTGCTGACTTTACCATCTGAGGCCACATCTGCTGAATG 1717
QY      157 GAGATTAATTAACATCTGATGAAACAGCAAGATGACATTAATGTCTAAGTGTGACATG 216
Db      1716 GAGATTAATTAACATCTGATGAAACAGCAAGATGACATTAATGTCTAAGTGTGACATG 1657
QY      217 TTTTTCACATTTTCCGCCCCCTTTAATTAATTCACACACAGCAAGGCAAAAAAGGAAGA 276
Db      1656 TTTTTCACATTTTCCGCCCCCTTTAATTAATTCACACACAGCAAGGCAAAAAAGGAAGA 1597
QY      277 CAGAGATCCCTGGGAGAAATGCCCCGCCATCTTGGGTCAATGATGAGCCCTCGCCCTG 336
Db      1596 CAGAGATCCCTGGGAGAAATGCCCCGCCATCTTGGGTCAATGATGAGCCCTCGCCCTG 1537
QY      337 TGCCTGTGCTCCGCTTGTGAGGAGAGACATTAAGAAATGATATGATGTCTTAAAG 396
Db      1536 TGCCTGTGCTCCGCTTGTGAGGAGAGACATTAAGAAATGATATGATGTCTTAAAG 1477
QY      397 ATGGGCGAGAAAAACAGATCTGTTGTGATATTTTGAAGGGATTAACAGATTGAAA 456
Db      1476 ATGGGCGAGAAAAACAGATCTGTTGTGATATTTTGAAGGGATTAACAGATTGAAA 1417
QY      457 TGAAGTCACAAAGTGAGCATTTACCAATGAGAGGAAAAACAGAGAAAAATCTTGATGCT 516
Db      1416 TGAAGTCACAAAGTGAGCATTTACCAATGAGAGGAAAAACAGAGAAAAATCTTGATGCT 1357
QY      517 TCACAAGACATGCACAAACAAATGGAATACTGTGATGACATGAGGCAGCCAGCTGGG 576
Db      1356 TCACAAGACATGCACAAACAAATGGAATACTGTGATGACATGAGGCAGCCAGCTGGG 1297
QY      577 GAGGAGATTAACACAGGGGCGAGAGGCTCAGAGATTCGCGCTGCTAACTGTCGCT 636
Db      1296 GAGGAGATTAACACAGGGGCGAGAGGCTCAGAGATTCGCGCTGCTAACTGTCGCT 1237
QY      637 CATTAACCAATATTCATATTTCTTAACCTCAAAACAAAGCTGTGTAATATCTGATCT 696
Db      1236 CATTAACCAATATTCATATTTCTTAACCTCAAAACAAAGCTGTGTAATATCTGATCT 1177
QY      697 CTACGGTTCCTTGCGGCCCAACATTCCTCCATATATCCAGCACACTCTATTTTAATAT 756
Db      1176 CTACGGTTCCTTGCGGCCCAACATTCCTCCATATATCCAGCACACTCTATTTTAATAT 1117
QY      757 TAGTCCCAAGATCTGTACTGTGACCTTTCTACACTGTAGATTAACATTTACTCATTTGTT 816
Db      1116 TAGTCCCAAGATCTGTACTGTGACCTTTCTACACTGTAGATTAACATTTACTCATTTGTT 1057
QY      817 CAAA 820
Db      1056 CAAA 1053

```

Search completed: September 26, 2003, 22:20:46
 Job time : 216.891 secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 26, 2003, 21:40:03 : Search time 47.0629 Seconds
(without alignments)
7690.430 Million cell updates/sec

Title: US-09-402-713A-4

Perfect score: 820

Sequence: 1 agaagctgcagtcagaaaaa.....cattactcatttgcataa 820

Scoring table: OLIGO_NUC

Gapop 60.0 , Gapext 60.0

Searched: 569978 seqs, 220691566 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Issued Patents-NA:*

1: /cgn2_6/ptodata/1/ina/5A.COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5B.COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A.COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B.COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PCUTS.COMB.seq:*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
C 1	812	99.0	812	4	US-09-439-313-471	Sequence 471, App
C 2	812	99.0	812	4	US-09-352-616A-471	Sequence 471, App
C 3	724	88.3	2229	4	US-09-439-313-469	Sequence 469, App
C 4	724	88.3	2229	4	US-09-352-616A-469	Sequence 469, App
C 5	724	88.3	2426	4	US-09-439-313-470	Sequence 470, App
C 6	724	88.3	2426	4	US-09-352-616A-470	Sequence 470, App
C 7	724	88.3	3112	4	US-09-439-313-468	Sequence 468, App
C 8	724	88.3	3112	4	US-09-352-616A-468	Sequence 468, App
C 9	257	31.3	718	4	US-09-439-313-313	Sequence 313, App
C 10	257	31.3	718	4	US-09-352-616A-313	Sequence 313, App
C 11	257	31.3	718	4	US-09-232-149A-313	Sequence 313, App
C 12	179	21.8	301	4	US-09-439-313-287	Sequence 287, App
C 13	179	21.8	301	4	US-09-352-616A-287	Sequence 287, App
C 14	179	21.8	301	4	US-09-232-149A-287	Sequence 287, App
C 15	20	2.4	164976	4	US-08-916-421B-1	Sequence 1, Appli
C 16	19	2.3	161	1	US-08-450-834-3	Sequence 3, Appli
C 17	18	2.2	4527	2	US-08-944-449-8	Sequence 8, Appli
C 18	18	2.2	4527	4	US-09-353-362-8	Sequence 8, Appli
C 19	18	2.2	8930	4	US-09-077-098A-1	Sequence 1, Appli
C 20	18	2.2	17000	4	US-09-679-299A-18	Sequence 18, Appli
C 21	17	2.1	590	4	US-09-364-206-25	Sequence 25, Appli
C 22	17	2.1	831	4	US-08-450-834-5	Sequence 5, Appli
C 23	17	2.1	1017	4	US-09-328-475C-104	Sequence 104, App
C 24	17	2.1	2920	4	US-08-976-259-10	Sequence 10, Appli
C 25	17	2.1	3247	3	US-08-718-388-4	Sequence 4, Appli
C 26	17	2.1	3661	3	US-08-718-388-5	Sequence 5, Appli
C 27	17	2.1	3675	3	US-08-793-331-5	Sequence 5, Appli

28	17	2.1	5128	4	US-09-364-206-1	Sequence 1, Appl
29	17	2.1	6792	4	US-09-374-454-20	Sequence 20, Appl
C 30	17	2.1	7824	3	US-08-718-388-6	Sequence 6, Appl
C 31	17	2.1	13857	4	US-09-620-312D-75	Sequence 75, Appl
C 32	17	2.1	15202	3	US-08-922-635-21	Sequence 21, Appl
C 33	17	2.1	16382	3	US-08-718-388-8	Sequence 8, Appl
C 34	17	2.1	16319	3	US-08-923-137-2	Sequence 2, Appl
C 35	17	2.1	46718	4	US-09-816-093-3	Sequence 3, Appl
C 36	17	2.1	64467	4	US-09-803-671B-3	Sequence 3, Appl
C 37	17	2.1	164976	4	US-08-916-421B-1	Sequence 1, Appl
C 38	16	2.0	20	4	US-09-705-299-79	Sequence 79, Appl
C 39	16	2.0	51	3	US-09-046-247-45	Sequence 45, Appl
C 40	16	2.0	89	2	US-08-379-482A-3	Sequence 3, Appl
C 41	16	2.0	219	4	US-09-328-352-2419	Sequence 2419, Ap
C 42	16	2.0	430	1	US-08-466-033-27	Sequence 27, Appl
C 43	16	2.0	430	1	US-08-444-733-27	Sequence 27, Appl
C 44	16	2.0	430	2	US-08-464-134-27	Sequence 27, Appl
C 45	16	2.0	430	2	US-08-461-361-27	Sequence 27, Appl

ALIGNMENTS

```
RESULT 1
US-09-439-313-471/c
; Sequence 471, Application US/09439313
; Patent No. 6329505
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan Louise
; APPLICANT: Jiang Yuqun
; APPLICANT: Reed, Steven G.
; APPLICANT: Kalos, Michael
; APPLICANT: Fanger, Gary
; APPLICANT: Retter, Mark
; APPLICANT: Solk, John
; APPLICANT: Day, Craig
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
; FILE REFERENCE: 210121.427C9
; CURRENT FILING DATE: 1999-11-12
; NUMBER OF SEQ ID NOS: 575
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 471
; LENGTH: 812
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-439-313-471
Query Match          99.0%; Score 812; DB 4; Length 812;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 812; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
6 CTGGCATGACAAAAACAGAGGGAGATTTGTGTGCTGACGCCGAGGAGACAGCAAGA 65
12 CTGGCATGACAAAAACAGAGGGAGATTTGTGTGCTGACGCCGAGGAGACAGCAAGA 65
812 CTGGCATGACAAAAACAGAGGGAGATTTGTGTGCTGACGCCGAGGAGACAGCAAGA 753
66 TCTGATGCTGGGAAGGACCTGATATACAGAGGTGAATAAAGAAAGCGCTGACCT 125
752 TCTGATGCTGGGAAGGACCTGATATACAGAGGTGAATAAAGAAAGCGCTGACCT 693
126 TACCATCTGAGGCCACACATCTGCTGAATATGAGATTAATTAACATCACTAGAACAGCA 185
692 TACCATCTGAGGCCACACATCTGCTGAATATGAGATTAATTAACATCACTAGAACAGCA 633
186 GATGCAATATATATCTTAAGTAGACATGTTTGGACATTTCCAGCCCTTTAATA 245
632 GATGCAATATATATCTTAAGTAGACATGTTTGGACATTTCCAGCCCTTTAATA 573
246 TCCACACACACAGGAAGCAAAAGAGACAGAGATCCCTGGGAGAAATGCCGCCGCGC 305
```

```
|||||
Db 572 TCCACACACAGAGAACACAAAAGAGACAGAGATCCCTGGAGAAAAGCCGCGG 513
QY 306 CCATCTTGGGTCATCATGAGACCCCTGCTGCTGCTGCTGCTGCTGAGGAGACA 365
Db 512 CCATCTTGGGTCATCATGAGACCCCTGCTGCTGCTGCTGCTGCTGAGGAGACA 453
QY 366 TTGAAAATGAATGATGTGTTCTTAAAGAGTGGGAGAAAACAGATCCTGTGTGGA 425
Db 452 TTGAAAATGAATGATGTGTTCTTAAAGAGTGGGAGAAAACAGATCCTGTGTGGA 393
QY 426 TATTATTTGAACGGGATTCAGATTGAATGAAGTACAAAAGTGGAGCATTTACCAATGA 485
Db 392 TATTATTTGAACGGGATTCAGATTGAATGAAGTACAAAAGTGGAGCATTTACCAATGA 333
QY 486 GAGGAAAACAGACAGAGAAAATCTTGATGCTTCCAAAGACATGCAACAAAACAAATGAAA 545
Db 332 GAGGAAAACAGACAGAGAAAATCTTGATGCTTCCAAAGACATGCAACAAAACAAATGAAA 273
QY 546 TACTGTATGATGATGAGGAGCCCAAGCTGGGAGAGAAATACACGCGGGGAGAGGTCAG 605
Db 272 TACTGTATGATGATGAGGAGCCCAAGCTGGGAGAGAAATACACGCGGGGAGAGGTCAG 213
QY 606 GATTCGGCCCTGCTGCTTAAACTGTGCTTCAATACCAATCATTTCTATTTCTAAC 665
Db 212 GATTCGGCCCTGCTGCTTAAACTGTGCTTCAATACCAATCATTTCTATTTCTAAC 153
QY 666 CTCAAAACAAAGCTGTTGTAATATCTGATCTACAGGTTCTTGGGCCCAACATTTCTC 725
Db 152 CTCAAAACAAAGCTGTTGTAATATCTGATCTACAGGTTCTTGGGCCCAACATTTCTC 93
QY 726 CATATATCCAGCACACACTCAATTTTAAATAGTCCAGATCTGACTGTGACTTTC 785
Db 92 CATATATCCAGCACACACTCAATTTTAAATAGTCCAGATCTGACTGTGACTTTC 33
QY 786 TACACTGTAGATTAACATTAATCAATTTTGTTC 817
Db 32 TACACTGTAGATTAACATTAATCAATTTTGTTC 1

RESULT 2
US-09-352-616A-471/C
: Sequence 471, Application US/09352616A
: Patent No. 6395278
: GENERAL INFORMATION:
: APPLICANT: Dillon, Davin C.
: APPLICANT: Harlocker, Susan Louise
: APPLICANT: Jiang, Yugu
: APPLICANT: Xu, Jiangchun
: APPLICANT: Mitcham, Jennifer Lynn
: TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
: FILE REFERENCE: 210121.427C8
: CURRENT APPLICATION NUMBER: US/09/352,616A
: CURRENT FILING DATE: 1999-07-13
: NUMBER OF SEQ ID NOS: 472
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 471
: LENGTH: 812
: TYPE: DNA
: ORGANISM: Homo sapiens
US-09-352-616A-471

Query Match 99.0%; Score 812; DB 4; Length 812;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 812; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 CTGGCATCAGAAAAACAGAGGAGATTTGTGTGCTGACGCGGAGGAGACAGAGAGA 65
Db 812 CTGGCATCAGAAAAACAGAGGAGATTTGTGTGCTGACGCGGAGGAGACAGAGAGA 753
QY 66 TCGCATGTGGGGAAGCACTGATGATACAGAGGTGAATAAGAAAGCTGTGACTT 125
|||||
```

```
Db 752 TCGCATGTGGGGAAGCACTGATGATACAGAGGTGAGAAATAGAAAGGCTGTGACTT 693
QY 126 TACCATCTGAGGCGCACACATCTGCTGAAAAGAGATATTTAACTCACTAGAAAACAGCAA 185
Db 692 TACCATCTGAGGCGCACACATCTGCTGAAAAGAGATATTTAACTCACTAGAAAACAGCAA 633
QY 186 GATGACAATATATGTTCTTAAGTAGTACATGTTTTTTCACATTTCCAGCCCTTTAAATA 245
Db 632 GATGACAATATATGTTCTTAAGTAGTACATGTTTTTTCACATTTCCAGCCCTTTAAATA 573
QY 246 TCCACACACAGAGAACACAAAAGAGAGACAGAGATCCCTGGAGAAAATGCCGCGCG 395
Db 572 TCCACACACAGAGAACACAAAAGAGAGACAGAGATCCCTGGAGAAAATGCCGCGCG 513
QY 306 CCATCTTGGGTCATCATGAGACCCCTGCTGCTGCTGCTGCTGCTGAGGAGAGACA 365
Db 512 CCATCTTGGGTCATCATGAGACCCCTGCTGCTGCTGCTGCTGCTGAGGAGAGACA 453
QY 366 TTGAAAATGAATGATGTGTTCTTAAAGAGTGGGAGAAAACAGATCCTGTGTGGA 425
Db 452 TTGAAAATGAATGATGTGTTCTTAAAGAGTGGGAGAAAACAGATCCTGTGTGGA 393
QY 426 TATTATTTGAACGGGATTCAGATTGAATGAAGTACAAAAGTGGAGCATTTACCAATGA 485
Db 392 TATTATTTGAACGGGATTCAGATTGAATGAAGTACAAAAGTGGAGCATTTACCAATGA 333
QY 486 GAGGAAAACAGACAGAGAAAATCTTGATGCTTCCAAAGACATGCAACAAAACAAATGAAA 545
Db 332 GAGGAAAACAGACAGAGAAAATCTTGATGCTTCCAAAGACATGCAACAAAACAAATGAAA 273
QY 546 TACTGTATGATGATGAGGAGCCCAAGCTGGGAGAGAAATACACGCGGGGAGAGGTCAG 605
Db 272 TACTGTATGATGATGAGGAGCCCAAGCTGGGAGAGAAATACACGCGGGGAGAGGTCAG 213
QY 606 GATTCGGCCCTGCTGCTTAAACTGTGCTTCAATACCAATCATTTCTATTTCTAAC 665
Db 212 GATTCGGCCCTGCTGCTTAAACTGTGCTTCAATACCAATCATTTCTATTTCTAAC 153
QY 666 CTCAAAACAAAGCTGTTGTAATATCTGATCTACAGGTTCTTGGGCCCAACATTTCTC 725
Db 152 CTCAAAACAAAGCTGTTGTAATATCTGATCTACAGGTTCTTGGGCCCAACATTTCTC 93
QY 726 CATATATCCAGCACACACTCAATTTTAAATAGTCCAGATCTGACTGTGACTTTC 785
Db 92 CATATATCCAGCACACACTCAATTTTAAATAGTCCAGATCTGACTGTGACTTTC 33
QY 786 TACACTGTAGATTAACATTAATCAATTTTGTTC 817
Db 32 TACACTGTAGATTAACATTAATCAATTTTGTTC 1

RESULT 3
US-09-439-313-469/C
: Sequence 469, Application US/09439313
: Patent No. 6329505
: GENERAL INFORMATION:
: APPLICANT: Xu, Jiangchun
: APPLICANT: Dillon, Davin C.
: APPLICANT: Mitcham, Jennifer L.
: APPLICANT: Harlocker, Susan Louise
: APPLICANT: Jiang Yugu
: APPLICANT: Reed, Steven G.
: APPLICANT: Kalos, Michael
: APPLICANT: Fanger, Gary
: APPLICANT: Relfer, Mark
: APPLICANT: Solk, John
: APPLICANT: Day, Craig
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
: FILE REFERENCE: 210121.427C9
: CURRENT APPLICATION NUMBER: US/09/439,313
: CURRENT FILING DATE: 1999-11-12
: NUMBER OF SEQ ID NOS: 575
```

	APPLICANT	Matcham, Jennifer Lynn
1	TITLE OF INVENTION:	COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
2	TITLE OF INVENTION:	OF PROSTATE CANCER AND METHODS FOR THEIR USE
3	FILE REFERENCE:	210121.427C8
4	CURRENT APPLICATION NUMBER:	US/09/352, 616A
5	CURRENT FILING DATE:	1999-07-13
6	NUMBER OF SEQ ID NOS:	472
7	SOFTWARE:	FastSeq for Windows Version 3.0
8	SEQ ID NO 469	
9	LENGTH:	2229
10	TYPE:	DNA
11	ORGANISM:	Homo sapiens
12	US-09-352-616A-469	
13	Query Match	88.3%; Score 724; DB 4; Length 2229;
14	Best Local Similarity	100.0%; Pred. No. 0;
15	Matches 724;	Conservative 0; Mismatches 0; Indels 0; Gaps 0;
16	QY	97 AGGTGAGAAATTAAGAAAGGCTGCTGACTTTTACCTGAGGCCACACATCTGCTGAATG 156
17	Db	1776 AGGTGAGAAATTAAGAAAGGCTGCTGACTTTTACCTGAGGCCACACATCTGCTGAATG 1717
18	QY	157 GAGTAATTTAATCAATCAGTAAGAAAGCAAGATGCAATTAATGTCGAAGAGACATG 216
19	Db	1716 GAGTAATTTAATCAATCAGTAAGAAAGCAAGATGCAATTAATGTCGAAGAGACATG 1657
20	QY	217 TTTTTCGACATTTTCAGCCCTTTTAAATATCCACACACAGAGAACAACAAAGAAACA 276
21	Db	1656 TTTTTCGACATTTTCAGCCCTTTTAAATATCCACACACAGAGAACAACAAAGAAACA 1597
22	QY	277 CAGAGATCCCTGGGAGAAATGCCCGGCCCATCTTGGGTCATCATGATGAGCTCGCCCTG 336
23	Db	1596 CAGAGATCCCTGGGAGAAATGCCCGGCCCATCTTGGGTCATCATGATGAGCTCGCCCTG 1537
24	QY	337 TGCCCTGGTCCCGCTTGAGAGGAGAGACATTAGAAATGSAATGATGTTGCTTAAAG 396
25	Db	1536 TGCCCTGGTCCCGCTTGAGAGGAGAGACATTAGAAATGSAATGATGTTGCTTAAAG 1477
26	QY	397 ATGGCGAGAAACAGATCCGTGTGTGATATTTTGAACGGATTTACAGATTTGAAA 456
27	Db	1476 ATGGCGAGAAACAGATCCGTGTGTGATATTTTGAACGGATTTACAGATTTGAAA 1417
28	QY	457 TGAAGTCAAAAGTGAGCATTTACCAATGAGAGAAAACAGACGAGAAAATCTTGATGCT 516
29	Db	1416 TGAAGTCAAAAGTGAGCATTTACCAATGAGAGAAAACAGACGAGAAAATCTTGATGCT 1357
30	QY	517 TCACAACACATGCAACAAACAAATGGAATATCTGATGACATGAGGACAGCAAGCTGGG 576
31	Db	1356 TCACAACACATGCAACAAACAAATGGAATATCTGATGACATGAGGACAGCAAGCTGGG 1297
32	QY	577 GAGGAGATTAACACAGGGGGCAGAGAGGTACAGATTTTGCCCTGCTGCTTAACTGTGCTT 636
33	Db	1296 GAGGAGATTAACACAGGGGGCAGAGAGGTACAGATTTTGCCCTGCTGCTTAACTGTGCTT 1237
34	QY	637 CATATACCAATCATTTCAATTTTCTAAACCTCAAAACAAAGCTGTGTAATCTGATCT 696
35	Db	1236 CATATACCAATCATTTCAATTTTCTAAACCTCAAAACAAAGCTGTGTAATCTGATCT 1177
36	QY	697 CTAGAGTTCCTTCGGGGCCCAACATTTTCCATATATCAGCGACACATCTTTTAATAT 756
37	Db	1176 CTAGAGTTCCTTCGGGGCCCAACATTTTCCATATATCAGCGACACATCTTTTAATAT 1117
38	QY	757 TAGTTCACAGATCTGTACTGTGACCTTTCTACACTGTAGATAATACATTACTCATTTGTT 816
39	Db	1116 TAGTTCACAGATCTGTACTGTGACCTTTCTACACTGTAGATAATACATTACTCATTTGTT 1057
40	QY	817 CAAA 820
41	Db	1056 CAAA 1053

Sequence 470, Application US/09439313
Patent No. 6329505
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Devin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan Louise
APPLICANT: Jiang, Yuqi
APPLICANT: Reed, Steven G.
APPLICANT: Kalos, Michael
APPLICANT: Fanger, Gary
APPLICANT: Retter, Mark
APPLICANT: Solk, John
APPLICANT: Day, Craig
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427C9
CURRENT APPLICATION NUMBER: US/09/439,313
CURRENT FILING DATE: 1999-11-12
NUMBER OF SEQ ID NOS: 575
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 470
LENGTH: 2426
TYPE: DNA
ORGANISM: Homo sapiens
US-09-439-313-470

Query Match 88.3%; Score 724; DB 4; Length 2426;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 724; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 97 AGGTGAGAAATTAAGAAAGGCTGCTGACTTTCACATCTGAGGCCACACATCTGCTGAATG 156
DB 1770 AGGTGAGAAATTAAGAAAGGCTGCTGACTTTCACATCTGAGGCCACACATCTGCTGAATG 1711
QY 157 GAGATAATTAACATCACTAGAAACAGACAGATGACATATATGCTTAAGTAGACATG 216
DB 1710 GAGATAATTAACATCACTAGAAACAGACAGATGACATATATGCTTAAGTAGACATG 1651
QY 217 TTTTGGACATTTCCAGCCCTTTAAATATCCACACACAGAGAACAAAGAAAGCA 276
DB 1650 TTTTGGACATTTCCAGCCCTTTAAATATCCACACACAGAGAACAAAGAAAGCA 1591
QY 277 CAGAGATCCCTGGGAGAAATGCCCGGCCCATCTTGGGTCATGATGAGCCCTGCCCTG 336
DB 1590 CAGAGATCCCTGGGAGAAATGCCCGGCCCATCTTGGGTCATGATGAGCCCTGCCCTG 1531
QY 337 TGCCTGGTCCCGCTTGTGAGGGAAGACATTAGAAATGAATGATGATGCTCTTAAGG 396
DB 1530 TGCCTGGTCCCGCTTGTGAGGGAAGACATTAGAAATGAATGATGATGCTCTTAAGG 1471
QY 397 ATGGGACGAGAAACAGATCCTGTTGTGATATTTTGAACGGGATTAAGATTTGAAA 456
DB 1470 ATGGGACGAGAAACAGATCCTGTTGTGATATTTTGAACGGGATTAAGATTTGAAA 1411
QY 457 TGAAGTACAAAGTACATTTACCATGAGAGGAAACAGACGAGAAATCTTGATGCT 516
DB 1410 TGAAGTACAAAGTACATTTACCATGAGAGGAAACAGACGAGAAATCTTGATGCT 1351
QY 517 TCACAGACATGCAACAAACAAATGGAATACGTGATGACATGAGGACAGCAAGCTGGG 576
DB 1350 TCACAGACATGCAACAAACAAATGGAATACGTGATGACATGAGGACAGCAAGCTGGG 1291
QY 577 GAGGAGATAACACAGGGGACAGAGGTCAGATTCTGGCCCTGCTGCTAAACCTGTGCTT 636
DB 1290 GAGGAGATAACACAGGGGACAGAGGTCAGATTCTGGCCCTGCTGCTAAACCTGTGCTT 1211
QY 637 CATTAACCAATCATTTATATTTCTAACCTCAAAACAAAGCTGTTGATATCTGATCT 696
DB 1230 CATTAACCAATCATTTATATTTCTAACCTCAAAACAAAGCTGTTGATATCTGATCT 1171
QY 697 CTACGGTCTCTTGCGCCCAACATCTCCATATATCCAGCAGACATCTTTTAATAT 756
DB 1171 CTACGGTCTCTTGCGCCCAACATCTCCATATATCCAGCAGACATCTTTTAATAT 756

DB 1170 CTACGGTCTCTTGCGCCCAACATCTCCATATATCCAGCAGACATCTTTTAATAT 1111
QY 757 TAGTCCAGATCTGTACTGTGACCTTTTACACTGTAGATAATCACTACTATTTGTT 816
DB 1110 TAGTCCAGATCTGTACTGTGACCTTTTACACTGTAGATAATCACTACTATTTGTT 1051
QY 817 CAAA 820
DB 1050 CAAA 1047

RESULT 6
US-09-352-616a-470/c

Sequence 470, Application US/09352616A
Patent No. 6395278
GENERAL INFORMATION:
APPLICANT: Dillon, Devin C.
APPLICANT: Harlocker, Susan Louise
APPLICANT: Jiang, Yuqi
APPLICANT: Xu, Jiangchun
APPLICANT: Mitcham, Jennifer Lynn
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
TITLE OF INVENTION: OF PROSTATE CANCER AND METHODS FOR THEIR USE
FILE REFERENCE: 210121.427C8
CURRENT APPLICATION NUMBER: US/09/352,616A
CURRENT FILING DATE: 1999-07-13
NUMBER OF SEQ ID NOS: 472
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 470
LENGTH: 2426
TYPE: DNA
ORGANISM: Homo sapiens
US-09-352-616a-470

Query Match 88.3%; Score 724; DB 4; Length 2426;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 724; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 97 AGGTGAGAAATTAAGAAAGGCTGCTGACTTTCACATCTGAGGCCACACATCTGCTGAATG 156
DB 1770 AGGTGAGAAATTAAGAAAGGCTGCTGACTTTCACATCTGAGGCCACACATCTGCTGAATG 1711
QY 157 GAGATAATTAACATCACTAGAAACAGACAGATGACATATATGCTTAAGTAGACATG 216
DB 1710 GAGATAATTAACATCACTAGAAACAGACAGATGACATATATGCTTAAGTAGACATG 1651
QY 217 TTTTGGACATTTCCAGCCCTTTAAATATCCACACACAGAGAACAAAGAAAGCA 276
DB 1650 TTTTGGACATTTCCAGCCCTTTAAATATCCACACACAGAGAACAAAGAAAGCA 1591
QY 277 CAGAGATCCCTGGGAGAAATGCCCGGCCCATCTTGGGTCATGATGAGCCCTGCCCTG 336
DB 1590 CAGAGATCCCTGGGAGAAATGCCCGGCCCATCTTGGGTCATGATGAGCCCTGCCCTG 1531
QY 337 TGCCTGGTCCCGCTTGTGAGGGAAGACATTAGAAATGAATGATGATGCTCTTAAGG 396
DB 1530 TGCCTGGTCCCGCTTGTGAGGGAAGACATTAGAAATGAATGATGATGCTCTTAAGG 1471
QY 397 ATGGGACGAGAAACAGATCCTGTTGTGATATTTTGAACGGGATTAAGATTTGAAA 456
DB 1470 ATGGGACGAGAAACAGATCCTGTTGTGATATTTTGAACGGGATTAAGATTTGAAA 1411
QY 457 TGAAGTACAAAGTACATTTACCATGAGAGGAAACAGACGAGAAATCTTGATGCT 516
DB 1410 TGAAGTACAAAGTACATTTACCATGAGAGGAAACAGACGAGAAATCTTGATGCT 1351
QY 517 TCACAGACATGCAACAAACAAATGGAATACGTGATGACATGAGGACAGCAAGCTGGG 576
DB 1350 TCACAGACATGCAACAAACAAATGGAATACGTGATGACATGAGGACAGCAAGCTGGG 1291
QY 577 GAGGAGATAACACAGGGGACAGAGGTCAGATTCTGGCCCTGCTGCTAAACCTGTGCTT 636
DB 1290 GAGGAGATAACACAGGGGACAGAGGTCAGATTCTGGCCCTGCTGCTAAACCTGTGCTT 1231

QY	97	AGGTGAGAAATAGAAAAGCGTCTGACTTTTACCATCTTGAGGCCACACATCTGCTGAATG	156
Db	1312	AGGTGAGAAATAGAAAAGCGTCTGACTTTTACCATCTTGAGGCCACACATCTGCTGAATG	1371
QY	157	GAGATTAATTAACATCCTCAGAAACAGCAAGATGACATATTAATGTCTTAAGTAGACATG	216
Db	1372	GAGATTAATTAACATCCTCAGAAACAGCAAGATGACATATTAATGTCTTAAGTAGACATG	1431
QY	217	TTTTTGACATTTCCAGCCCTTTTAAATATCCACACACAGAGAGCAAAAAGAAACA	276
Db	1432	TTTTTGACATTTCCAGCCCTTTTAAATATCCACACACAGAGAGCAAAAAGAAACA	1491
QY	277	CAGAGATTCCTGGAGAAATGCCCCGCCCATCTTGATGATCATGATGAGCTCGCCCTG	336
Db	1492	CAGAGATTCCTGGAGAAATGCCCCGCCCATCTTGATGATCATGATGAGCTCGCCCTG	1551

```
QY 337 TCCCTGTCCTCCCTTGTGAGGAAAGACATTGAAATGATGTGTTCTTAAAG 396
Db 1552 TGCCCTGTCCTCCCTTGTGAGGAAAGACATTGAAATGATGTGTTCTTAAAG 1611
QY 397 ATGGCAGGAAAGACATCTGTTGTGATTTTATTTGAACGGGATACGATTTGAA 456
Db 1612 ATGGCAGGAAAGACATCTGTTGTGATTTTATTTGAACGGGATACGATTTGAA 1671
QY 457 TGAAGTCACAAAGTGAGCATTACCAATGAGAGAAACAGACGAGAAATCTTTCATGCT 516
Db 1672 TGAAGTCACAAAGTGAGCATTACCAATGAGAGAAACAGACGAGAAATCTTTCATGCT 1731
QY 517 TCACAGACATGCAACAAATGCAATGATGATGATGATGAGCAGCAGCAGCAGCAG 576
Db 1732 TCACAGACATGCAACAAATGCAATGATGATGATGATGAGCAGCAGCAGCAGCAG 1791
QY 577 GAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 636
Db 1792 GAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1851
QY 637 CATACCAATCATTTCTATTTCTAACCTCAAAACAAAGCTGTTGATATGATGAT 696
Db 1852 CATACCAATCATTTCTATTTCTAACCTCAAAACAAAGCTGTTGATATGATGAT 1911
QY 697 CTACGTTCTTCTGAGGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 756
Db 1912 CTACGTTCTTCTGAGGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 1971
QY 757 TAGTCCAGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGAT 816
Db 1972 TAGTCCAGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGAT 2031
QY 817 CAAA 820
Db 2032 CAAA 2035

RESULT 9
US-09-439-313-313
: Sequence 313, Application US/09439313
: Patent No. 6329505
: GENERAL INFORMATION:
: APPLICANT: Xu, Jiangchun
: APPLICANT: Dillon, Davin C.
: APPLICANT: Mitcham, Jennifer L.
: APPLICANT: Harlocker, Susan Louise
: APPLICANT: Jiang Yuqi
: APPLICANT: Reed, Steven G.
: APPLICANT: Katos, Michael
: APPLICANT: Fanger, Gary
: APPLICANT: Reltter, Mark
: APPLICANT: Solk, John
: APPLICANT: Day, Craig
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
: TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
: FILE REFERENCE: 210121.427C9
: CURRENT APPLICATION NUMBER: US/09/439,313
: NUMBER OF SEQ ID NOS: 575
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 313
: LENGTH: 718
: TYPE: DNA
: ORGANISM: Homo sapien
: FEATURE:
: NAME/KEY: misc_feature
: LOCATION: (1)...(718)
: OTHER INFORMATION: n = A,T,C or G
US-09-439-313-313

Query Match 31.3%; Score 257; DB 4; Length 718;
Best Local Similarity 99.4%; Pred. No. 3.1e-125;
```

```
Matches 357; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 42 TGCAGCCGAGGAGAGCCAGGAAGATCTGATGTTGGGAGGAGCCTGATGATACAGAGGTG 101
Db 17 TGCAGCCGAGGAGAGCCAGGAAGATCTGATGTTGGGAGGAGCCTGATGATACAGAGGTG 76
QY 102 AGAATTAAGAAAGGCTGCTGACTTTACCATCTGAGGCCACACATCTGCTGAATGAGAT 161
Db 77 AGAATTAAGAAAGGCTGCTGACTTTACCATCTGAGGCCACACATCTGCTGAATGAGAT 136
QY 162 AATTACATCTAGAAACAGCAGATGACATTAATGCTAGTGTGATGATGATGATGAT 221
Db 137 AATTACATCTAGAAACAGCAGATGACATTAATGCTAGTGTGATGATGATGATGAT 196
QY 222 GCACATTTCCAGCCCTTTAATATCCACACACAGAGAGCAGAGAGAGAGAGAGAGAG 281
Db 197 GCACATTTCCAGCCCTTTAATATCCACACACAGAGAGAGAGAGAGAGAGAGAGAGAG 256
QY 282 ATCCCTGGGAGAAATGCCCGCCGATCTTGGTCAATGATGATGATGATGATGATGAT 341
Db 257 ATCCCTGGGAGAAATGCCCGCCGATCTTGGTCAATGATGATGATGATGATGATGAT 316
QY 342 GTCCTGCTGTGAGGAGAGACATTTAGAAATGATGATGATGATGATGATGATGATGAT 400
Db 317 GTCCTGCTGTGAGGAGAGACATTTAGAAATGATGATGATGATGATGATGATGATGAT 375

RESULT 10
US-09-352-616A-313
: Sequence 313, Application US/09352616A
: Patent No. 6395278
: GENERAL INFORMATION:
: APPLICANT: Dillon, Davin C.
: APPLICANT: Harlocker, Susan Louise
: APPLICANT: Jiang, Yuqi
: APPLICANT: Xu, Jiangchun
: APPLICANT: Mitcham, Jennifer Lynn
: TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
: TITLE OF INVENTION: OF PROSTATE CANCER AND METHODS FOR THEIR USE
: FILE REFERENCE: 210121.427C8
: CURRENT APPLICATION NUMBER: US/09/352,616A
: NUMBER OF SEQ ID NOS: 472
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 313
: LENGTH: 718
: TYPE: DNA
: ORGANISM: Homo sapien
: FEATURE:
: NAME/KEY: misc_feature
: LOCATION: (1)...(718)
: OTHER INFORMATION: n = A,T,C or G
US-09-352-616A-313

Query Match 31.3%; Score 257; DB 4; Length 718;
Best Local Similarity 99.4%; Pred. No. 3.1e-125;
Matches 357; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 42 TGCAGCCGAGGAGAGCCAGGAAGATCTGATGTTGGGAGGAGCCTGATGATACAGAGGTG 101
Db 17 TGCAGCCGAGGAGAGCCAGGAAGATCTGATGTTGGGAGGAGCCTGATGATACAGAGGTG 76
QY 102 AGAATTAAGAAAGGCTGCTGACTTTACCATCTGAGGCCACACATCTGCTGAATGAGAT 161
Db 77 AGAATTAAGAAAGGCTGCTGACTTTACCATCTGAGGCCACACATCTGCTGAATGAGAT 136
QY 162 AATTACATCTAGAAACAGCAGATGACATTAATGCTAGTGTGATGATGATGATGAT 221
Db 137 AATTACATCTAGAAACAGCAGATGACATTAATGCTAGTGTGATGATGATGATGAT 196
QY 222 GCACATTTCCAGCCCTTTAATATCCACACACAGAGAGAGAGAGAGAGAGAGAGAGAG 281
Db 197 GCACATTTCCAGCCCTTTAATATCCACACACAGAGAGAGAGAGAGAGAGAGAGAGAG 256
QY 342 GTCCTGCTGTGAGGAGAGACATTTAGAAATGATGATGATGATGATGATGATGATGAT 400
Db 317 GTCCTGCTGTGAGGAGAGACATTTAGAAATGATGATGATGATGATGATGATGATGAT 375
```


RESULT 12
US-09-439-113-287/c
Sequence 287, Application US/09439313
Patent No 6329505
GENERAL INFORMATION:
APPLICANT: Xu, Jlangchun
APPLICANT: Dillon, Devin C.
APPLICANT: Mitchem, Jennifer L.
APPLICANT: Hatlocker, Susan Louise

	Query Match	Similarity	99.6%	Score	179	DB	4	Length	301
Best Local	Similarity	99.6%	Pred.	No.	7.8e-84				
Matches	229	Conservative	0	Mismatches	1	Indels	0	Gaps	0
Oy	472	AGCATTTACCAATGAGAGGAAAAACAGACGAGAAAAATCTTGATGCGCTTCAACAAGACATGCCAA	531						
Db	301	AGCATTTACCAATGAGAGGAAAAACAGACGAGAAAAATCTTGATGCGCTTCAACAAGACATGCCAA	242						
Oy	532	CAAAACAAAATGGAATACTGTGATATACATGAGAGGCCCAAGCTGGGGAGAGCAATAAACCG	591						

```
Db      241 CAAACAAAATGAACTGATGATACATGAGCAGCAGCCAGCTGGGAGAGATTAACACAG 182
Oy      592 GGGCAGAGGCTCAGGATTCGGCCCTGCTGCTAAACGTGGTTCATTAACCAATCATT 651
Db      181 GGGCAGAGGCTCAGGATTCGGCCCTGCTGCTAAACGTGGTTCATTAACCAATCATT 122
Oy      652 TCATATTCTTAACCTCAAAACAAAGCTGTTGTAATATCTGATCTCTACG 701
Db      121 TCATATTCTTAACCTCAAAACAAAGCTGTTGTAATATCTGATCTCTACG 72

RESULT 14
US-09-232-149A-287/c
; Sequence 287, Application US/09232149A
; Patent No. 6465611
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer Lynn
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE
; FILE REFERENCE: 210121.427C6
; CURRENT APPLICATION NUMBER: US/09/232.149A
; CURRENT FILING DATE: 1999-01-15
; NUMBER OF SEQ ID NOS: 338
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 287
; LENGTH: 301
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-232-149A-287

Query Match      21.8%; Score 179; DB 4; Length 301;
Best Local Similarity 99.6%; Pred. No. 2.8e-84;
Matches 229; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy      472 AGCATTTACCAATGAGAGAAACAGACGAGAAATCTTGATGCTTCAAGACATGCAA 531
Db      301 AGCATTTACCAATGAGAGAAACAGACGAGAAATCTTGATGCTTCAAGACATGCAA 242
Oy      532 CAAACAAAATGGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 591
Db      241 CAAACAAAATGGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 182
Oy      592 GGGCAGAGGCTCAGGATTCGGCCCTGCTGCTAAACGTGGTTCATTAACCAATCATT 651
Db      181 GGGCAGAGGCTCAGGATTCGGCCCTGCTGCTAAACGTGGTTCATTAACCAATCATT 122
Oy      652 TCATATTCTTAACCTCAAAACAAAGCTGTTGTAATATCTGATCTCTACG 701
Db      121 TCATATTCTTAACCTCAAAACAAAGCTGTTGTAATATCTGATCTCTACG 72

RESULT 15
US-08-916-421B-1
; Sequence 1, Application US/08916421B
; Patent No. 6503729
; GENERAL INFORMATION:
; APPLICANT: Bull et al.
; TITLE OF INVENTION: Complete Genome Sequence of the Methanogenic Archaeon, Methanococ
; Patent No. 6503729
; FILE OF INVENTION: jannasch1
; FILE REFERENCE: PB275
; CURRENT APPLICATION NUMBER: US/08/916.421B
; CURRENT FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: US 60/024,428
; PRIOR FILING DATE: 1996-08-22
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 1664976
; TYPE: DNA
```

```
ORGANISM: Methanococcus jannaschii
FEATURE:
NAME/KEY: misc_feature
LOCATION: (28222)..(28222)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc_feature
LOCATION: (28257)..(28258)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc_feature
LOCATION: (84773)..(84773)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc_feature
LOCATION: (84808)..(84808)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc_feature
LOCATION: (84812)..(84812)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc_feature
LOCATION: (98120)..(98120)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc_feature
LOCATION: (98159)..(98159)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc_feature
LOCATION: (98239)..(98239)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc_feature
LOCATION: (98266)..(98266)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc_feature
LOCATION: (98343)..(98343)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc_feature
LOCATION: (103998)..(103998)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc_feature
LOCATION: (148948)..(148948)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc_feature
LOCATION: (163385)..(163385)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc_feature
LOCATION: (191989)..(191989)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc_feature
LOCATION: (191995)..(191995)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc_feature
LOCATION: (231980)..(231980)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc_feature
LOCATION: (234187)..(234187)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc_feature
LOCATION: (234220)..(234220)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc_feature
LOCATION: (309398)..(309398)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc_feature
LOCATION: (234814)..(234814)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc_feature
LOCATION: (309418)..(309418)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc_feature
LOCATION: (312837)..(312837)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc_feature
LOCATION: (312993)..(312993)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc_feature
LOCATION: (319226)..(319226)
```

```
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc_feature
LOCATION: (559167)..(559167)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc_feature
LOCATION: (559241)..(559241)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc_feature
LOCATION: (600992)..(600992)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc_feature
LOCATION: (622708)..(622708)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc_feature
LOCATION: (657081)..(657081)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc_feature
LOCATION: (657203)..(657203)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc_feature
LOCATION: (674435)..(674435)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc_feature
LOCATION: (682442)..(682442)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc_feature
LOCATION: (713652)..(713652)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc_feature
LOCATION: (741684)..(741684)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc_feature
LOCATION: (779455)..(779455)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc_feature
LOCATION: (779676)..(779676)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc_feature
LOCATION: (855539)..(855539)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc_feature
LOCATION: (871619)..(871619)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc_feature
LOCATION: (1084830)..(1084830)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc_feature
LOCATION: (1096846)..(1096846)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc_feature
LOCATION: (1119881)..(1119881)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc_feature
LOCATION: (1130881)..(1130881)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc_feature
LOCATION: (1310988)..(1310988)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc_feature
LOCATION: (1313224)..(1313224)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc_feature
LOCATION: (1349473)..(1349473)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc_feature
LOCATION: (1349491)..(1349491)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc_feature
LOCATION: (1470091)..(1470091)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc_feature
LOCATION: (1569020)..(1569020)
OTHER INFORMATION: n equals a, t, c, or g
```

```
NAME/KEY: misc_feature
LOCATION: (1602912)..(1602912)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc_feature
LOCATION: (1603734)..(1603734)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc_feature
LOCATION: (1637998)..(1637998)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc_feature
LOCATION: (1664854)..(1664854)
OTHER INFORMATION: n equals a, t, c, or g
US-08-916-421B-1
```

```
Query Match      2.4% Score 20; DB 4; Length 1664976;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      740 CACGCATTTTATATATTTAG 759
Db      1520938 CACGCATTTTATATATTTAG 1520957
```

```
Search completed: September 27, 2003, 11:43:56
Job time : 51.0629 secs
```

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 26, 2003, 21:44:18 : Search time 190.028 Seconds
(without alignments)
10742.554 Million cell updates/sec

Title: US-09-402-713a-4

Perfect score: 820

Sequence: 1 agaagctgcacatcagaagaa.....cattactcatttgcacaa 820

Scoring table:

Gapop 60.0 , Gapext 60.0

Searched: 1678620 seqs, 1244745471 residues

Word size : 0

Total number of hits satisfying chosen parameters: 3357240

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : Published_Applications_NA.*

1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/2/pubpna/PCF_NEW_PUB.seq:*
3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
6: /cgn2_6/ptodata/2/pubpna/PCFUS_PUBCOMB.seq:*
7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
9: /cgn2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
10: /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
13: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
14: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
15: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
16: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
17: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	820	100.0	876	11 US-09-957-708-3	Sequence 3, Appli
2	812	99.0	812	9 US-09-759-143-471	Sequence 471, App
3	812	99.0	812	9 US-09-780-669-471	Sequence 471, App
4	812	99.0	812	9 US-09-822-827-471	Sequence 471, App
5	812	99.0	812	10 US-09-895-793-471	Sequence 471, App
6	812	99.0	812	10 US-09-895-814-471	Sequence 471, App
7	812	99.0	812	12 US-10-144-678A-471	Sequence 471, App
8	812	99.0	812	13 US-10-012-896-471	Sequence 471, App
9	812	99.0	812	14 US-10-010-940-471	Sequence 471, App
10	724	88.3	2229	9 US-09-759-143-469	Sequence 469, App
11	724	88.3	2229	9 US-09-780-669-469	Sequence 469, App
12	724	88.3	2229	9 US-09-822-827-469	Sequence 469, App
13	724	88.3	2229	10 US-09-895-793-469	Sequence 469, App
14	724	88.3	2229	10 US-09-895-814-469	Sequence 469, App
15	724	88.3	2229	12 US-10-144-678A-469	Sequence 469, App
16	724	88.3	2229	13 US-10-012-896-469	Sequence 469, App

C 17	724	88.3	2229	14 US-10-010-940-469	Sequence 469, App
C 18	724	88.3	2426	9 US-09-759-143-470	Sequence 470, App
C 19	724	88.3	2426	9 US-09-780-669-470	Sequence 470, App
C 20	724	88.3	2426	9 US-09-822-827-470	Sequence 470, App
C 21	724	88.3	2426	10 US-09-895-793-470	Sequence 470, App
C 22	724	88.3	2426	10 US-09-895-814-470	Sequence 470, App
C 23	724	88.3	2426	12 US-10-144-678A-470	Sequence 470, App
C 24	724	88.3	2426	13 US-10-012-896-470	Sequence 470, App
C 25	724	88.3	2426	14 US-10-010-940-470	Sequence 470, App
C 26	724	88.3	2426	14 US-10-205-823-448	Sequence 448, App
C 27	724	88.3	3112	9 US-09-759-143-468	Sequence 468, App
C 28	724	88.3	3112	9 US-09-780-669-468	Sequence 468, App
C 29	724	88.3	3112	9 US-09-822-827-468	Sequence 468, App
C 30	724	88.3	3112	10 US-09-895-793-468	Sequence 468, App
C 31	724	88.3	3112	10 US-09-895-814-468	Sequence 468, App
C 32	724	88.3	3112	12 US-10-144-678A-468	Sequence 468, App
C 33	724	88.3	3112	13 US-10-012-896-468	Sequence 468, App
C 34	724	88.2	3923	14 US-10-010-940-468	Sequence 468, App
C 35	723	88.2	3923	9 US-09-759-143-650	Sequence 650, App
C 36	723	88.2	3923	9 US-09-780-669-650	Sequence 650, App
C 37	723	88.2	3923	9 US-09-822-827-650	Sequence 650, App
C 38	723	88.2	3923	10 US-09-895-793-650	Sequence 650, App
C 39	723	88.2	3923	10 US-09-895-814-650	Sequence 650, App
C 40	723	88.2	3923	12 US-10-144-678A-650	Sequence 650, App
C 41	723	88.2	3923	13 US-10-012-896-650	Sequence 650, App
C 42	723	88.2	3923	14 US-10-205-823-316	Sequence 316, App
C 43	473	57.7	597	12 US-10-195-730-46	Sequence 46, Appl
C 44	467	57.0	1102	14 US-10-198-846-11000	Sequence 11000, A
C 45	287	35.0	4097	12 US-09-814-353-20144	Sequence 20144, A

ALIGNMENTS

RESULT 1					
US-09-957-708-3					
Sequence 3, Application US/09957708					
Publication No. US20030031678A1					
GENERAL INFORMATION:					
APPLICANT: Sun, Yongming					
APPLICANT: Recipon, Hervé					
APPLICANT: Cafferey, Robert					
APPLICANT: Ali, Shujath					
TITLE OF INVENTION: Compositions and Methods Relating to Prostate Specific					
TITLE OF INVENTION: Genes					
FILE REFERENCE: DEX-0239					
CURRENT APPLICATION NUMBER: US/09/957,708					
PRIOR FILING DATE: 2001-09-19					
PRIOR APPLICATION NUMBER: 60/233,746					
PRIOR FILING DATE: 2000-09-19					
NUMBER OF SEQ ID NOS: 40					
SOFTWARE: Patentin Ver. 2.1					
SEQ ID NO 3					
LENGTH: 876					
TYPE: DNA					
ORGANISM: Homo sapiens					
US-09-957-708-3					
Query Match					
Best Local Similarity 100.0%; Score 820; DB 11; Length 876;					
Matches 820; Conservative 0; Mismatches 0; Indels 0; Gaps 0;					
OY	1	AGAACTGGCATCAGAAAAACAGAGAGGAGATTTGTGTGGCTGCAGCCGAGGAGACACAG	60		
DB	30	AGAACTGGCATCAGAAAAACAGAGGAGATTTGTGTGGCTGCAGCCGAGGAGACACAG	89		
OY	61	GAAGATTCGATGTCGAGGAGACCTGATGATACAGAGTGAATAAAGAAAGCTCT	120		
DB	90	GAAGATTCGATGTCGAGGAGACCTGATGATACAGAGTGAATAAAGAAAGCTCT	149		
OY	121	GACTTACCATCTGAGGACACACATCTGCTGAATGAGATTAATTAACATCACTGAAC	180		
DB	150	GACTTACCATCTGAGGACACACATCTGCTGAATGAGATTAATTAACATCACTGAAC	209		

QY	181	AGCAATATACATATATATATAGTCTAAGTAGTGACATGTTTTGACATTTCCAGCCCTT	240
Db	210	AGCAAGATGCACAATATATATAGTCTAAGTAGTGACATGTTTTGACATTTCCAGCCCTT	269
QY	241	AAATATCCACACACACAGBACACAAAAAGBACACAGATCCCTGGGAGAAATCCC	300
Db	270	AAATATCCACACACACAGBACACAAAAAGBACACAGATCCCTGGGAGAAATCCC	329
QY	301	GGCCGCATCTTGGGTCATCGATGAGCCCTCGCCCTGTGCTGTGCCGTGTGAGGAA	360
Db	330	GGCCGCATCTTGGGTCATCGATGAGCCCTCGCCCTGTGCTGTGCCGTGTGAGGAA	389
QY	361	GGCATTAGAAAATGATATGATGTCTTCTTAAGAGATGGCAGAGAAAACGATCCGTT	420
Db	390	GGCATTAGAAAATGATATGATGTCTTCTTAAAGATGGCAGAGAAAACGATCCGTT	449
QY	421	GTGGATATTTATTTTGAACGGATTCAGATTTGGAATTAAGTCAAAAGTGACATTACC	480
Db	450	GTGGATATTTATTTTGAACGGATTCAGATTTGGAATTAAGTCAAAAGTGACATTACC	509
QY	481	AATGABAGGAAAACAGACAGAAAATCTTGATGGCTTACAAAGCATGCAACAAACAAA	540
Db	510	AATGABAGGAAAACAGACAGAAAATCTTGATGGCTTACAAAGCATGCAACAAACAAA	569
QY	541	TGGAATACTGTGATGCATGAGGACGCAAGCTGGGGAGAGATTAACGAGGGGACAGG	600
Db	570	TGGAATACTGTGATGCATGAGGACGCAAGCTGGGGAGAGATTAACGAGGGGACAGG	629
QY	601	GTGAGATTCTGGCCCTGCTGCCCTTAACGTGAGCGCTTAAACCAAAATCTCATATTTC	660
Db	630	GTGAGATTCTGGCCCTGCTGCCCTTAAACTGTGCTTAAACCAAAATCTCATATTTC	689
QY	661	TAAACCTCAAAACAAAGCTGTGTAATATCTGATCTTACGGTTCTTCTGGGCCAACA	720
Db	690	TAAACCTCAAAACAAAGCTGTGTAATCTGATCTTACCGTTCTTCTGGGCCAACA	749
QY	721	TTTCTCATTTATCCAGCCACACTCTATTTTAAATATTTAGTCCAGATCTGTACTGGAC	780
Db	750	TTTCTCATTTATCCAGCCACACTCTATTTTAAATATTTAGTCCAGATCTGTACTGGAC	809
QY	781	CTTTCACACCTAGAAATACATTACTCATTTTGTCAA	820
Db	810	CTTTCACACCTAGAAATACATTACTCATTTTGTCAA	849

```

RESULT 2
: US-09-759-143-471/C
: Sequence 471, Application US/09759143
: Patent No. US2002002248A1
: GENERAL INFORMATION:
: APPLICANT: Xu, Jiangchun
: APPLICANT: Dillon, Davin C.
: APPLICANT: Mitcham, Jennifer L.
: APPLICANT: Harlocker, Susan L.
: APPLICANT: Jiang, Yugu
: APPLICANT: Henderson, Robert A.
: APPLICANT: Kalos, Michael D.
: APPLICANT: Fanger, Gary R.
: APPLICANT: Retter, Marc W.
: APPLICANT: Stolk, John A.
: APPLICANT: Day, Craig H.
: APPLICANT: Vedvick, Thomas S.
: APPLICANT: Carter, Darlick
: APPLICANT: Li, Samuel
: APPLICANT: Wang, Aijun
: APPLICANT: Skeiky, Yasir A.W.
: APPLICANT: Hepler, William
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
: TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
: FILE REFERENCE: 210121.427023
: CURRENT APPLICATION NUMBER: US/09/759.143
: CURRENT FILING DATE: 2001-01-12

```

```

; NUMBER OF SEQ ID NOS: 934
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 471
; LENGTH: 812
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-759-143-471

```

Query Match	99.0%	Score 812	DB 9	Length 812
Best Local Similarity	100.0%	Pred. No.	0	
Matches 812, Conservative	0	Mismatches	0	Gaps 0

QY	6	TTGGCATTCAAAAAACAGAGGGAGATTGGTGGCTCGACGCCGAGGGAGACACAGAAGA	65
Db	812	CTGGCATTCAAAAAACAGAGGGAGATTGGTGGCTCGACGCCGAGGGAGACACAGAAGA	753
QY	66	TCTGCATGTTGGGAAGACCTGATGATACAGAGGTGAGAAATTAAGAAAGGCTGCTGACTT	125
Db	752	TCTGCATGTTGGGAAGACCTGATGATACAGAGGTGAGAAATTAAGAAAGGCTGCTGACTT	693
QY	126	TACCATCTGAGGCCACACATCTGCTGAAATGGAGATTAATTAACTACTAGAAACAGCA	185
Db	692	TACCATCTGAGGCCACACATCTGCTGAAATGGAGATTAATTAACTACTAGAAACAGCA	633
QY	186	GATCAACAATTAATGTTCTTAAGTAGAGCATGTTTTTGACAATTTCCACCCCTTTAAATA	245
Db	632	GATCAACAATTAATGTTCTTAAGTAGAGCATGTTTTTGACAATTTCCACCCCTTTAAATA	573
QY	246	TCCACACACAGAGGAAGACAAAAGGAAGCACAGATCCCTGGGAGAAATGCCCGGCG	305
Db	572	TCCACACACAGAGGAAGACAAAAGGAAGCACAGATCCCTGGGAGAAATGCCCGGCG	513
QY	306	CCATCTGGGGTCATCGATGAGCCCTCGCCCTGCTGGTCCCGCTTGGAGGAAGGACA	365
Db	512	CCATCTGGGGTCATCGATGAGCCCTCGCCCTGCTGGTCCCGCTTGGAGGAAGGACA	453
QY	366	TTAAGAAAATGAATTGATGTGTTCCTTAAGAGATGGGACGAGAAAACAGATCCGTGTGGA	425
Db	452	TTAAGAAAATGAATTGATGTGTTCCTTAAGAGATGGGACGAGAAAACAGATCCGTGTGGA	393
QY	426	TATTTTATTTGAAACGGGATTACAGATTTGAAATGAAGTACAAAGTGAGCATTTACCAATGA	485
Db	392	TATTTTATTTGAAACGGGATTACAGATTTGAAATGAAGTACAAAGTGAGCATTTACCAATGA	333
QY	486	GAGGAAAAACAGCGAAATCCTTGATGGCTTCCAAACATGCAACAAACAAATGGAA	545
Db	332	GAGGAAAAACAGCGAAATCCTTGATGGCTTCCAAACATGCAACAAACAAATGGAA	273
QY	546	TACTGTGATGATGAGGACAGCAAGCTGGGGAGAGATTAACACAGGGGACAGAGGCTGAG	605
Db	272	TACTGTGATGATGAGGACAGCAAGCTGGGGAGAGATTAACACAGGGGACAGAGGCTGAG	213
QY	606	GATTCTGGCCCTGCTGCTTAACGTGCGTTCAATACCAAAATCATTTTATTTCTAAAC	665
Db	212	GATTCTGGCCCTGCTGCTTAACGTGCGTTCAATACCAAAATCATTTTATTTCTAAAC	153
QY	666	CTCAAAACAAAGCTGTTGTAATATCTGATCTCTACAGTTCCTTGCGGGCCCAACATTTCTC	725
Db	152	CTCAAAACAAAGCTGTTGTAATATCTGATCTCTACAGTTCCTTGCGGGCCCAACATTTCTC	93
QY	726	CATATATTCAGCCACACACTCATTTTAAATTTAGTTCCAGATCTGTACTGTGACCTTTC	785
Db	92	CATATATTCAGCCACACACTCATTTTAAATTTAGTTCCAGATCTGTACTGTGACCTTTC	33
QY	786	TACACTGTAGAATAAATTAATCTATTTTGTTC	817
Db	32	TACACTGTAGAATAAATTAATCTATTTTGTTC	1

RESULT 3
US-09-780-669-471/c
; Sequence 471, Application US/09780665
; Patent No. US20020051977A1

```
/ GENERAL INFORMATION:
/ APPLICANT: Xu, Jiangchun
/ APPLICANT: Dillon, Davin C.
/ APPLICANT: Mitcham, Jennifer L.
/ APPLICANT: Harlocker, Susan L.
/ APPLICANT: Jiang, Yuqi
/ APPLICANT: Henderson, Robert A.
/ APPLICANT: Kalos, Michael D.
/ APPLICANT: Fanger, Gary R.
/ APPLICANT: Ketter, Marc W.
/ APPLICANT: Stolk, John A.
/ APPLICANT: Day, Craig H.
/ APPLICANT: Vedvick, Thomas S.
/ APPLICANT: Carter, Darriick
/ APPLICANT: Li, Samuel
/ APPLICANT: Wang, Aijun
/ APPLICANT: Skelky, Yasir A.W.
/ APPLICANT: Hepler, William
/ APPLICANT: Hural, John
/ APPLICANT: McNeill, Patricia D.
/ APPLICANT: Houghton, Raymond L.
/ TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
/ FILE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
/ FILE REFERENCE: 210121.427C24
/ CURRENT APPLICATION NUMBER: US/09/780,669
/ CURRENT FILING DATE: 2001-02-09
/ NUMBER OF SEQ ID NOS: 943
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 471
/ LENGTH: 812
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-09-780-669-471
```

```
Query Match          99.0%; Score 812; DB 9; Length 812;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 812; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      6 CTGGCATCAGAAAAACAGAGGGAGATTGTGTGCTGCAGCCGAGGGAGACCAGAGAA 65
DB      812 CTGGCATCAGAAAAACAGAGGGAGATTGTGTGCTGCAGCCGAGGGAGACCAGAGAA 753
QY      66 TCTGCATGTTGGGAAGGACCTGATGATACAGAGGTGAGAAATTAAGAAAGCTGCTGACTT 125
DB      752 TCTGCATGTTGGGAAGGACCTGATGATACAGAGGTGAGAAATTAAGAAAGCTGCTGACTT 693
QY      126 TACCATCTGAGGCCACACATCTGCTGAATGAGATATTTAACTACTAGAAACAGCAA 185
DB      692 TACCATCTGAGGCCACACATCTGCTGAATGAGATATTTAACTACTAGAAACAGCAA 633
QY      186 GATGACAAATATATGCTTAAGTAGACATGTTTTTGCACATTTCCAGCCCTTTAAATA 245
DB      632 GATGACAAATATATGCTTAAGTAGACATGTTTTTGCACATTTCCAGCCCTTTAAATA 573
QY      246 TCCACACACACAGAAAGCAAAAGAGACAGAGATCCCTGGGAGAAATGCCGCGCG 305
DB      572 TCCACACACACAGAAAGCAAAAGAGACAGAGATCCCTGGGAGAAATGCCGCGCG 513
QY      306 CCATCTTGGGTCATGATGAGCCTGCGCTGTGCTGCTGCCGCTTGTGAGGGAAGACA 365
DB      512 CCATCTTGGGTCATGATGAGCCTGCGCTGTGCTGCTGCCGCTTGTGAGGGAAGACA 453
QY      366 TTAGAAATGAAATGATGTTCTTTAAAGATGGGCAAGAAACAGATCCTGTTGTGA 425
DB      452 TTAGAAATGAAATGATGTTCTTTAAAGATGGGCAAGAAACAGATCCTGTTGTGA 393
QY      426 TATTTTATTTGAAGGGATTACAGATTGAAATGAAGTCAAAAGTGAAGATTACCAATGA 485
DB      392 TATTTTATTTGAAGGGATTACAGATTGAAATGAAGTCAAAAGTGAAGATTACCAATGA 333
QY      486 GAGGAAACAGAGAGAAATCTGTATGCTTCACAAAGACATGCAACAAACAAATGGA 545
DB      332 GAGGAAACAGAGAGAAATCTGTATGCTTCACAAAGACATGCAACAAACAAATGGA 273
```

```
QY      546 TACTGTGATGATGAGGACGACCAAGCTGGGAGAGATTAACAGGGGACAGGCTGAC 605
DB      272 TACTGTGATGATGAGGACGACCAAGCTGGGAGAGATTAACAGGGGACAGGCTGAC 213
QY      606 GATTCTGGCCCTGCTGACCTTAAGTGTGCTTATTAACCAATTCATTATTTTAAAC 665
DB      212 GATTCTGGCCCTGCTGACCTTAAGTGTGCTTATTAACCAATTCATTATTTTAAAC 153
QY      666 CTCAAAACAAAGCTGTTGAATATCTGATCTCTAGCGTTCTTGGGCCCAACATCTC 725
DB      152 CTCAAAACAAAGCTGTTGAATATCTGATCTCTAGCGTTCTTGGGCCCAACATCTC 93
QY      726 CATATATCAGCAGACACTATTTTATATTTAGTTCCAGATTCCTACTGTGACCTTTC 785
DB      92 CATATATCAGCAGACACTATTTTATATTTAGTTCCAGATTCCTACTGTGACCTTTC 33
QY      786 TACACTGTAGAAATTAACATTACTCATTTTGTTC 817
DB      32 TACACTGTAGAAATTAACATTACTCATTTTGTTC 1
```

```
RESULT 4
US-09-822-827-471/c
; Sequence 471, Application US/09822827
; Patent No. US20020081680A1
/ GENERAL INFORMATION:
/ APPLICANT: Xu, Jiangchun
/ TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
/ FILE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
/ FILE REFERENCE: 210121.534C1
/ CURRENT APPLICATION NUMBER: US/09/822,827
/ CURRENT FILING DATE: 2001-03-28
/ NUMBER OF SEQ ID NOS: 982
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 471
/ LENGTH: 812
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-09-822-827-471
```

```
Query Match          99.0%; Score 812; DB 9; Length 812;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 812; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      6 CTGGCATCAGAAAAACAGAGGGAGATTGTGTGCTGCAGCCGAGGGAGACCAGAGAA 65
DB      812 CTGGCATCAGAAAAACAGAGGGAGATTGTGTGCTGCAGCCGAGGGAGACCAGAGAA 753
QY      66 TCTGCATGTTGGGAAGGACCTGATGATACAGAGGTGAGAAATTAAGAAAGCTGCTGACTT 125
DB      752 TCTGCATGTTGGGAAGGACCTGATGATACAGAGGTGAGAAATTAAGAAAGCTGCTGACTT 693
QY      126 TACCATCTGAGGCCACACATCTGCTGAATGAGATATTTAACTACTAGAAACAGCAA 185
DB      692 TACCATCTGAGGCCACACATCTGCTGAATGAGATATTTAACTACTAGAAACAGCAA 633
QY      186 GATGACAAATATATGCTTAAGTAGACATGTTTTTGCACATTTCCAGCCCTTTAAATA 245
DB      632 GATGACAAATATATGCTTAAGTAGACATGTTTTTGCACATTTCCAGCCCTTTAAATA 573
QY      246 TCCACACACACAGAAAGCAAAAGAGACAGAGATCCCTGGGAGAAATGCCGCGCG 305
DB      572 TCCACACACACAGAAAGCAAAAGAGACAGAGATCCCTGGGAGAAATGCCGCGCG 513
QY      306 CCATCTTGGGTCATGATGAGCCTGCGCTGTGCTGCTGCCGCTTGTGAGGGAAGACA 365
DB      512 CCATCTTGGGTCATGATGAGCCTGCGCTGTGCTGCTGCCGCTTGTGAGGGAAGACA 453
QY      366 TTAGAAATGAAATGATGTTCTTTAAAGATGGGCAAGAAACAGATCCTGTTGTGA 425
DB      452 TTAGAAATGAAATGATGTTCTTTAAAGATGGGCAAGAAACAGATCCTGTTGTGA 393
```



```

; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepier, William T.
; APPLICANT: Henderson, Robert A.
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Vinals de Bassols, Carlota
; APPLICANT: Foy, Teresa
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C26
; CURRENT APPLICATION NUMBER: US/09/895,814
; NUMBER OF SEQ ID NOS: 990
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 471
; LENGTH: 812
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-895-814-471

Query Match
Best Local Similarity 99.0%; Score 812; DB 10; Length 812;
Matches 812; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 CTGGCATCAGAAAAACAGAGGGGAGATTGTGTGCTGCGAGCCGAGAGAGACAGAGAGA 65
DB 812 CTGGCATCAGAAAAACAGAGGGGAGATTGTGTGCTGCGAGCCGAGAGAGACAGAGAGA 753
OY 66 TCTGATGATGGGAAAGGACCTGATATACAGAGGTGAGCAATTAAGAAAGGCTGCTGACTT 125
DB 752 TCTGATGATGGGAAAGGACCTGATATACAGAGGTGAGCAATTAAGAAAGGCTGCTGACTT 693
OY 126 TACCATCTGAGGCCACACATCTGCTGAATGAGATTAATTAACATCAGTACAGAAACAGCA 185
DB 692 TACCATCTGAGGCCACACATCTGCTGAATGAGATTAATTAACATCAGTACAGAAACAGCA 633
OY 186 GATGACAATATATATGCTTAAGTAGTACATGTTTTTGGCATTTCAGCCCTTTAAATA 245
DB 632 GATGACAATATATGCTTAAGTAGTACATGTTTTTGGCATTTCAGCCCTTTAAATA 573
OY 246 TCCACACACACAGAGACCAAAAGAGACACAGAGATCCCTGGGAAATGCCGCGCG 305
DB 572 TCCACACACACAGAGACCAAAAGAGACACAGAGATCCCTGGGAAATGCCGCGCG 513
OY 306 CCATCTGGGTCATGATGAGGCTGCGCCCTGTGCGTCCGCTTGTGAGGGAAGGACA 365
DB 512 CCATCTGGGTCATGATGAGGCTGCGCCCTGTGCGTCCGCTTGTGAGGGAAGGACA 453
OY 366 TTAGAANAATGATGATGTTCTCTTAAGATGGGAGAGAAACAGATCCTGTTGTGA 425
DB 452 TTAGAANAATGATGATGTTCTCTTAAGATGGGAGAGAAACAGATCCTGTTGTGA 393
OY 426 TATTTATTTGAACGGGATTACAGATTGAATGAAGTCAAAAGTAGAGCATTAACCAATGA 485
DB 392 TATTTATTTGAACGGGATTACAGATTGAATGAAGTCAAAAGTAGAGCATTAACCAATGA 333
OY 486 GAGGAAAACAGAGGAAAATCTTGATGGCTTCAAGACATGCAAAACAAATGGA 545
DB 332 GAGGAAAACAGAGGAAAATCTTGATGGCTTCAAGACATGCAAAACAAATGGA 273
OY 546 TACTGTGATGATGAGGAGCCCAAGCTGGGAGAGATTAACAGGAGGAGAGGAGTCA 605
DB 272 TACTGTGATGATGAGGAGCCCAAGCTGGGAGAGATTAACAGGAGGAGAGGAGTCA 213
OY 606 GATTTGCGCCCTGCTGCTTAAACGTGCTTATTAACCAATTCATTAATTTTCAACC 665
DB 212 GATTTGCGCCCTGCTGCTTAAACGTGCTTATTAACCAATTCATTAATTTTCAACC 153
OY 666 CTCAAAACAAAGCTGTTGTAATATCTGATCTCTAGGGTTCCTTCTGGGCGCAACATCTC 725
```

```

DB 152 CTCAAAACAAAGCTGTTGTAATATCTGATCTCTAGGGTTCCTTGGGCGCAACATCTC 93
OY 726 CATATATCCAGCCACACATCTTTTAATATTAAGTCCAGATCTGTACTGTGACCTTTC 785
DB 92 CATATATCCAGCCACACATCTTTTAATATTAAGTCCAGATCTGTACTGTGACCTTTC 33
OY 786 TACACTGTGATTAACATTAACATTTTGTTC 817
DB 32 TACACTGTGATTAACATTAACATTTTGTTC 1

RESULT 7
US-10-144-678A-471/C
; Sequence 471, Application US/10144678A
; Publication No. US20030157089A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvyck, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A. W.
; APPLICANT: Hepier, William T.
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Vinals y de Bassols, Carlota
; APPLICANT: Foy, Teresa M.
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Deng, Ta
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C28
; CURRENT APPLICATION NUMBER: US/10/144,678A
; NUMBER OF SEQ ID NOS: 1033
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 471
; LENGTH: 812
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-144-678A-471

Query Match
Best Local Similarity 99.0%; Score 812; DB 12; Length 812;
Matches 812; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 CTGGCATCAGAAAAACAGAGGGGAGATTGTGTGCTGCGAGCCGAGAGAGACAGAGAGA 65
DB 812 CTGGCATCAGAAAAACAGAGGGGAGATTGTGTGCTGCGAGCCGAGAGAGACAGAGAGA 753
OY 66 TCTGATGATGGGAAAGGACCTGATATACAGAGGTGAGCAATTAAGAAAGGCTGCTGACTT 125
DB 752 TCTGATGATGGGAAAGGACCTGATATACAGAGGTGAGCAATTAAGAAAGGCTGCTGACTT 693
OY 126 TACCATCTGAGGCCACACATCTGCTGAATGAGATTAATTAACATCAGTACAGAAACAGCA 185
DB 692 TACCATCTGAGGCCACACATCTGCTGAATGAGATTAATTAACATCAGTACAGAAACAGCA 633
OY 186 GATGACAATATATATGCTTAAGTAGTACATGTTTTTGGCATTTCAGCCCTTTAAATA 245
DB 632 GATGACAATATATATGCTTAAGTAGTACATGTTTTTGGCATTTCAGCCCTTTAAATA 573
```

QY	246	TCACACACACAGAGCAAGCAAAAGAGACACACAGAGATCCCTGGAGAAATGCCGCCG	305
Db	572	TCACACACACAGAGCAAGCAAAAGAGACACACAGATCCCTGGAGAAATGCCGCCG	513
QY	306	CCATCTTGGGTATGATGATAGCCTCGCCTGTGCTCGTCCGCTTGTGAGGAAAGACA	365
Db	512	CCATCTTGGGTATGATGATAGCCTCGCCTGTGCTCGTCCGCTTGTGAGGAAAGACA	453
QY	366	TTAGAAAATGAATTTGATGTGTTCTCTTAAAGGATGGGACAGAAAACAGATCCTTGGGA	425
Db	452	TTAGAAAATGAATTTGATGTGTTCTCTTAAAGGATGGGACAGAAAACAGATCCTTGGGA	393
QY	426	TATTTTATTTGAAAGGGATTACAGATTTGAAATGAAAGTCAACAAAGTAGCATTTACCAATGA	485
Db	392	TATTTTATTTGAAAGGGATTACAGATTTGAAATGAAAGTCAACAAAGTAGCATTTACCAATGA	333
QY	486	GAGGAAAACAGCGAGAAAATCTTATGTGCTTCACAAAGCATGTCAACAAAATATGGA	545
Db	332	GAGGAAAACAGCGAGAAAATCTTATGTGCTTCACAAAGCATGTCAACAAAATATGGA	273
QY	546	TACTGTGATGACATGAGCGAGCCAAAGCTTGGGAGAGAGATTAACACGGGGCAGAGGTCAG	605
Db	272	TACTGTGATGACATGAGCGAGCCAAAGCTTGGGAGAGAGATTAACACGGGGCAGAGGTCAG	213
QY	606	GATTTGGCCCTGCTGCTCTTAAACTGTGCTTATAACCAATCATTTATTTCTAAC	665
Db	212	GATTTGGCCCTGCTGCTCTTAAACTGTGCTTATAACCAATCATTTATTTCTAAC	153
QY	666	CTCAAAACAAAGCTTTTGAATATGTGATCTGACGGTCTCTGGGCCCAACATTTCTC	725
Db	152	CTCAAAACAAAGCTTTTGAATATGTGATCTGACGGTCTCTGGGCCCAACATTTCTC	93
QY	726	CATATATCGAGCCACACATCATTTTAAATTTAGTTCCAGATCTGTACTGTGACCTTTC	785
Db	92	CATATATCGAGCCACACATCATTTTAAATTTAGTTCCAGATCTGTACTGTGACCTTTC	33
QY	786	TACACTGTAGATAATACATTACTCATTTTGTTC	817
Db	32	TACACTGTAGATAATACATTACTCATTTTGTTC	1

RESULT 8
US-10-012-896-471/c
Sequence 471, Application US/10012896
Publication No. US20020183251A1
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Devin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Jiang, Yugu
APPLICANT: Kalos, Michael D.
APPLICANT: Retter, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Day, Craig H.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Darriek
APPLICANT: Li, Samuel X.
APPLICANT: Wang, Aijun
APPLICANT: Skelky, Yasir A.W.
APPLICANT: Hepler, William T.
APPLICANT: Henderson, Robert A.
APPLICANT: McNeill, Patricia D.
APPLICANT: Houghton, Raymond L.
APPLICANT: Vinals de Bassols, Carlota
APPLICANT: Foy, Teresa
APPLICANT: Fanger, Gary R.
APPLICANT: Mantanabe, Yoshihiro
APPLICANT: Meagher, Madeleine Joy
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER

Query Match	99.0%;	Score 812;	DB 13;	Length 812;	
Best Local Similarity	100.0%;	Pred. No. 0;			
Matches 812;	Conservative	0;	Mismatches	0;	Indels
					Gaps 0;
Query	CTGGATCAGAAAAACAGAGGGAGATTTGGTGGCTGCAGCCGAGGGAGACCCAGGAAGA	65			
Ds	CTGGATCAGAAAAACAGAGGGAGATTTGGTGGCTGCAGCCGAGGGAGACCCAGGAAGA	753			
Qy	CTGGATCAGAAAAACAGAGGGAGATTTGGTGGCTGCAGCCGAGGGAGACCCAGGAAGA	125			
Ds	CTGGATCAGAAAAACAGAGGGAGATTTGGTGGCTGCAGCCGAGGGAGACCCAGGAAGA	693			
Qy	TACCATCTGAGGCCACACATCTGCTGGAATGAGATTAATTAACATCTAGTAACAGCA	185			
Ds	TACCATCTGAGGCCACACATCTGCTGGAATGAGATTAATTAACATCTAGTAACAGCA	633			
Qy	TACCATCTGAGGCCACACATCTGCTGGAATGAGATTAATTAACATCTAGTAACAGCA	245			
Ds	TACCATCTGAGGCCACACATCTGCTGGAATGAGATTAATTAACATCTAGTAACAGCA	573			
Qy	TCCACACACACAGGAGACCAAAAGGAGACACAGATCCCTGGAGAAATGCCCCGCC	305			
Ds	TCCACACACACAGGAGACCAAAAGGAGACACAGATCCCTGGAGAAATGCCCCGCC	513			
Qy	CCATCTGGGATCAGATGAGAGCCCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	365			
Ds	CCATCTGGGATCAGATGAGAGCCCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	453			
Qy	TTAGAAAAATGATGATGCTGCTTAAAGGATGGGAGGAAAAACAGATCCTGTTGTGGA	425			
Ds	TTAGAAAAATGATGATGCTGCTTAAAGGATGGGAGGAAAAACAGATCCTGTTGTGGA	393			
Qy	TATTTATTTGAACGGGATTAAGATTTGAATGAAGTCCACAAAGTGAACATTTACCAATGA	485			
Ds	TATTTATTTGAACGGGATTAAGATTTGAATGAAGTCCACAAAGTGAACATTTACCAATGA	333			
Qy	TATTTATTTGAACGGGATTAAGATTTGAATGAAGTCCACAAAGTGAACATTTACCAATGA	333			
Ds	TATTTATTTGAACGGGATTAAGATTTGAATGAAGTCCACAAAGTGAACATTTACCAATGA	333			
Qy	GAGGAAAAACAGGAGAAATCTTGATGGCTTCAAGACATGCAACAAACAAATGGAA	545			
Ds	GAGGAAAAACAGGAGAAATCTTGATGGCTTCAAGACATGCAACAAACAAATGGAA	273			
Qy	TACTGTGATGACATGAGGACCCAAAGCTGGGAGAGATTAACCAAGGGGACAGAGGCTAG	605			
Ds	TACTGTGATGACATGAGGACCCAAAGCTGGGAGAGATTAACCAAGGGGACAGAGGCTAG	213			
Qy	GATTCATGGCCCTGCTGCTTAAAGTGGGCTTCAATTAACCAATTAATTAATTTCTAAC	665			
Ds	GATTCATGGCCCTGCTGCTTAAAGTGGGCTTCAATTAACCAATTAATTAATTTCTAAC	153			
Qy	CTCAAAACAAAGCTGTGTATATCTGATCTCTCAAGGTTCTCTGCGGGCCCAACATCTC	93			
Ds	CTCAAAACAAAGCTGTGTATATCTGATCTCTCAAGGTTCTCTGCGGGCCCAACATCTC	725			
Qy	CATATATTCAGCCACACATCTTAAATTAATTAATTAATTAATTAATTAATTAATTAAT	785			
Ds	CATATATTCAGCCACACATCTTAAATTAATTAATTAATTAATTAATTAATTAATTAAT	33			
Qy	TACACGTAGAAATTAACATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT	817			
Ds	TACACGTAGAAATTAACATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT	1			

```

US-10-010-940-471/c
Sequence 471, Application US/10010940
Publication No. US20030088062A1
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan Louise
APPLICANT: Jiang Yuqi
APPLICANT: Reed, Steven G.
APPLICANT: Kalos, Michael
APPLICANT: Fanger, Gary
APPLICANT: Retter, Mark
APPLICANT: Solk, John
APPLICANT: Day, Craig
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.42733
CURRENT APPLICATION NUMBER: US/10/010,940
CURRENT FILING DATE: 2001-12-05
NUMBER OF SEQ ID NOS: 575
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 471
LENGTH: 812
TYPE: DNA
ORGANISM: Homo sapiens
US-10-010-940-471

```

Query Match	99.0%;	Score 812;	DB 14;	length 812;
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches 812; Conservative	0;	Mismatches 0;	Indels 0;	Gaps 0;

QY	6	CTGCATCAGAAAAACAGAGGGAGATTGTGTGGCTCAGCCGAGGGAGACAGAGA	65
Db	812	CTGGCATCAGAAAAACAGAGGGAGATTGTGTGGCTCAGCCGAGGGAGACAGAGA	753
QY	66	TCTGCATGTGGGAAGGACCTGATGTATCAGAGGTGAGAAATTAAGAAAGGCTGTGACTT	125
Db	752	TCTGCATGTGGGAAGGACCTGATGTATCAGAGGTGAGAAATTAAGAAAGGCTGTGACTT	693
QY	126	TACCATCTGAGGCCACACATCTGCTGAAATGGAGATAATTAACTACCTAGAACACAA	185
Db	692	TACCATCTGAGGCCACACATCTGCTGAAATGGAGATAATTAACTACCTAGAACACAA	633
QY	186	GATGACATATAATAGTCTTAAGTAGAGCATGTGTTTGGACATTTCCACCCCTTTAAATA	245
Db	632	GATGACATATAATAGTCTTAAGTAGAGCATGTGTTTGGACATTTCCACCCCTTTAAATA	573
QY	246	TCCACACACACAGGAAGCAGAAAAAGGAAGCAGAGATCCCTGGGAGAAATGCCGGCG	305
Db	572	TCCACACACACAGGAAGCAGAAAAAGGAAGCAGAGATCCCTGGGAGAAATGCCGGCG	513
QY	306	CCATCTTGGGTATCATGATGAGCCTGCGCCTGTGCTGGTCCCGCTTGTGAGGGAAGACA	365
Db	512	CCATCTTGGGTATCATGATGAGCCTGCGCCTGTGCTGGTCCCGCTTGTGAGGGAAGACA	453
QY	366	TTAAGAAATGAATTGATGTGTTCCCTTAAGATGGGACAGAAAAACAGATCCGTGTGGA	425
Db	452	TTAAGAAATGAATTGATGTGTTCCCTTAAGATGGGACAGAAAAACAGATCCGTGTGGA	393
QY	426	TATTTATTTGAACGGGATTACAGATTTTGAATGAAGTCACAAAGTGACATTAACCATGA	485
Db	392	TATTTATTTGAACGGGATTACAGATTTTGAATGAAGTCACAAAGTGACATTAACCATGA	333
QY	486	GAGAGAAACAGACAGAAAAATCTTGATGTGCTTCACAGACATGCACAAACAAATTCGAA	545
Db	332	GAGAGAAACAGACAGAAAAATCTTGATGTGCTTCACAGACATGCACAAACAAATTCGAA	273
QY	546	TATCTGTGATGATGAGGACAGCAAGCTGGGGAGAGATTAACACAGGGGACAGAGGTGAG	605
Db	272	TATCTGTGATGATGAGGACAGCAAGCTGGGGAGAGATTAACACAGGGGACAGAGGTGAG	213
QY	606	GATTCGTGGCCCTGCTGCTTAACTGATGCTTCATTAACCAAAATCATTTATATTTCTAAC	665

Db	212	GATTCGGCCCTGCTCCCTAAACTGGGTTCCATACCAAAATCATTTTCATTTTCTAAC	153
QY	666	CTCAAAACAAGCTGTGTATATATCATGATCTACGTTCTCTCGGGCCCAACATCTC	725
Db	152	CTCAAAACAAGCTGTGTATATATCTGATCTACGTTCTCTCGGGCCCAACATCTC	93
QY	726	CATATATCCGACACACTATTTTAAATTTAGTTTCCAGATCGTACTGTGACCTTTC	785
Db	92	CATATATCCGACACACTATTTTAAATTTAGTTTCCAGATCTGTACTGTGACCTTTC	33
QY	786	TACACTGTAGAAATTAACATTACTCATTTTGTTC	817
Db	32	TACACTGTAGAAATTAACATTACTCATTTTGTTC	1

RESULT 10
US-09-759-143-469/c
; Sequence 469, Application US/09759143
; Patent No. US20020022248A1

```

GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Jiang, Yuqi
APPLICANT: Henderson, Robert A.
APPLICANT: Kalos, Michael D.
APPLICANT: Fanger, Gary R.
APPLICANT: Reller, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Day, Craig H.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Darick
APPLICANT: Li, Samuel
APPLICANT: Wang, Aijun
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Hepler, William
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427C23
CURRENT APPLICATION NUMBER: US/09/759,143
CURRENT FILING DATE: 2001-01-12
NUMBER OF SEQ ID NOS: 934
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 469
LENGTH: 2229
TYPE: DNA
ORGANISM: Homo sapiens
US-09-759-143--469

```

Query Match	88.3%;	Score 724;	DB 9;	Length 2229;
Best Local Similarity	100.0%;	Pred. No. 0;		

OY	9	AGGGAGAAATTAAGAAAGCTGCTGACTTACCATCTGAGGCAACACTTCGTGAAATG	15
Db	1776	AGGTGAGAAATTAAGAAAGCTGCTGACTTACCATCTGAGGCAACACTTCGTGAAATG	1775
OY	157	GAGATAATTAATACATCACTGTAAGAAACAGCAAGATGACATAATATGCTTAAGTAGACATG	218
Db	1716	GAGATAATTAATACATCACTGTAAGAAACAGCAAGATGACATAATATGCTTAAGTAGACATG	1655
OY	217	TTTTTTCACATTTTCCAGCCCCCTTTTAAATTTCCACACACACAGGAAGCAACAAAGGAAGCA	2787
Db	1656	TTTTTTCACATTTTCCAGCCCCCTTTTAAATTTCCACACACACAGGAAGCAACAAAGGAAGCA	1595
OY	277	CAGAGATCCCTGGGAGAAATATGCCGGCGCCCATCTTGGGTATGATGATGAAAGCTCGCCCTG	3385
Db	1596	CAGAGATCCCTGGGAGAAATATGCCGGCGCCCATCTTGGGTATGATGATGAAAGCTCGCCCTG	1595
OY	337	TGCCTGATCCCGCTTGTGAGGAGAGACATTGAAATGAATTGATGTGTCCTTAAAGG	396

Db 1536 TGCTGCTCCGCTTGTGAGGGAAGACATTAGAAAATGAATTGATGTCTTAAAG 1477
QY 397 ATGGGACAGAAAACAGATCCTGTGTGATATTTATTTGAAGGGATTCAGATTTGAAA 456
Db 1476 ATGGGACAGAAAACAGATCCTGTGTGATATTTATTTGAAGGGATTCAGATTTGAAA 1417
QY 457 TGAAGTACAAAGTACGATTTACCAATGAGGAAAACAGAGAAAATCTTGATGGCT 516
Db 1416 TGAAGTACAAAGTACGATTTACCAATGAGGAAAACAGAGAAAATCTTGATGGCT 1357
QY 517 TCACAGACATGCAACAACAAATGAATGATCTGATGATGAGGAGGACGACGCTGG 576
Db 1356 TCACAGACATGCAACAACAAATGATCTGATGATGAGGAGGACGACGCTGG 1297
QY 577 GAGGAGATTAACACAGGGGACAGAGGTCAGATTCCTGCTGCTTAACTGCTGCT 636
Db 1296 GAGGAGATTAACACAGGGGACAGAGGTCAGATTCCTGCTGCTTAACTGCTGCT 1237
QY 637 CATACCAAAATCATTTATTTCTAATCCTCAAAACAAAGCTGTGTAATCTGATCT 696
Db 1236 CATACCAAAATCATTTATTTCTAATCCTCAAAACAAAGCTGTGTAATCTGATCT 1177
QY 697 CTACGTTCTCTTGGGCCCCAACATCTCCATATATCCAGCAGACATTTTAATAT 756
Db 1176 CTACGTTCTCTTGGGCCCCAACATCTCCATATATCCAGCAGACATTTTAATAT 1117
QY 757 TAGTCCAGATCTGTACTGTGACCTTTCTACACTGTAGATTAAGATTAATCTGATCT 816
Db 1116 TAGTCCAGATCTGTACTGTGACCTTTCTACACTGTAGATTAATCTGATCT 1057
QY 817 CAAA 820
Db 1056 CAAA 1053

RESULT 11

US-09-780-669-469/c
Sequence 469, Application US/09780669
Patent No. US20020051977A1
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, David C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Jiang, Yugu
APPLICANT: Henderson, Robert A.
APPLICANT: Kalos, Michael D.
APPLICANT: Fanger, Gary R.
APPLICANT: Retter, Marc W.
APPLICANT: Stolck, John A.
APPLICANT: Day, Craig H.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Darriek
APPLICANT: Li, Samuel
APPLICANT: Wang, Aijun
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Hepler, William
APPLICANT: Hurst, John
APPLICANT: McNeill, Patricia D.
APPLICANT: Houghton, Raymond L.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
FILE REFERENCE: 210121.427C24
CURRENT APPLICATION NUMBER: US/09/780,669
CURRENT FILING DATE: 2001-02-09
NUMBER OF SEQ ID NOS: 943
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 469
LENGTH: 2229
TYPE: DNA
ORGANISM: Homo sapiens
US-09-780-669-469

Query Match 88.3%; Score 724; DB 9; Length 2229;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 724; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 97 AGGTGAGAAATTAAGAAAGGCTGCTGACTTTCACATCTGAGGCGCACATCTGCGAATG 156
Db 1776 AGGTGAGAAATTAAGAAAGGCTGCTGACTTTCACATCTGAGGCGCACATCTGCGAATG 1717
QY 157 GAGATTAATTAATCATCTAGTAAGAACAGCAAGATGCAATATATATCTTAAGTACATG 216
Db 1716 GAGATTAATTAATCATCTAGTAAGAACAGCAAGATGCAATATATATCTTAAGTACATG 1657
QY 217 TTTTGCACATTTTCAGCCCTTTAATATTCACACACACAGAGAACCAAAAGAGCA 276
Db 1656 TTTTGCACATTTTCAGCCCTTTAATATTCACACACACAGAGAACCAAAAGAGCA 1597
QY 277 CAGAGATCCCTGGGAGAAATCCCGGCGCATCTGTGGGTATGATGATGAGGCTGCGCTG 336
Db 1596 CAGAGATCCCTGGGAGAAATCCCGGCGCATCTGTGGGTATGATGATGAGGCTGCGCTG 1537
QY 337 TGCTGTGCTCCGCTTGTGAGGAGAGACATTAGAAATGAATGATGTCTTAAAG 396
Db 1536 TGCTGTGCTCCGCTTGTGAGGAGAGACATTAGAAATGAATGATGTCTTAAAG 1477
QY 397 ATGGGACAGAAAACAGATCCTGTGTGATTTTATTTGAACGGATTCAGATTTGAAA 456
Db 1476 ATGGGACAGAAAACAGATCCTGTGTGATTTTATTTGAACGGGATTCAGATTTGAAA 1417
QY 457 TGAAGTCAAAAGTACGATTAACCAATGAGGAAAACAGAGAAAATCTGATGGCT 516
Db 1416 TGAAGTCAAAAGTACGATTAACCAATGAGGAAAACAGAGAAAATCTGATGGCT 1357
QY 517 TCACAGACATGCAACAACAAATGAATCTGTGATGACATGAGGAGGCAAGCTGG 576
Db 1356 TCACAGACATGCAACAACAAATGAATCTGTGATGATGAGGAGGCAAGCTGG 1297
QY 577 GAGGAGATTAACACAGGGGACAGAGGTCAGATTCCTGCTGCTTAACTGCTGCT 636
Db 1296 GAGGAGATTAACACAGGGGACAGAGGTCAGATTCCTGCTGCTTAACTGCTGCT 1237
QY 637 CATACCAAAATCATTTATTTCTAATCCTCAAAACAAAGCTGTGTAATCTGATCT 696
Db 1236 CATACCAAAATCATTTATTTCTAATCCTCAAAACAAAGCTGTGTAATCTGATCT 1177
QY 697 CTACGTTCTCTTGGGCCCCAACATCTCCATATATCCAGCAGACATTTTAATAT 756
Db 1176 CTACGTTCTCTTGGGCCCCAACATCTCCATATATCCAGCAGACATTTTAATAT 1117
QY 757 TAGTCCAGATCTGTACTGTGACCTTTCTACACTGTAGATTAAGATTAATCTGATCT 816
Db 1116 TAGTCCAGATCTGTACTGTGACCTTTCTACACTGTAGATTAATCTGATCT 1057
QY 817 CAAA 820
Db 1056 CAAA 1053

RESULT 12

US-09-822-827-469/c
Sequence 469, Application US/09822827
Patent No. US20020081680A1
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
FILE REFERENCE: 210121.534C1
CURRENT APPLICATION NUMBER: US/09/822,827
CURRENT FILING DATE: 2001-03-28
NUMBER OF SEQ ID NOS: 982
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 469
LENGTH: 2229
TYPE: DNA

```
; ORGANISM: Homo sapiens
US-09-822-827-469

Query Match      88.3%; Score 724; DB 9; Length 2229;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 724; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  97 AGGTAGAATAAGAAAGGCTGCTGACTTACCATCTGTAGGCGCACGATCTGCTGAAG 156
    |||||||
DB  1776 AGGTAGAATAAGAAAGGCTGCTGACTTACCATCTGTAGGCGCACGATCTGCTGAAG 1717
QY  157 GAGATAATTAACATCACTGAAACAGCAAGATGACATATTAATGCTAAGTGTGACATG 216
    |||||||
DB  1716 GAGATAATTAACATCACTGAAACAGCAAGATGACATATTAATGCTAAGTGTGACATG 1657
QY  217 TTTTTCACATTTCCAGCCCTTTAAATATCCACACACACAGAGAACACAAAGAGCA 276
    |||||||
DB  1656 TTTTTCACATTTCCAGCCCTTTAAATATCCACACACACAGAGAACACAAAGAGCA 1597
QY  277 CAGAGATCCCTGGAGAAATGCCCGCCGCTCTTGCGTCATCCATGAGCCTCGCCCTG 336
    |||||||
DB  1596 CAGAGATCCCTGGAGAAATGCCCGCCGCTCTTGCGTCATCCATGAGCCTCGCCCTG 1537
QY  337 TCCCTGATCCGCTTGTGAGGAGAGACATTAAGAAATGATGATGCTTCTCTTAAAG 396
    |||||||
DB  1536 TCCCTGATCCGCTTGTGAGGAGAGACATTAAGAAATGATGATGCTTCTCTTAAAG 1477
QY  397 ATGGCAGGAAACAGATCTCTGTGATATTTATTTGACGGGATTACAGATTTGAAA 456
    |||||||
DB  1476 ATGGCAGGAAACAGATCTCTGTGATATTTATTTGACGGGATTACAGATTTGAAA 1417
QY  457 TGAATGCAAAAGTAGCATTTACCATGAGAGAAACAGAGAGAAATCTTGATGGCT 516
    |||||||
DB  1416 TGAATGCAAAAGTAGCATTTACCATGAGAGAAACAGAGAGAAATCTTGATGGCT 1357
QY  517 TCACAAGACATGCAACAAACAAATGATGATGATGATGATGATGATGATGATGATG 576
    |||||||
DB  1356 TCACAAGACATGCAACAAACAAATGATGATGATGATGATGATGATGATGATG 1297
QY  577 GAGGAGATTAACACAGGGGAGAGGGTCAGGATTTGGCCCTGCTTAACTGTGCGTT 636
    |||||||
DB  1296 GAGGAGATTAACACAGGGGAGAGGGTCAGGATTTGGCCCTGCTTAACTGTGCGTT 1237
QY  637 CATTAACCAATATTTCAATTTCAACCTCAAAACAAAGCTGTTGTAATATGATCT 696
    |||||||
DB  1236 CATTAACCAATATTTCAATTTCAACCTCAAAACAAAGCTGTTGTAATATGATCT 1177
QY  697 CTACGGTTCCTCTGTGGGCCAACAATTCATATATCCAGCCACACTATTTTAAATTT 756
    |||||||
DB  1176 CTACGGTTCCTCTGTGGGCCAACAATTCATATATCCAGCCACACTATTTTAAATTT 1117
QY  757 TAGTTCACAGATCTGTACTGTGACCTTTTACACTGTAGAAATTAACATTAATTTGTT 816
    |||||||
DB  1116 TAGTTCACAGATCTGTACTGTGACCTTTTACACTGTAGAAATTAACATTAATTTGTT 1057
QY  817 CAAA 820
    |||||
DB  1056 CAAA 1053

RESULT 13
US-09-895-793-469/c
; Sequence 469, Application US/09895793
; Publication No. US20020192763A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yugu
; APPLICANT: Kalos, Michael D.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
```

```
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Ajun
; APPLICANT: Skelky, Yasir A.W.
; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Vinals de Bassols, Carlota
; APPLICANT: Foy, Teresa
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.534C2
; CURRENT APPLICATION NUMBER: US/09/895,793
; CURRENT FILING DATE: 2001-06-29
; NUMBER OF SEQ ID NOS: 982
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 469
; LENGTH: 2229
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-895-793-469

Query Match      88.3%; Score 724; DB 10; Length 2229;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 724; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  97 AGGTAGAATAAGAAAGGCTGCTGACTTACCATCTGTAGGCGCACGATCTGCTGAAG 156
    |||||||
DB  1776 AGGTAGAATAAGAAAGGCTGCTGACTTACCATCTGTAGGCGCACGATCTGCTGAAG 1717
QY  157 GAGATAATTAACATCACTGAAACAGCAAGATGACATATTAATGCTAAGTGTGACATG 216
    |||||||
DB  1716 GAGATAATTAACATCACTGAAACAGCAAGATGACATATTAATGCTAAGTGTGACATG 1657
QY  217 TTTTTCACATTTCCAGCCCTTTAAATATCCACACACACAGAGAACACAAAGAGCA 276
    |||||||
DB  1656 TTTTTCACATTTCCAGCCCTTTAAATATCCACACACACAGAGAACACAAAGAGCA 1597
QY  277 CAGAGATCCCTGGAGAAATGCCCGCCGCTCTTGCGTCATCCATGAGCCTCGCCCTG 336
    |||||||
DB  1596 CAGAGATCCCTGGAGAAATGCCCGCCGCTCTTGCGTCATCCATGAGCCTCGCCCTG 1537
QY  337 TCCCTGATCCGCTTGTGAGGAGAGACATTAAGAAATGATGATGATGATGATGATGATG 396
    |||||||
DB  1536 TCCCTGATCCGCTTGTGAGGAGAGACATTAAGAAATGATGATGATGATGATGATGATG 1477
QY  397 ATGGCAGGAAACAGATCTCTGTGATATTTATTTGACGGGATTACAGATTTGAAA 456
    |||||||
DB  1476 ATGGCAGGAAACAGATCTCTGTGATATTTATTTGACGGGATTACAGATTTGAAA 1417
QY  457 TGAATGCAAAAGTAGCATTTACCATGAGAGAAACAGAGAGAAATCTTGATGGCT 516
    |||||||
DB  1416 TGAATGCAAAAGTAGCATTTACCATGAGAGAAACAGAGAGAAATCTTGATGGCT 1357
QY  517 TCACAAGACATGCAACAAACAAATGATGATGATGATGATGATGATGATGATGATG 576
    |||||||
DB  1356 TCACAAGACATGCAACAAACAAATGATGATGATGATGATGATGATGATGATG 1297
QY  577 GAGGAGATTAACACAGGGGAGAGGGTCAGGATTTGGCCCTGCTTAACTGTGCGTT 636
    |||||||
DB  1296 GAGGAGATTAACACAGGGGAGAGGGTCAGGATTTGGCCCTGCTTAACTGTGCGTT 1237
QY  637 CATTAACCAATATTTCAATTTCAACCTCAAAACAAAGCTGTTGTAATATGATCT 696
    |||||||
DB  1236 CATTAACCAATATTTCAATTTCAACCTCAAAACAAAGCTGTTGTAATATGATCT 1177
QY  697 CTACGGTTCCTCTGTGGGCCAACAATTCATATATCCAGCCACACTATTTTAAATTT 756
    |||||||
```

Db 1176 CTAGGTTCTTCTGGGCCCAACATCTCCATATATCCAGCCACACTATTTTATATTT 1117
QY 757 TAGTCCCGAGATCTGTACTGTGACCTTTCTACACTGTAGAAATAACATTACTCATTTTGT 816
Db 1116 TAGTCCCGAGATCTGTACTGTGACCTTTCTACACTGTAGAAATAACATTACTCATTTTGT 1057
QY 817 CAAA 820
Db 1056 CAAA 1053

RESULT 14
US-09-895-814-469/C
; Sequence 469, Application US/09895814
; Publication No. US20020193296A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yugu
; APPLICANT: Kalos, Michael D.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stoik, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Derrick
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghlon, Raymond L.
; APPLICANT: Vinals de Bassols, Carlota
; APPLICANT: Foy, Teresa
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C26
; CURRENT APPLICATION NUMBER: US/09/895, 814
; CURRENT FILING DATE: 2001-06-29
; NUMBER OF SEQ ID NOS: 990
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 469
; LENGTH: 2229
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-895-814-469

Query Match 88.3%; Score 724; DB 10; Length 2229;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 724; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 97 AGTGGAATAATGAAGAAGGCTGCTGACTTACCATCTGAGGCCACACATCTGCTGAATG 156
Db 1776 AGGTGAATAATGAAGAAGGCTGCTGACTTACCATCTGAGGCCACACATCTGCTGAATG 1717
QY 157 GAGATAATTAACATCACTAGAAACAGACAGATGACATATATGTCTAAGTAGATG 216
Db 1716 GAGATAATTAACATCACTAGAAACAGACAGATGACATATATGTCTAAGTAGATG 1657
QY 217 TTTTTCGACATTTTCAGCCCTTTAAATATCCACACACAGAGCAAAAGAGCA 276
Db 1656 TTTTTCGACATTTTCAGCCCTTTAAATATCCACACACAGAGCAAAAGAGCA 1597
QY 277 CAGAGATCCCTGGAGAAATGCCCGGCCCATCTTGGGTCATGATGAGCCTGCCCTG 336
Db 1596 CAGAGATCCCTGGAGAAATGCCCGGCCCATCTTGGGTCATGATGAGCCTGCCCTG 1537
QY 337 TGCTGTGCTCCGCTTGAGAGGAAGACATTAGAAATGATGATGTTCTTAAGG 396
|||||

Db 1536 TGCTGTGCTCCGCTTGAGAGGAAGACATTAGAAATGATGATGTTCTTAAGG 1477
QY 397 ATGGCAGAGAAAGACATCTGTGTGTGATATTTATTTGAAGGGATTAACATTTGAAA 456
Db 1476 ATGGCAGAGAAAGACATCTGTGTGTGATATTTATTTGAAGGGATTAACATTTGAAA 1417
QY 457 TGAAGTCAGAAATGAGCATTAACATGAGAGAAACAGACAGAAATCTTGATGCT 516
Db 1416 TGAAGTCAGAAATGAGCATTAACATGAGAGAAACAGACAGAAATCTTGATGCT 1357
QY 517 TCACAGACATGCAACAAAGAAATGAAATCTGTGATGATGAGGAGGCAAGCTGGG 576
Db 1356 TCACAGACATGCAACAAAGAAATGAAATCTGTGATGATGAGGAGGCAAGCTGGG 1297
QY 577 GAGGATTAACACAGGGGAGAGGTCAGATTTGCGCTGCTGCTTAACTGCGCTT 636
Db 1296 GAGGATTAACACAGGGGAGAGGTCAGATTTGCGCTGCTGCTTAACTGCGCTT 1237
QY 637 CATACCAATCATTTCTATTTCTTAACCTCAAAACAAAGCTGTTGTAATCTGATCT 696
Db 1236 CATACCAATCATTTCTATTTCTTAACCTCAAAACAAAGCTGTTGTAATCTGATCT 1177
QY 697 CTAGGTTCTTCTGGGCCCAACATCTCCATATATCCAGCCACACTATTTTAAATTT 756
Db 1176 CTAGGTTCTTCTGGGCCCAACATCTCCATATATCCAGCCACACTATTTTAAATTT 1117
QY 757 TAGTCCCGAGATCTGTACTGTGACCTTTCTACACTGTAGAAATAACATTACTCATTTTGT 816
Db 1116 TAGTCCCGAGATCTGTACTGTGACCTTTCTACACTGTAGAAATAACATTACTCATTTTGT 1057
QY 817 CAAA 820
Db 1056 CAAA 1053

RESULT 15
US-10-144-678A-469/C
; Sequence 469, Application US/10144678A
; Publication No. US20030157089A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yugu
; APPLICANT: Kalos, Michael D.
; APPLICANT: Henderson, Robert A.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stoik, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Derrick
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William T.
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghlon, Raymond L.
; APPLICANT: Vinals y de Bassols, Carlota
; APPLICANT: Foy, Teresa M.
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Deng, Ta
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C28
; CURRENT APPLICATION NUMBER: US/10/144,678A
; CURRENT FILING DATE: 2002-08-12
; NUMBER OF SEQ ID NOS: 1003
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 469
; LENGTH: 2229

```

; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-144-678A-469

```

```

Query Match      88.3%; Score 724; DB 12; Length 2229;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 724; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY	97	AGGTGAGAAATTAAGAAAGGCTGCTGACTTTACCATCTGAGGCCACACATCTGCTGAATG	156
DB	1776	AGGTGAGAAATTAAGAAAGGCTGCTGACTTTACCATCTGAGGCCACACATCTGCTGAATG	1717
QY	157	GAGATATTAACATCACTGAACAGCAAGATGACATTAATGTCTAAGTAGTGACATG	216
DB	1716	GAGATATTAACATCACTGAACAGCAAGATGACATTAATGTCTAAGTAGTGACATG	1657
QY	217	TTTTTGACATTTCCAGCCCTTTAAATATCCACACACAGAGAACACAAAAGAAAGCA	276
DB	1656	TTTTTGACATTTCCAGCCCTTTAAATATCCACACACAGAGAACACAAAAGAAAGCA	1597
QY	277	CAGAGATCCCTGGAGAAATGCCCGGCCCATCTTTGGTCAATGATGAGCCTCGCCCTG	336
DB	1596	CAGAGATCCCTGGAGAAATGCCCGGCCCATCTTTGGTCAATGATGAGCCTCGCCCTG	1537
QY	337	TGCTGTGTCCTGCTGTGAGGAGGACATTAAGAAATGAATGATGTGTTCTTAAAG	396
DB	1536	TGCTGTGTCCTGCTGTGAGGAGGACATTAAGAAATGAATGATGTGTTCTTAAAG	1477
QY	397	ATGGGCGAGAAACAGATCCTGTGTGATATTTATTTGACGGATTAACAGATTTGAAA	456
DB	1476	ATGGGCGAGAAACAGATCCTGTGTGATATTTATTTGACGGATTAACAGATTTGAAA	1417
QY	457	TGAAGTCACAAAGTGAGCATTTACCAATGAGAGAAACAGACAGAAAACTTTGATGCT	516
DB	1416	TGAAGTCACAAAGTGAGCATTTACCAATGAGAGAAACAGACAGAAAACTTTGATGCT	1357
QY	517	TCACAAGACATGCAACAAACAAATGATGATGATGATGATGATGATGATGATGATG	576
DB	1356	TCACAAGACATGCAACAAACAAATGATGATGATGATGATGATGATGATGATGATG	1297
QY	577	GAGAGATTAACACAGGGGCGAGAGGTACAGATTTGCCCCGCTGAACGTGCGTT	636
DB	1296	GAGAGATTAACACAGGGGCGAGAGGTACAGATTTGCCCCGCTGAACGTGCGTT	1237
QY	637	CATTAACCAATCATTTCAATTTCTAACCCTCAAAAAGCTGTTGTAATCTGATCT	696
DB	1236	CATTAACCAATCATTTCAATTTCTAACCCTCAAAAAGCTGTTGTAATCTGATCT	1177
QY	697	CTACGGTTCCTCTGGGGCCCAACATCTCCATATATCCAGCCACACTCAATTTTAAATT	756
DB	1176	CTACGGTTCCTCTGGGGCCCAACATCTCCATATATCCAGCCACACTCAATTTTAAATT	1117
QY	757	TAGTTCOCAGATCTGTACTGTGACCTTTCTACACTGTAGAAATACATTAATTTGTT	816
DB	1116	TAGTTCOCAGATCTGTACTGTGACCTTTCTACACTGTAGAAATACATTAATTTGTT	1057
QY	817	CAAA 820	
DB	1056	CAAA 1053	

Search completed: September 27, 2003, 12:16:10
 Job time : 192.028 secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 26, 2003, 21:39:38 ; Search time 1720.81 Seconds
(without alignments)
11581.589 Million cell updates/sec

Title: US-09-402-713A-4

Perfect score: 820
Sequence: 1 agaagctgcatcagaagaa.....cattactcatttgcacaa 820

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 22781392 seqs, 12152238056 residues

Word size : 0

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

EST:*
1: em_estba:*
2: em_esthum:*
3: em_estlin:*
4: em_estlinu:*
5: em_estlov:*
6: em_estlpl:*
7: em_estro:*
8: em_hic:*
9: gb_est1:*
10: gb_est2:*
11: gb_hic:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estlinu:*
16: em_estom:*
17: em_gss_hum:*
18: em_gss_liv:*
19: em_gss_pln:*
20: em_gss_vrt:*
21: em_gss_fun:*
22: em_gss_mam:*
23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_rod:*
26: em_gss_phg:*
27: em_gss_vrl:*
28: gb_gss1:*
29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	367	44.8	402 9	AA578773 nh24a04.s
2	238	29.0	290 10	BF373619 MR0-FT017
3	213	26.0	332 10	BF858286 RC5-FT019
4	199	24.3	226 10	BF858371 RC5-FT019

Result No.	Score	Query Match Length	ID	Description
5	198	24.1	282 10	BF373581 MR0-FT017
6	167	20.4	167 10	BF373406 IL2-FT015
7	103	12.6	394 28	AQ206972 HS_3238.B
8	100	12.2	572 13	BQ292550 PM0-AN008
9	86	10.5	657 9	A1557495 PT2.1_7.H
10	22	2.7	349 10	BE904264 601494521
11	22	2.7	569 13	B0836203 rF43b09.Y
12	22	2.7	804 10	BG119805 602352140
13	21	2.6	334 28	A2418181 1M0194J09
14	21	2.6	416 28	AQ712816 HS_5387.A
15	21	2.6	416 29	B2292184 SALK_1235
16	21	2.6	484 28	BH072026 RPCI-24-2
17	21	2.6	666 28	BZ007435 oeh26f11.
18	20	2.4	54 28	A2306177 1M0007G11
19	20	2.4	336 9	AV552477 AVS52477
20	20	2.4	480 14	T43985 Lambda
21	20	2.4	539 9	AV553868 AVS53868
22	20	2.4	547 28	A2812467 2M0079H11
23	20	2.4	565 9	AV881136 AV881136
24	20	2.4	571 29	B2630161 PUAAB40TD
25	20	2.4	575 13	BM185716 BM185716
26	20	2.4	575 29	B2630159 PUAAB40TB
27	20	2.4	577 29	B2630476 PUAAB89TB
28	20	2.4	597 29	B2630479 PUAAB89TD
29	20	2.4	601 13	BM143969 BM143969
30	20	2.4	603 29	CNS02108 Tetradon
31	20	2.4	605 13	BM110589 BM110589
32	20	2.4	617 14	CB003211 VVB027F07
33	20	2.4	626 13	BM253300 BM253300
34	20	2.4	632 13	BM093085 BM093085
35	20	2.4	632 14	CB004149 VVB036D02
36	20	2.4	643 13	BM094987 BM094987
37	20	2.4	645 13	BM135051 BM135051
38	20	2.4	645 13	BM165500 BM165500
39	20	2.4	647 13	BM143965 BM143965
40	20	2.4	652 9	AV871969 AV871969
41	20	2.4	656 13	BM119156 BM119156
42	20	2.4	658 13	BU742900 UT-E-FO1-
43	20	2.4	659 14	CA345815 676555 NC
44	20	2.4	661 9	AV983992 AV983992
45	20	2.4	669 9	AV850520 AV850520

ALIGNMENTS

RESULT 1
AA578773
LOCUS
DEFINITION
nh24a04.s1 NCI-CGAP_Prl Homo sapiens CDNA clone IMAGE:953262, mRNA
Sequence.
AA578773
VERSION
AA578773.1 GI:2356957
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE
1 (bases 1 to 402)
NCI-CGAP <http://www.ncbi.nlm.nih.gov/cgap>.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgabs-r@mail.nih.gov
Tissue Procurement: W. Marston Linehan, M.D., Rodrigo Chuagui, M.D.
, Michael Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: David B. Kitzman, Ph.D.
CDNA Sequencing by: Genome Systems Inc., Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www.bio.lnl.gov/dbp/image/image.html

Insert Length: 565 Std Error: 0.00
Seq primer: -40m13 fwd. ET from Amersham
High quality sequence stop: 373.
Location/Qualifiers

FEATURES

SOURCE

```
1..402
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:953262"
/sex="Male"
/dev_stage="45 years old"
/lab_host="DH10B"
/clone_lib="NCL_CGAP_Pri1"
/note="Vector: PAMPI0; Site_1: NotI; Site_2: EcoRI; 1st
strand cDNA was primed with oligo(dT)17 on 50 ng of
DNase-treated, total cellular RNA obtained from 5,000-10
,000 microdissected, histologically normal prostate
epithelial cells. Double-stranded cDNA was ligated to
EcoRI adaptors, 5 cycles of PCR applied to the cDNA with
an adaptor-specific primer, and the resulting PCR product
subcloned into PAMPI0 by the UDG-cloning method (Life
Technologies). Average insert size is 600 bp. NOTE: Not
directionally cloned. This library was constructed by
David Krizman."
BASE COUNT      128 a      86 c      84 g      104 t
ORIGIN
```

Query Match
Best Local Similarity 100.0%; Score 367; DB 9; Length 402;
Matches 367; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
430 TATTTGAACGGGATTACAGATTGAAATGAAGTCAACAAGTGACATTACCAATGAGAGG 489
|||||
36 TATTTGAACGGGATTACAGATTGAAATGAAGTCAACAAGTGACATTACCAATGAGAGG 95
490 AAAACAGACGAGAAATCTGATGCTTCAACAAGACATGCAACAACAAATGGAATCT 549
|||||
96 AAAACAGACGAGAAATCTGATGCTTCAACAAGACATGCAACAACAAATGGAATCT 155
550 GTGATGACATGAGGCGAGCAAGCTGGGGAGAGATTAACACAGGGGCGAGGGTCAAGATT 609
|||||
156 GTGATGACATGAGGCGAGCAAGCTGGGGAGAGATTAACACAGGGGCGAGGGTCAAGATT 215
610 CTGGCCCTGCTGCTTAAACTGTGGTTCATTAACCAATCATTTTCTTAACCTCA 669
Db 216 CTGGCCCTGCTGCTTAAACTGTGGTTCATTAACCAATCATTTTCTTAACCTCA 275
Qy 670 AAAACAGCTGTGTAATATCTGANTCTAGTCTTCTGGGGCCCAACATTCGCCATA 729
Db 276 AAAACAGCTGTGTAATATCTGANTCTAGTCTTCTGGGGCCCAACATTCGCCATA 335
Qy 730 TATCCAGCCACATCATTTTAAATATTTAGTCCAGATCTGACTGTGACCTTCTACA 789
Db 336 TATCCAGCCACATCATTTTAAATATTTAGTCCAGATCTGACTGTGACCTTCTACA 395
Qy 790 CTGTAGA 796
Db 396 CTGTAGA 402
```

RESULT 2
BP373619 290 bp mRNA linear EST 24-NOV-2000
DEFINITION MR0-FT0175-310800-106-n09 FT0175 Homo sapiens cDNA, mRNA sequence.
ACCESSION BP373619
VERSION BP373619.1 GI:11335644
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 290)
AUTHORS Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,

TITLE
JOURNAL
MEDLINE
PUBMED
COMMENT
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
Brunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
Simpson,A.J.G.
Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
10737800

Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?rl=MR06t2-MR0-FT0175-
310800-106-h09&t3=2000-08-31&t4=1)
Seq primer: puc 18 forward
High quality sequence stop: 290.
Location/Qualifiers

FEATURES

SOURCE

```
1..290
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="FT0175"
/note="Organ: prostate,tumor; Vector: puc18; Site_1: SmaI;
Site_2: SmaI; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the puc 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."
BASE COUNT      78 a      73 c      53 g      86 t
ORIGIN
```

Query Match
Best Local Similarity 100.0%; Score 238; DB 10; Length 290;
Matches 238; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
575 GGGAGGAGATTAACACGCGGCGAGAGGTCAGATTGCGCTGCTCTAACTGCG 634
|||||
21 GGGAGGAGATTAACACGCGGCGAGAGGTCAGATTGCGCTGCTCTAACTGCG 80
Qy 635 TTCAATACCAATCATTTTCAATTTCTAACCCCTCAAAACAAAGCTGTTGTAATCTGAT 694
Db 81 TTCAATACCAATCATTTTCAATTTCTAACCCCTCAAAACAAAGCTGTTGTAATCTGAT 140
Qy 695 CTCAGGCTTCCTTGGGGCCCAACATTCCTCAATATCCAGCCACACTCTTTTATA 754
Db 141 CTCAGGCTTCCTTGGGGCCCAACATTCCTCAATATCCAGCCACACTCTTTTATA 200
Qy 755 TTTAGTCCAGATCTGACTGTGACCTTTCTACAGCTGTAATATGATTTT 812
Db 201 TTTAGTCCAGATCTGACTGTGACCTTTCTACAGCTGTAATATGATTTT 258
```

RESULT 3
BF858286 332 bp mRNA linear EST 16-JAN-2001
DEFINITION RC5-FT0193-201100-012-D06 FT0193 Homo sapiens cDNA, mRNA sequence.
ACCESSION BF858286
VERSION BF858286.1 GI:12246030
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
AUTHORS
1 (bases 1 to 332)
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,
Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,
Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H.,
Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare,
M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
Simpson, A.J.
Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
JOURNAL
MEDLINE
PUBMED
10737800
COMMENT
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=RC5&t2=RC5-FT0193-
201100-012-D06&t3=2000-11-20&t4=1)
Seq primer: puc 18 forward
High quality sequence stop: 332.
FEATURES
source
1..332
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="FT0193"
/note="Organ: prostate_tumor; Vector: puc18; Site_1: Sma1;
Site_2: Sma1; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the puc 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."
BASE COUNT
90 a 84 c 64 g 94 t
ORIGIN
Query Match 26.0%; Score 213; DB 10; Length 332;
Best Local Similarity 100.0%; Pred. No. 1e-99;
Matches 213; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 576 GGAGGAGATTAACACGCGGCGACAGGAGTCTGGCCCTGCTCAAACTGCGCT 635
|||||
DB 61 GGAGGAGATTAACACGCGGCGACAGGAGTCTGGCCCTGCTCAAACTGCGCT 120
QY 636 TCATACCAATCATTTTCATATTTTCATACCTCAAAACAAAGCTGTTGAATATCGATC 695
|||||
DB 121 TCATACCAATCATTTTCATATTTTCATACCTCAAAACAAAGCTGTTGAATATCGATC 180
QY 636 TCTAGGTTCTCTTGGGCGCAACATTCATATATCCAGCCACACTATTTAATAT 755
|||||
DB 181 TCTAGGTTCTCTTGGGCGCAACATTCATATATCCAGCCACACTATTTAATAT 240
QY 756 TTAGTTCCAGATCTGTACTGTGACCTTTCTAC 788
|||||
DB 241 TTAGTTCCAGATCTGTACTGTGACCTTTCTAC 273
RESULT 4
BF858371/c 226 bp mRNA linear EST 16-JAN-2001
LOCUS
DEFINITION
RC5-FT0193-211100-012-E11 FT0193 Homo sapiens cDNA, mRNA sequence.
ACCESSION
BF858371 GI:12246115
VERSION
KEYWORDS
EST.
SOURCE
ORGANISM Homo sapiens (human)

REFERENCE
AUTHORS
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
1 (bases 1 to 226)
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,
Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,
Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H.,
Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare,
M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
Simpson, A.J.
Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
JOURNAL
MEDLINE
PUBMED
10737800
COMMENT
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=RC5&t2=RC5-FT0193-
211100-012-E11&t3=2000-11-21&t4=1)
Seq primer: puc 18 forward
High quality sequence stop: 226.
FEATURES
source
1..226
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="FT0193"
/note="Organ: prostate_tumor; Vector: puc18; Site_1: Sma1;
Site_2: Sma1; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the puc 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."
BASE COUNT
79 a 29 c 59 g 59 t
ORIGIN
Query Match 24.3%; Score 199; DB 10; Length 226;
Best Local Similarity 100.0%; Pred. No. 1.8e-92;
Matches 199; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 622 CCTAAACGTGGGCTCATACCAATCATTTGATATTTTACCCCTCAAAACAAAGCTGT 681
|||||
DB 226 CCTAAACGTGGGCTCATACCAATCATTTGATATTTTACCCCTCAAAACAAAGCTGT 167
QY 682 TGTAAATATGATCTCTACGAGTCTTGGGCGCAACATTCATATATCCAGCCACA 741
|||||
DB 166 TGTAAATATGATCTCTACGAGTCTTGGGCGCAACATTCATATATCCAGCCACA 107
QY 742 CTCATTTTAAATTTAGTCCAGATCTGTACTGTGACCTTTCTACACTGTAGAAATAC 801
|||||
DB 106 CTCATTTTAAATTTAGTCCAGATCTGTACTGTGACCTTTCTACACTGTAGAAATAC 47
QY 802 ATTACGATTTTGTCAAA 820
|||||
DB 46 ATTACGATTTTGTCAAA 28
RESULT 5
BF373581/c 282 bp mRNA linear EST 24-NOV-2000
LOCUS
DEFINITION
MR0-FT0175-210800-101-d05 FT0175 Homo sapiens cDNA, mRNA sequence.
ACCESSION
BF373581 GI:11335606
VERSION
KEYWORDS
EST.

	SOURCE	ORGANISM
	Homo sapiens (human)	Homo sapiens
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.	
REFERENCE	1 (bases 1 to 282)	
AUTHORS	Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Britones, M.R., Nagai, M.A., da Silva, M. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bala, G.S., Simpson, D.H., Brunstein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.V. and Simpson, A.J.	
TITLE	Shotgun sequencing of the human transcriptome with ORF expressed sequence tags	
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)	
MEDLINE	20202663	
PUBMED	10737800	
COMMENT	Contact: Simpson A.J.G. Laboratory of Cancer Genetics Ludwig Institute for Cancer Research Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil Tel: +55-11-2704922 Fax: +55-11-2707001 Email: asimpson@ludwig.org.br This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?l1=MR0&t2=MR0-FT0175-210800-101-d05&t3=2000-08-21&t4=1) Seq primer: puc 18 forward High quality sequence start: 35 High quality sequence stop: 282. Location/Qualifiers 1..282 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /dev_stage="Adult" /clone_lib="FT0175" /note="Organ: prostate,tumor; Vector: puc18; Site:1: Sma1; Site:2: Sma1; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the puc 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions." BASE COUNT 85 a 51 c 70 g 76 t ORIGIN	
	Query Match 24.1%; Score 198; DB 10; Length 282; Best Local Similarity 100.0%; P-rod. No. 6.0e-92; Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
OY	588 CACGGGGAGAGGGGTACAGATTCTGGCCCTCTGCTCTAACTGTCGCTTAACCAAT 647	
DBD	262 CACGGGGAGAGGGGTACAGATTCTGGCCCTCTGCTCTAACTGTCGCTTAACCAAT 203	
OY	648 CATTTCATATTTCTAACCCCTCAAAACAAGGCTGTGTAATATCTGATCTACAGGTTCC 707	
DB	202 CATTTCATATTTCTAACCCCTCAAAACAAGGCTGTGTAATATCTGATCTACAGGTTCC 143	
OY	708 TCTGGGGCCCAACATTTCTCATATATCCAGCCACACTCTTTTAAATATTTAGTCCAGA 767	
DB	142 TCTGGGGCCCAACATTTCTCATATATCCAGCCACACTCTTTTAAATATTTAGTCCAGA 83	
OY	768 TCTGTACGTGACCTTC 785	
DB	82 TCTGTACGTGACCTTC 65	
RESULT 6	BP373406 167 bp mRNA linear EST 24-NOV-2000	
LOCUS	BP373406	
DEFINITION	112-FT0159-070800-120-H01 FT0159 Homo sapiens CDNA, mRNA sequence.	

ACCESSION	BF373406
VERSION	BF373406.1
KEYWORDS	GI:11335431
SOURCE	EST.
ORGANISM	Homo sapiens (human)
REFERENCE	Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eumetazoa; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 167) Dias Neto, E., Garcia Correa, R., Verjovsky-Almeida, S., Brito, M.R., Nagel, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bala, G.S., Simpson, D.H., Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.
TITLE	Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE	20202663
PUBMED	10737800
COMMENT	Contact: Simpson A.J.G. Laboratory of Cancer Genetics Ludwig Institute for Cancer Research Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil Tel: +55-11-2704922 Fax: +55-11-2707001 Email: asimpson@ludwig.org.br This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?cl=IL2&t2=IL2-FT0159 070800-12c-H01&t3=2000-08-07&t4=1) Seq primer: puc 18 forward High quality sequence stop: 167. Location/Qualifiers 1..167 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /dev_stage="Adult" /clone_1lb="FT0159" /note="Organ: prostate.tumor; Vector: puc18; Site.1: Smal; Site.2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the puc 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
BASE COUNT	47 a 38 c 49 g 33 t
ORIGIN	
Query Match	20.4%; Score 167; DB 10; Length 167;
Best Local Similarity	100.0%; Pred. No. 8.3e-76;
Matches	167; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY	254 CACAGGAAGCACAAAAGGAGACACAGATCCCTGGGAAATGCCGCCCATCTTG 313 Db 1 CACAGGAAGCAAAAAGGAGACACAGATCCCTGGGAAATGCCGCCCATCTTG 60 OY 314 GGTATCGATAGAGCCTGCCTGTCCTGGTCCGCTTGCGCTTGAGAGAAGACATTAGAAAA 373 Db 61 GGTCATCGATAGAGCCTGCCTGTCCTGGTCCGCTTGCGCTTGAGAGAAGACATTAGAAAA 120 OY 374 TGAATTGATGTGTTCTTAAGAGATGGGACAGAAAACAGATCTGTT 420 Db 121 TGAATTGATGTGTTCTTAAGAGATGGGACAGAAAACAGATCTGTT 167
RESULT 7	
A0206972/c	394 bp DNA linear GSS 17-SEP-1998
Locus	HS-3238_B1_G11_MR CIT Approved Human Genomic Sperm Library D Homo
DEFINITION	sapiens genomic clone Plate-338 Col-21 Row-N, genomic survey sequence.

ACCESSION AQ206972.1 GI:3617542
VERSION GSS.
KEYWORDS Homo sapiens (human)
SOURCE
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 394)
AUTHORS Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T., Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and Hood,L.
TITLE Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
MEDLINE 99380589
PUBMED 10449764
COMMENT Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Sequence Tagged Connector
Plate: 3238 row: N column: 21
Class: BAC ends
High quality sequence stop: 394.
FEATURES
source
1..394
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/clone="Plate=3238 Col=21 Row=N"
/sex="male"
/clone_1lb="CIR Approved Human Genomic Sperm Library D"
/note="Organ: sperm; Vector: pBelOBAC11; BAC Clones in E-Coli DH10B"
BASE COUNT 134 a 62 c 93 g 103 t 2 others
ORIGIN
Query Match 12.6%; Score 103; DB 28; Length 394;
Best Local Similarity 100.0%; Pred. No. 3.2e-42;
Matches 103; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 718 ACATTCCTCATATCCACGCCACTGATTTTAAATTAATTAATCCAGATCTGACTGT 777
DB 381 ACATTCCTCATATATCCACGCCACTGATTTTAAATTAATTAATTAATCCAGATCTGACTGT 322
QY 778 GACCTTCTACACTGTAGATATACATTAATCTCAATTTTGTTCAGAA 820
DB 321 GACCTTCTACACTGTAGATATACATTAATCTCAATTTTGTTCAGAA 279
RESULT 8
LOCUS BQ292550 572 bp mRNA linear EST 15-MAY-2002
DEFINITION PMO-AN0087-240501-019-a06 AN0087 Homo sapiens cDNA, mRNA sequence.
ACCESSION BQ292550
VERSION BQ292550.1 GI:20801500
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 572)
AUTHORS Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Brlones,M.R., Nagai,M.A., da Silva,M. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.
TITLE Shotgun sequencing of the human transcriptome with ORF expressed sequence tags

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE 20202663
PUBMED 10737800
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=PM06t2-PM0-AN0087-240501-019-a06t3-2001-05-24&t=1)
Seq primer: puc 18 forward
High quality sequence stop: 572.
FEATURES
source
1..572
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_1lb="AN0087"
/note="Organ: amnion,normal; Vector: puc18; Site:1: Sma1; Site:2: Sma1; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
BASE COUNT 150 a 90 c 169 g 163 t
ORIGIN
Query Match 12.2%; Score 100; DB 13; Length 572;
Best Local Similarity 100.0%; Pred. No. 1.4e-40;
Matches 100; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AGACCTGGCATCAGAAACAGAGGGAGATTTGTGTCGCCAGCCAGAGACCGAG 60
DB 116 AGACCTGGCATCAGAAACAGAGGGAGATTTGTGTCGCCAGCCAGAGACCGAG 175
QY 61 GAAGATCTGCATGTCGGAAGACCTGATGATACAGAGCT 100
DB 176 GAAGATCTGCATGTCGGAAGACCTGATGATACAGAGCT 215
RESULT 9
LOCUS AI557495 657 bp mRNA linear EST 09-AUG-1999
DEFINITION PT2.1.7_H12.r tumor2 Homo sapiens cDNA 3', mRNA sequence.
ACCESSION AI557495
VERSION AI557495.1 GI:4489858
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 657)
AUTHORS Huang,G.M., Ng,W.L., Farkas,J., He,L., Liang,H.A., Gordon,D., Yu,J. and Hood,L.
TITLE Prostate cancer expression profiling by cDNA sequencing analysis
JOURNAL Genomics 59 (2), 178-186 (1999)
MEDLINE 9935982
PUBMED 10409429
COMMENT Contact: Guyang Mathew Huang
Leroy Hood
University of Washington
Department of Molecular Biotechnology, Box 357730, University of Washington, Seattle, WA 98195
Tel: 5106280100
Fax: 5106280108
Email: huanggm@yahoo.com.

```

FEATURES
  source
    Location/Qualifiers
      1. .657
        /organism="Homo sapiens"
        /mol_type="mRNA"
        /db_xref="taxon:9606"
        /clone_lib="tumor2"
        /note="Organ: Prostate; Vector: pBluescript; Directional
        cDNA library was constructed using Lambda ZP II kit
        (Stratagene). mRNA was extracted from a frozen prostate
        tumor tissue (Mayo Clinics)."
BASE COUNT      179 a      112 c      153 g      166 t      47 others
ORIGIN
Query Match      10.5%; Score 86; DB 9; Length 657;
Best Local Similarity 100.0%; Pred. No. 3e-33;
Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 CAGAAAACAGAGGGGAGATTGTGTGCTCCAGCCGAGGAGACGAGAAATCTGCAT 72
    |||||||
Db 14 CAGAAAACAGAGGGGAGATTGTGTGCTCCAGCCGAGGAGACGAGAAATCTGCAT 73
    |||||||
QY 73 GGTGGAAGAGACTGATGATACAGAG 98
    |||||||
Db 74 GGTGGAAGAGACTGATGATACAGAG 99
    |||||||

RESULT 10
BE904264/c 349 bp mRNA linear EST 20-OCT-2000
LOCUS 601494521F2 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3896348 5',
DEFINITION mRNA sequence.
ACCESSION BE904264
VERSION BE904264.1 GI:10396339
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 349)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LMN)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LMN at:
http://image.llnl.gov
Plate: LLM9689 row: j column: 05
High quality sequence start: 3
High quality sequence stop: 10.
Location/Qualifiers
  1. .349
    /organism="Homo sapiens"
    /mol_type="mRNA"
    /db_xref="taxon:9606"
    /clone="IMAGE:3896348"
    /tissue_type="epithelioid carcinoma"
    /lab_host="DH10B (phage-resistant)"
    /clone_lib="NIH_MGC_70"
    /note="Organ: pancreas; Vector: pCMV-SPORT6; Site.1: NotI;
    Site.2: SalI; Cloned unidirectionally. Primer: Oligo dT.
    Average insert size 1.1 kb. Library constructed by Life
    Technologies."
BASE COUNT      114 a      61 c      93 g      81 t
ORIGIN
Query Match      2.7%; Score 22; DB 10; Length 349;
Best Local Similarity 100.0%; Pred. NO. 6.3;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 757 TAGTCCAGATCTGACTGTG 778
    |||||||
Db 64 TAGTCCAGATCTGACTGTG 433

RESULT 11
B0836203 569 bp mRNA linear EST 09-JAN-2003
LOCUS r143b09.y1 Meloidogyne hapla J2 PAMP1 v1 Meloidogyne hapla cDNA 5',
DEFINITION r143b09.y1 Meloidogyne hapla J2 PAMP1 v1 Meloidogyne hapla cDNA 5',
mRNA sequence.
ACCESSION B0836203
VERSION B0836203.1 GI:22140517
KEYWORDS EST.
SOURCE Meloidogyne hapla
ORGANISM Meloidogyne hapla
Eukaryota; Metazoa; Nematoda; Chromadorea; Tylenchida; Tylenchina;
Tylenchoidea; Heteroderidae; Meloidogyninae; Meloidogyne.
REFERENCE 1 (bases 1 to 569)
AUTHORS McCarter,J., Clifton,S., Chapell,B., Pape,D., Martin,J., Wylie,T.,
Dante,M., Marra,M., Hillier,L., Kucaba,T., Thelning,B., Bowers,Y.,
Gibbons,M., Ritter,E., Bennett,J., Franklin,C., Tsagarisbill,R.,
Ronko,I., Kennedy,S., McGuire,L., Beck,C., Underwood,K., Steptoe
,M., Allen,M., Person,B., Swaller,T., Harvey,N., Schurk,R., Kohn,S.,
Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. and
Wilson,R.
TITLE The Washington Univ. Nematode EST Project, 1999
JOURNAL Unpublished
COMMENT Contact: McCarter JP
The Washington Univ. Nematode EST Project, 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@wustl.wustl.edu
This clone will not be made available due to an unidentified
microbial contamination of the source material.
Seq primer: -40RP from gibco
High quality sequence stop: 423.
Location/Qualifiers
  1. .569
    /organism="Meloidogyne hapla"
    /mol_type="mRNA"
    /db_xref="taxon:6305"
    /dev_stage="J2"
    /lab_host="DH10B"
    /clone_lib="Meloidogyne hapla J2 PAMP1 v1"
    /note="Vector: pAMP1 (Gibco); Site.1: NotI; Site.2: SalI;
    The library was constructed by Claire Murphy and Dr. James
    McCarter at Washington University, St. Louis. The cDNA was
    made by using Dynabead oligo-dT priming (Dynal). PCR based
    library using a modified protocol from the SMART PCR cDNA
    Synthesis kit from Clontech. Directionally cloned into the
    UDG sites of PAMP1. J2 were provided by Dr. Valerie
    Williamson of the University of California at Davis
    (vwilliams@ucdavis.edu)."
BASE COUNT      248 a      86 c      56 g      179 t
ORIGIN
Query Match      2.7%; Score 22; DB 13; Length 569;
Best Local Similarity 100.0%; Pred. NO. 7.7;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 499 GAGAAATCTTGATGGCTTCAC 520
    |||||||
Db 336 GAGAAATCTTGATGGCTTCAC 357

RESULT 12
B0119805 804 bp mRNA linear EST 30-JAN-2001
LOCUS 602352140F1 NIH_MGC_90 Homo sapiens cDNA clone IMAGE:4450424 5',
DEFINITION mRNA sequence.

```

ACCESSION BG119805
 VERSION BG119805.1 GI:12613311
 KEYWORDS EST
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 804)
 NIH-MGC <http://mgs.nci.nih.gov/>
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgabs-remail.nih.gov
 Tissue Procurement: ATCC
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILN)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/ILN at:
<http://image.llnl.gov>
 Plate: LLM10235 row: p column: 09
 High quality sequence stop: 310.
 Location/Qualifiers
 1..804
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:4450424"
 /tissue_type="adenocarcinoma, cell line"
 /lab_host="DH10B (phage-resistant)"
 /note="Organ: liver; Vector: pCMV-SPORT6; Site:1; NotI; Site:2; SalI; Cloned unidirectionally; oligo-dT primed. Average insert size 1.7 kb. Library enriched for full-length clones and constructed by Life Technologies. Note: this is a NIH-MGC Library."
 BASE COUNT 283 a 200 c 202 g 119 t
 ORIGIN
 Query Match 2.7%; Score 22; DB 10; Length 804;
 Best Local Similarity 100.0%; Pred. No. 8.9;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 483 TGAGAGGAAACAGACGAGAA 504
 ||||||||||||||||||||
 DB 734 TGAGAGGAAACAGACGAGAA 755
 ||||||||||||||||||||
 RESULT 13
 AZ418181/c 334 bp DNA linear GSS 03-OCT-2000
 LOCUS 1M019409F Mouse 10kb plasmid UGCG1M library Mus musculus genomic
 DEFINITION clone UGCG1M019409 F, genomic survey sequence.
 ACCESSION AZ418181
 VERSION AZ418181.1 GI:10542194
 KEYWORDS GSS
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 334)
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamli, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tinney, A., von Niederhausen, A. and Wright, D., Weiss, R.
 TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
 JOURNAL Unpublished
 COMMENT Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT 84112, USA

tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0194 row: j column: 09
 Seq primer: CGTGTAAACGACGCGCCAGT
 Class: plasmid ends
 High quality sequence stop: 334.
 Location/Qualifiers
 1..334
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UGCG1M019409F"
 /sex="Male"
 /lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UGCG1M library"
 /note="Vector: PMD42uv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
 (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (q147321419b1AF129072.1), a copy-number inducible derivative of plasmid RL. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
 BASE COUNT 59 a 53 c 99 g 123 t
 ORIGIN
 Query Match 2.6%; Score 21; DB 28; Length 334;
 Best Local Similarity 100.0%; Pred. No. 20;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 248 CACACACACGAGACGACAAA 268
 ||||||||||||||||||||
 DB 147 CACACACACGAGACGACAAA 127
 ||||||||||||||||||||
 RESULT 14
 A0712816 416 bp DNA linear GSS 13-JUL-1999
 LOCUS HS_5387_A2_E08-SP6E RPCI-11 Human Male BAC library Homo sapiens
 DEFINITION genomic clone Plate=963 Col=16 Row=I, genomic survey sequence.
 ACCESSION A0712816
 VERSION A0712816.1 GI:5462132
 KEYWORDS GSS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 416)
 Mahairas, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T., Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D. and Hood, L.
 TITLE Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
 MEDLINE 99380589
 PUBMED 10449764
 COMMENT Contact: Mahairas GG, Wallace JC, Hood L
 High Throughput Sequencing Center
 University of Washington

401 Queen Anne Avenue North, Seattle, WA 98109, USA
 Tel: (206) 616-3618
 Fax: (206) 616-3887
 Email: jwallace@u.washington.edu
 Clones are derived from the human BAC library RPCI-11. For BAC library availability, please contact Pieter de Jong (pieter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm) or from Research Genetics (info@resgen.com). BAC end Web Server: http://www.htsc.washington.edu
 Plate: 963 row: I column: 16
 Seq primer: SP6
 Class: BAC ends
 High quality sequence stop: 416.

FEATURES

source

Location/Qualifiers
 1. .416

/organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"
 /clone="Plate=963 Col=16 Row=1"
 /sex="male"

/note="Vector: pBAC3.6; Site_1: EcoRI; Site_2: EcoRI; Male blood DNA was isolated from one randomly chosen donor and partially digested with a combination of EcoRI and EcoRI Methylase. Size selected DNA was cloned into the pBAC3.6 vector at EcoRI sites"

BASE COUNT

122 a 101 c 75 g 118 t

ORIGIN

Query Match 2.6%; Score 21; DB 28; Length 416;
 Best Local Similarity 100.0%; Pred. No. 22;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 660 CTAACTCAAAACAAAGCTG 680
 ||||||||||||||||||
 Db 186 CTAACTCAAAACAAAGCTG 206

RESULT 15 416 bp DNA linear GSS 24-OCT-2002
 B2292184 SALK_123591.42.40.x Arabidopsis thaliana TDNA insertion lines
 LOCUS Arabidopsis thaliana genomic clone SALK_123591.42.40.x, genomic
 DEFINITION survey sequence.

ACCESSION B2292184

VERSION B2292184.1 GI:24338800

KEYWORDS GSS.
 SOURCE Arabidopsis thaliana (thale cress)

ORGANISM

Arabidopsis thaliana
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids
 ; eurosids II; Brassicales; Brassicaceae; Arabidopsids.
 1 (bases 1 to 416)

REFERENCE

Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Gadrinab,
 C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P.,
 Zimmerman,J. and Ecker,J.R.
 A Sequence-Indexed Library of Insertion Mutations in the
 Arabidopsis Genome

TITLE

Unpublished

JOURNAL

Contact: Joseph R. Ecker
 Salk Institute Genomic Analysis Laboratory (SIGNAL)
 The Salk Institute for Biological Studies
 10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
 Tel: 858 453 4100 x1752
 Fax: 858 558 6379

Email: ecker@salk.edu
 This is single pass sequence recovered from the left border of
 TDNA. This sequence lies within an annotated exon of At2g01770.
 Class: TDNA tagged.

FEATURES

source

Location/Qualifiers
 1. .416
 /organism="Arabidopsis thaliana"

/mol_type="genomic DNA"
 /strain="Columbia 0"
 /db_xref="taxon:3702"
 /clone="SALK_123591.42.40.x"
 /note="PCR was performed on Arabidopsis thaliana TDNA insertion lines
 each of which contains one or more TDNA insertion
 elements. The resultant fragment for each line was
 directly sequenced to determine the genomic sequence at
 the site of insertion. Details of the protocols used can
 be found at http://signal.salk.edu/cdna_protocols.html"

BASE COUNT 115 a 77 c 81 g 141 t
 ORIGIN

Query Match 2.6%; Score 21; DB 29; Length 416;
 Best Local Similarity 100.0%; Pred. No. 22;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 518 CACAAGACATGCACAAACAA 538
 ||||||||||||||||||
 Db 216 CACAAGACATGCACAAACAA 196

Search completed: September 27, 2003, 11:35:46
 Job time : 1722.81 secs

XX 09-APR-1998; 98WO-CA00346.
PF Best Local Similarity 98.6%; Score 3531; DB 19; Length 3582;
XX 10-APR-1997; 97US-0041836.
XX (DIAG-) DIAGNOCURE INC.
XX Bussemakers MUG;
PI WPI: 1998-568347/48.
DR P-Psdb: AAM79738.
XX

PT New nucleic acid encoding prostate cancer antigen 3 - for diagnosis,
XX prevention and treatment of prostatic cancer
XX

PS Claim 3; Fig 5B-5F; 11pp; English.

CC The present sequence represents the prostate cancer antigen (PCA3)
CC wild-type cDNA sequence comprising of exons 1, 2, 3, 4a-4d of the
CC PCA3 gene. The invention claims for PCA3 cDNA variants and the
CC proteins they encode. The invention also claims for antibodies
CC against PCA3 protein. The antibodies are claimed to be useful for
CC detecting PCA3 protein in immunosay tests, for diagnosing, assessing
CC and prognosis of prostatic cancer (PC). Antibodies, optionally
CC coupled to a cytotoxin or radioisotope, and nucleic acids antisense
CC to PCA3 cDNA are claimed to be useful for treating PC, while determining
CC elevated levels of PCA3 (as RNA or protein) is useful for detecting a
CC predisposition to development of PC, e.g. in prenatal tests. Detecting
CC PCA3 protein allows differentiation between malignant and benign
CC prostatic disease, and the level of PCA3 expression allows correlation
CC with the grade of tumour. PCA3 protein and its fragments are also
CC claimed to be useful in vaccines for preventing PC; in drug screens
CC for identifying specific (ant)agonists (potentially useful
CC therapeutically) and for studying protein-DNA interactions.

XX Sequence 3582 BP; 1052 A; 788 C; 679 G; 1063 T; 0 other;

Query Match 98.6%; Score 3531; DB 19; Length 3582;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3581; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ACAGAGAAATATAGCAAGTGGCGAGAGTGGCATCAGAAAAACAGAGGGGAGATTGTGT 60
DB 1 ACAGAGAAATATAGCAAGTGGCGAGAGTGGCATCAGAAAAACAGAGGGGAGATTGTGT 60
QY 61 GGTGCGACCGGAGGAGACAGAGATCTGCATGTGGAGAGACCTGATGATACAGAG 120
DB 61 GGTGCGACCGGAGGAGACAGAGATCTGCATGTGGAGAGACCTGATGATACAGAG 120
QY 121 GAATTACAAACATATCTAGTGTTCATGAAACACCAAGATTAATAGTGAAGAGCTA 180
DB 121 GAATTACAAACATATCTAGTGTTCATGAAACACCAAGATTAATAGTGAAGAGCTA 180
QY 181 GTCCGTGTGAGTCTCCATGACAGACAGGGCTGATCACCATGAGGGGCTTTCTGAG 240
DB 181 GTCCGTGTGAGTCTCCATGACAGACAGGGCTGATCACCATGAGGGGCTTTCTGAG 240
QY 241 TACTCAGTGCAGCAAGAAAGACTACAGACATCTCAATGCGAGGGGTGAGAAATAGAAA 300
DB 241 TACTCAGTGCAGCAAGAAAGACTACAGACATCTCAATGCGAGGGGTGAGAAATAGAAA 300
QY 301 GGGCTGACCTTTTCCATCTGAGGCGACACATCTGCGTAATGAGAGATTAATACATCAC 360
DB 301 GGGCTGACCTTTTCCATCTGAGGCGACACATCTGCGTAATGAGAGATTAATACATCAC 360
QY 361 TAGAAGACGCAAGATGACATATATATGCTAAGTAGTGAATGTTTGGCATTTCCAG 420
DB 361 TAGAAGACGCAAGATGACATATATATGCTAAGTAGTGAATGTTTGGCATTTCCAG 420
QY 421 CCCCTTTAAATATATCCACACACAGAGAAACCAAAAGAGACACAGAGATCCCTGGGAGA 480
DB 421 CCCCTTTAAATATATCCACACACAGAGAAACCAAAAGAGACACAGAGATCCCTGGGAGA 480

QY 481 AATGCCGCGCCCATCTTGGGTGATGATAGACCTCGCCCTGTGCTGCCGCTTGT 540
DB 481 AATGCCGCGCCCATCTTGGGTGATGATAGACCTCGCCCTGTGCTGCCGCTTGT 540
QY 541 GAGGGAAGACATTGAAATGAATGATGTGCTTAAAGAGATGGGACAGAAACAGA 600
DB 541 GAGGGAAGACATTGAAATGAATGATGTGCTTAAAGAGATGGGACAGAAACAGA 600
QY 601 TCTGTGTGATATTTTGAACGCGGATACAGATTTGAATGAAGTCAAAAGTGAG 660
DB 601 TCTGTGTGATATTTTGAACGCGGATACAGATTTGAATGAAGTCAAAAGTGAG 660
QY 661 CATTAACATAGAGAGAAACAGACAGAGAAATCTTGATGCTTACAGACATGACA 720
DB 661 CATTAACATAGAGAGAAACAGACAGAGAAATCTTGATGCTTACAGACATGACA 720
QY 721 AACAAAATGGAATCTGATGACATGAGGAGCCACCTGGGAGGAGATTAACACGGG 780
DB 721 AACAAAATGGAATCTGATGACATGAGGAGCCACCTGGGAGGAGATTAACACGGG 780
QY 781 GCAGAGGTCAGAGATTCGGCCCTGCTCCTAACTGCGCTGATACCAAAATCATTTG 840
DB 781 GCAGAGGTCAGAGATTCGGCCCTGCTCCTAACTGCGCTGATACCAAAATCATTTG 840
QY 841 ATATTTCTAACCTCAAAACAAAGCTGTGTAATATCTGATCTAGGCTTCTTGGG 900
DB 841 ATATTTCTAACCTCAAAACAAAGCTGTGTAATATCTGATCTAGGCTTCTTGGG 900
QY 901 CCCAATCTTCATATCTGACGACACACCTATTTAATTTAGTTCCAGATTCGTA 960
DB 901 CCCAATCTTCATATCTGACGACACACCTATTTAATTTAGTTCCAGATTCGTA 960
QY 961 CTGTGACCTTCTACACTGTAGATTAACATTAATCTTTGTTGTTGTTGTTGTTGTT 1020
DB 961 CTGTGACCTTCTACACTGTAGATTAACATTAATCTTTGTTGTTGTTGTTGTTGTT 1020
QY 1021 GCTGCTTAATATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1080
DB 1021 GCTGCTTAATATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1080
QY 1081 AACAGGCTGGGAGACATCTCAAGATCTTCCAGAGGTTATCTTACACACAGCATGA 1140
DB 1081 AACAGGCTGGGAGACATCTCAAGATCTTCCAGAGGTTATCTTACACACAGCATGA 1140
QY 1141 TCATTAGGAGTGAATATCTAATCAACATCATCTCAGTGTCTTGGCCATCTGAAT 1200
DB 1141 TCATTAGGAGTGAATATCTAATCAACATCATCTCAGTGTCTTGGCCATCTGAAT 1200
QY 1201 TCATTTCCTCCTTTTGTGCTCCTTCTCAAGACCTCAAAATGTCTCATTTAATATCA 1260
DB 1201 TCATTTCCTCCTTTTGTGCTCCTTCTCAAGACCTCAAAATGTCTCATTTAATATCA 1260
QY 1261 GGATTAACCTTTTAACTGGAAGATTCATGATGATGATGATGATGATGATGATGAT 1320
DB 1261 GGATTAACCTTTTAACTGGAAGATTCATGATGATGATGATGATGATGATGATGAT 1320
QY 1321 ATTAATATATTTGTTTCCAGTGCAGAGATGATGATGATGATGATGATGATGATGAT 1380
DB 1321 ATTAATATATTTGTTTCCAGTGCAGAGATGATGATGATGATGATGATGATGATGAT 1380
QY 1381 GATTTTTCCTCAATATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1440
DB 1381 GATTTTTCCTCAATATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1440
QY 1441 AGCCTTCCTCCATCTCCAGCCTTATCTGATCAGACATCAACCCCTCCATACACCT 1500
DB 1441 AGCCTTCCTCCATCTCCAGCCTTATCTGATCAGACATCAACCCCTCCATACACCT 1500
QY 1501 AAACAAATCTAATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1560
DB 1501 AAACAAATCTAATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1560
QY 1561 GAGAGAGCTTCTTGTCTTAAATCTAGATGATGATGATGATGATGATGATGATGAT 1620

Dp	1561	GAGAGCTCTTCTTGTCTCTTAATCTAGATATGTAAGTTTGATTAAGTTGACTA	1620
Qy	1561	TCTTACTTTCATGCAAAAGAGGACACATATAGATTATCATCTCATGAGACACAAATA	1680
Dp	1561	TCTTACTTTCATGCAAAAGAGGACACATATAGATTATCATCTCATGAGACACAAATA	1680
Qy	1561	CTAAAGTGTAATTTGATTATAGATTTAGATTAATATATGAATGCAAGGCCACAGA	1740
Dp	1561	CTAAAGTGTAATTTGATTATAGATTTAGATTAATATATGAATGCAAGGCCACAGA	1740
Qy	1741	GGGAATGTTATGGGGACGTTTGTAGCCCTGGGATGGAGCAAAAGCAGGAACCTCA	1800
Dp	1741	GGGAATGTTATGGGGACGTTTGTAGCCCTGGGATGGAGCAAAAGCAGGAACCTCA	1800
Qy	1801	TAGATATGTAATATATATCTTCTATCTATCTATCTATCTATCTATCTATCTATCT	1860
Dp	1801	TAGATATGTAATATATATCTTCTATCTATCTATCTATCTATCTATCTATCTATCT	1860
Qy	1861	CACAGAATTCATGCAATGCAATCCCAAGGTAACCTTATCCATTTTCATGATGATGC	1920
Dp	1861	CACAGAATTCATGCAATGCAATCCCAAGGTAACCTTATCCATTTTCATGATGATGC	1920
Qy	1921	GCTTATGAAATTTGGCAATCATATCTGTCCTTATCTCAACTTTGAAATGTTGTGCC	1980
Dp	1921	GCTTATGAAATTTGGCAATCATATCTGTCCTTATCTCAACTTTGAAATGTTGTGCC	1980
Qy	1981	TTTGTAGTTAATTTGAAAGAAATAGGGACACTGTTGAGGACACTTTAGGTTGACCTGAC	2040
Dp	1981	TTTGTAGTTAATTTGAAAGAAATAGGGACACTGTTGAGGACACTTTAGGTTGACCTGAC	2040
Qy	2041	AATTAAGATTTTACAAAGAGCTACTCAGAGCAGTTGTTAAGAGCTCTGTGTGTGTGT	2100
Dp	2041	AATTAAGATTTTACAAAGAGCTACTCAGAGCAGTTGTTAAGAGCTCTGTGTGTGTGT	2100
Qy	2101	GTTGT	2160
Dp	2101	GTTGT	2160
Qy	2161	TTTAAAGCAGCATTTTTCAAATGGACATAGACTGGCAATGATGTTATCCACACCATAT	2220
Dp	2161	TTTAAAGCAGCATTTTTCAAATGGACATAGACTGGCAATGATGTTATCCACACCATAT	2220
Qy	2221	CTCATTTATCTCCAGTAATGTGATTAATGTGATCTGTTAACATATTAATAAAGTTGAC	2280
Dp	2221	CTCATTTATCTCCAGTAATGTGATTAATGTGATCTGTTAACATATTAATAAAGTTGAC	2280
Qy	2281	TTTCAAAAAGCAGCTGGAATGACACACACATATGATATCTATCTCTACATCA	2340
Dp	2281	TTTCAAAAAGCAGCTGGAATGACACACACATATGATATCTATCTCTACATCA	2340
Qy	2341	GCTCACACCTGTTGACATATATGTTTGAAGACACACCTGTTGGGCTCTCTTAAGC	2400
Dp	2341	GCTCACACCTGTTGACATATATGTTTGAAGACACACCTGTTGGGCTCTCTTAAGC	2400
Qy	2401	AAATTAATCTGATTAAGTCTGAGCTGGGGCTGTGCATCAGGCGGTTTGAGAAATTTCAA	2460
Dp	2401	AAATTAATCTGATTAAGTCTGAGCTGGGGCTGTGCATCAGGCGGTTTGAGAAATTTCAA	2460
Qy	2461	TTTCTACAGCAGACCCAGATTTGAAATTCCTCATCTTTTAAAGAAATCAATTTACAGGTTTG	2520
Dp	2461	TTTCTACAGCAGACCCAGATTTGAAATTCCTCATCTTTTAAAGAAATCAATTTACAGGTTTG	2520
Qy	2521	GAGAGAAATTCAGACAGCTCAGGCTGTTACTATATGTCCTGAACTTCTGCTCTGTTG	2580
Dp	2521	GAGAGAAATTCAGACAGCTCAGGCTGTTACTATATGTCCTGAACTTCTGCTCTGTTG	2580
Qy	2581	TGTTTCATGGAATGCAATTAATATGTTATCTTTGAACATGATGCTCATAGAGAGATA	2640
Dp	2581	TGTTTCATGGAATGCAATTAATATGTTATCTTTGAACATGATGCTCATAGAGAGATA	2640
Qy	2641	TAAAGACTCTGAGTGAATATCAACTTTAGGATTCAAAGAAATTTAGATTTAAGCTCACA	2700
Dp	2641	TAAAGACTCTGAGTGAATATCAACTTTAGGATTCAAAGAAATTTAGATTTAAGCTCACA	2700

Db	2641	TTAAGACTCTGATGATATATCAACTTTAGGATTCTAAAGAAATATTAGATTTTAAAGCTACA	2700
OY	2701	CTGGTCTAAAAGAACCAAGATATCAAGAAGACTGTAGCTGTCTAGCTGCCCATCTCTGTGA	2760
Db	2701	CTGGTCTAAAAGAACCAAGATATCAAGAAGACTGTAGCTGTCTAGCTGCCCATCTCTGTGA	2760
OY	2761	GCCACAAACCAACAGCAGAGACCCAAACGCATGTCTAGATCCTTAAATCAAGAAACCACTG	2820
Db	2761	GCCACAAACCAACAGCAGAGACCCAAACGCATGTCTAGATCCTTAAATCAAGAAACCACTG	2820
OY	2821	TCATGAGTGTGAATTCCTCTATTATTAAGATGCTAGCTGTGGCCATCTGTGGCTCTCTCTT	2880
Db	2821	TCATGAGTGTGAATTCCTCTATTATTAAGATGCTAGCTGTGGCCATCTGTGGCTCTCTCTT	2880
OY	2881	GACACATATTAAGCTTCTAGCCTTTGCTTCCAGCACTTTTATCTTTTCTCAACACATCGC	2940
Db	2881	GACACATATTAAGCTTCTAGCCTTTGCTTCCAGCACTTTTATCTTTTCTCAACACATCGC	2940
OY	2941	TTACCAATCCTCTCTCTGTCTGTGGCTTTGGACTTCCCCAAAGATTTTAAAGACTCT	3000
Db	2941	TTACCAATCCTCTCTCTGTCTGTGGCTTTGGACTTCCCCAAAGATTTTAAAGACTCT	3000
OY	3001	CAAGCTTTTCTTCCATCCCCACACACTAAGCTGAATTTGGCCAGACCCCTTATTTATTTAA	3060
Db	3001	CAAGCTTTTCTTCCATCCCCACACACTAAGCTGAATTTGGCCAGACCCCTTATTTATTTAA	3060
OY	3061	TTTCCAAATAGATGCTGCTATAGGGCTTAATATGGCTTTAGATGAACATTAGATATTTAAAG	3120
Db	3061	TTTCCAAATAGATGCTGCTATAGGGCTTAATATGGCTTTAGATGAACATTAGATATTTAAAG	3120
OY	3121	TCCTAAGAGGTTCAAAATATCCAACTATATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	3180
Db	3121	TCCTAAGAGGTTCAAAATATCCAACTATATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	3180
OY	3181	CCCATATATTAAGTATGATCAACGTAAGAGATGTGCCCAAGATGCCAGTCAAAATGAAGAAC	3240
Db	3181	CCCATATATTAAGTATGATCAACGTAAGAGATGTGCCCAAGATGCCAGTCAAAATGAAGAAC	3240
OY	3241	CAGTGGCTCCTGTGGATCATGCATGCAAGACTCTGAAGCCAGAGAGTACTGATTACG	3300
Db	3241	CAGTGGCTCCTGTGGATCATGCATGCAAGACTCTGAAGCCAGAGAGTACTGATTACG	3300
OY	3301	CCTCATGGGTGGAGGGGACCACTCCTGGGCTCTGTGATGTGCAGAGCAAGACCTGAGA	3360
Db	3301	CCTCATGGGTGGAGGGGACCACTCCTGGGCTCTGTGATGTGCAGAGCAAGACCTGAGA	3360
OY	3361	TGCTGCCCTGCTTCAAGTCTCTCTGCAATCTCCCTTTCTAATGAAGATCCATATAATTTG	3420
Db	3361	TGCTGCCCTGCTTCAAGTCTCTCTGCAATCTCCCTTTCTAATGAAGATCCATATAATTTG	3420
OY	3421	CTACATTTGAGAAATTTCCAAATAGGAAGTCAATGTTATATCGGCCATATCAATTTTTTAA	3480
Db	3421	CTACATTTGAGAAATTTCCAAATAGGAAGTCAATGTTATATCGGCCATATCAATTTTTTAA	3480
OY	3481	ACTTGGCTGAATAATTAAGTTTTTTTCAAAATCTGTCTGTAAATTAATCTTTTCTTACAGTG	3540
Db	3481	ACTTGGCTGAATAATTAAGTTTTTTTCAAAATCTGTCTGTAAATTAATCTTTTCTTACAGTG	3540
OY	3541	TCTTGGCATACTATATCAACTTTGATTTCTTTGTTTACAACTTT	3582
Db	3541	TCTTGGCATACTATATCAACTTTGATTTCTTTGTTTACAACTTT	3582
RESULT 2			
AAS64026			
ID AAS64026 standard; cDNA: 3923 BP.			
AAS64026;			
AC			
29-JAN-2002 (first entry)			
Human CDNA encoding DD3.			

Human; prostate cancer; ss; cytostatic; immunostimulant; tumour.
Homo sapiens.
WO2001/3032-A2.
04-OCT-2001.
27-MAR-2001; 2001WO-US09919.
27-MAR-2000; 2000US-0536857.
09-MAY-2000; 2000US-0568100.
12-MAY-2000; 2000US-0570737.
13-JUN-2000; 2000US-0593793.
27-JUN-2000; 2000US-0605783.
10-AUG-2000; 2000US-0636215.
29-AUG-2000; 2000US-0651236.
06-SEP-2000; 2000US-0652729.
02-OCT-2000; 2000US-0679426.
10-OCT-2000; 2000US-0685166.
(CORI-) CORIXA CORP.
XU J, DILLON DC, MITCHAM JL, HARLOCKER SL, JIANG Y, KALOS MD;
PANGER GR, RETTER MW, STOIK JA, DAY CH, VEDVICK TS, CARTER D;
LI SX, WANG A, SKEIKY YAW, HEPLER WT, HENDERSON RA;
WPI; 2001-639232/73.
New human prostate-specific polypeptides and polynucleotides useful for
the diagnosis and treatment of cancer, especially prostate cancer -
Claim 1; Page 473-474; 579pp; English.
The invention relates to isolated prostate-specific
polynucleotides, polypeptides, fusion proteins of the polypeptides,
antibodies raised against the polypeptides (or antigenic epitopes
derived from them) and antigen-presenting cells expressing the
polypeptides. The antibodies are useful for detecting the presence of
cancer, especially prostate cancer. The polypeptides, polynucleotides and
the antigen-presenting cells are useful for stimulating and/or expanding
T cells specific for a tumour protein, and for inhibiting the development
of cancer especially prostate cancer. Compositions comprising the
polynucleotide and/or polypeptide are useful for stimulating an immune
response, and for treating cancer. The oligonucleotide is useful for
detecting cancer. The present sequence is a prostate specific
polynucleotide of the invention.
Sequence 3923 BP; 1157 A; 840 C; 740 G; 1186 T; 0 other;
Query Match 84.8%; Score 3036; DB 22; Length 3923;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3036; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 ACAGAGAAATAGAGAGCGGAGAGCTGGCATCAGAAAAACAGAGGGAGATTTCGT 60
DB 1 ACAGAGAAATAGAGAGCGGAGAGCTGGCATCAGAAAAACAGAGGGAGATTTCGT 60
OY 61 GGTGACAGCGAGGAGACCGAGAAATCTCATGTGGGAGAGACCTGATGATACAGAG 120
DB 61 GGTGACAGCGAGGAGACCGAGAAATCTCATGTGGGAGAGACCTGATGATACAGAG 120
OY 121 GAATTACACACATATCTAGTGTTCATGAACACCCAGATAAATAGTGAAGAGCTA 180
DB 121 GAATTACACACATATCTAGTGTTCATGAACACCCAGATAAATAGTGAAGAGCTA 180
OY 181 GTCCGCTGTAGTCTCTCATGTACACAGGGCTGGATCACCATGAGCGCACTTTCGAG 240
DB 181 GTCCGCTGTAGTCTCTCATGTACACAGGGCTGGATCACCATGAGCGCACTTTCGAG 240
OY 241 TACTCAGTGCAGCAAGAAAGACTACAGACATCTCATGAGGAGGAGGAGAAATAGAAA 300
DB 241 TACTCAGTGCAGCAAGAAAGACTACAGACATCTCATGAGGAGGAGGAGAAATAGAAA 300

OY 301 GGTGCTGACTTTTACCATCTGAGCCACACATCTGCTGAATGAGATATTAACATCAC 360
DB 301 GGTGCTGACTTTTACCATCTGAGCCACACATCTGCTGAATGAGATATTAACATCAC 360
OY 361 TAGAACAAGACAGATGACAAATATATGCTTAAGTAGACATGTTTTTGCACATTTCCAG 420
DB 361 TAGAACAAGACAGATGACAAATATATGCTTAAGTAGACATGTTTTTGCACATTTCCAG 420
OY 421 CCCCTTAAATATCCACACACAGAGGAGCAAAAGACACAGATCCCTGGGAGA 480
DB 421 CCCCTTAAATATCCACACACAGAGGAGCAAAAGACACAGATCCCTGGGAGA 480
OY 481 AATGCCCGCCCATCTTTGGGTATCGATGAGCCCTGCTGCTGCTCCGCTTGT 540
DB 481 AATGCCCGCCCATCTTTGGGTATCGATGAGCCCTGCTGCTGCTCCGCTTGT 540
OY 541 GAGGAGAGACATTAGAAATGAAATGATGTGTCCTTAAAGATGGCAGAAACAGA 600
DB 541 GAGGAGAGACATTAGAAATGAAATGATGTGTCCTTAAAGATGGCAGAAACAGA 600
OY 601 TCTGTGTGATATTTATTTGAACGGGATACAGATTTGAATGAAGTCCAAAGTGAG 660
DB 601 TCTGTGTGATATTTATTTGAACGGGATACAGATTTGAATGAAGTCCAAAGTGAG 660
OY 661 CATTACCAATGAGAGAGAAACAGACAGAGAAATCTTGTGCTTACAAAGCATGCAACA 720
DB 661 CATTACCAATGAGAGAGAAACAGACAGAGAAATCTTGTGCTTACAAAGCATGCAACA 720
OY 721 AACCAATGGAATCTGTGATGACATGAGGACGCAAGCTGGGAGGAGATMACCGGG 780
DB 721 AACCAATGGAATCTGTGATGACATGAGGACGCAAGCTGGGAGGAGATMACCGGG 780
OY 781 GCAGAGGTCAGGATTCGGCCCTGCTGCCATACTGGCTCATACCAATCATTTTC 840
DB 781 GCAGAGGTCAGGATTCGGCCCTGCTGCCATACTGGCTCATACCAATCATTTTC 840
OY 841 ATATTTCTAACCCCTCAAAACAAAGCTGTTGAATATCTGATCTGACGGTCTCTTGGC 900
DB 841 ATATTTCTAACCCCTCAAAACAAAGCTGTTGAATATCTGATCTGACGGTCTCTTGGC 900
OY 901 CCCCAACATCTCCATATATCCAGCACACATCTTTTAATTTAGTTCCAGATCTGTA 960
DB 901 CCCCAACATCTCCATATATCCAGCACACATCTTTTAATTTAGTTCCAGATCTGTA 960
OY 961 CTGTGACCTTCTACCTGTGATGATTAACATTAATCTTTGTTCAAGACCTTCGTG 1020
DB 961 CTGTGACCTTCTACCTGTGATGATTAACATTAATCTTTGTTCAAGACCTTCGTG 1020
OY 1021 GCTGCTTAATATGAGCTGACTGTTTTTCTAAGAGCTGTTGGCCAGGGATCTGTG 1080
DB 1021 GCTGCTTAATATGAGCTGACTGTTTTTCTAAGAGCTGTTGGCCAGGGATCTGTG 1080
OY 1081 AACAGGCTGGGAACATCTCAAGATCTTCCAGGGTTATCTTAATCTGACACAGCATGA 1140
DB 1081 AACAGGCTGGGAACATCTCAAGATCTTCCAGGGTTATCTTAATCTGACACAGCATGA 1140
OY 1141 TCATTAGGAGTGAATATCATCAACATCATCTGAGTCTGTTGCCATACCTGTAAT 1200
DB 1141 TCATTAGGAGTGAATATCATCAACATCATCTGAGTCTGTTGCCATACCTGTAAT 1200
OY 1201 TCATTTCCACTTTTGTGCCATTTCTCAAGACCTCAAAAGTCAATTCATTAATATGACA 1260
DB 1201 TCATTTCCACTTTTGTGCCATTTCTCAAGACCTCAAAAGTCAATTCATTAATATGACA 1260
OY 1261 GGATTAACCTTTTTTTTAACTGGAAGATTCATATGTCATGACCTATGGAAATTTA 1320
DB 1261 GGATTAACCTTTTTTTTAACTGGAAGATTCATATGTCATGACCTATGGAAATTTA 1320
OY 1321 ATTACATATTTGTTTCCAGTGAAGATGACATACTGTTATCCCTCCCTTGTGTT 1380
DB 1321 ATTACATATTTGTTTCCAGTGAAGATGACATACTGTTATCCCTCCCTTGTGTT 1380

OY		1381	TATTTTTTTCACGATAAAGTTAAATGGCTTAGCCGTGTACTGAGCGTGATACAGAC	1440
Db		1381	GATTTTTTTTTCCAGTAATAAGTTAAAAGCTTTACCCTTTGACTGAGCGCTGATACAGAC	1440
OY		1441	AGCCTCCGCCATCCCCTCACGCCTTAATCTGCATCACCATCAACCCCTCCCATACACCT	1500
Db		1441	AGCCTCCGCCATCCCCTCACGCCTTAATCTGCATCACCATCAACCCCTCCCATACACCT	1500
OY		1501	AAACAAAATCTAACCTGTAATTCCCTGMAACTGTGAGGACATATATTCCTCTGCGCT	1560
Db		1501	AAACAAAATCTAACCTGTAATTCCCTGMAACTGTGAGGACATATATTCCTCTGCGCT	1560
OY		1561	GAGAAGCCTTCCTTGCTCTTAATCTAGATGTGAAGTTTGGATTAAGTTGACTA	1620
Db		1561	GAGAAGCCTTCCTTGCTCTTAATCTAGATGTGAAGTTTGGATTAAGTTGACTA	1620
OY		1621	TCCTACCTTCAGCAAGAGAGGACACATATAGATATCATCTCATATGAGACACAATA	1680
Db		1621	TCCTACCTTCAGCAAGAGAGGACACATATAGATATCATCTCATATGAGACACAATA	1680
OY		1681	CTAAAGGTATTTGATTTATPAAGAGTTTATGATAAATATPAGAAATGCAAGGACACAGA	1740
Db		1681	CTAAAGGTATTTGATTTATPAAGAGTTTATGATAAATATPAGAAATGCAAGGACACAGA	1740
OY		1741	GGGAATGTTTAVGGGGCAGCTTTGTAAAGCCCTGGAGTGAAGCAAAGGACGGAACCTCA	1800
Db		1741	GGGAATGTTTAVGGGGCAGCTTTGTAAAGCCCTGGAGTGAAGCAAAGGACGGAACCTCA	1800
OY		1801	TAGATATCTTATATATATATCTTCATTTCTCTATCTCTATCAATATTCACAAGCTTTT	1860
Db		1801	TAGATATCTTATATATATATCTTCATTTCTCTATCTCTATCAATATTCACAAGCTTTT	1860
OY		1861	CACAGAATTCATGAGAGTCAAAATCCCCAAAGGTAAACCTTATGCCATTTGCATGGAGAGC	1920
Db		1861	CACAGAATTCATGAGAGTCAAAATCCCCAAAGGTAAACCTTATGCCATTTGCATGGAGAGC	1920
OY		1921	GCTTTAGATTTTGGCAATATCATCTGCTCATTCACATTTGAGATGTGTTGTCC	1980
Db		1921	GCTTTAGATTTTGGCAATATCATCTGCTCATTCACATTTGAGATGTGTTGTCC	1980
OY		1981	TTGTAGTTAATTGAAAAAGAAATAGGGCACTCTTGTGAGCCACTTTAAGGTTTACCTCTGGC	2040
Db		1981	TTGTAGTTAATTGAAAAAGAAATAGGGCACTCTTGTGAGCCACTTTAAGGTTTACCTCTGGC	2040
OY		2041	AATPAAGAATTTACAAAAGAGCTACTCAGAGCAGTGTGTAGAGCTGCTGTGTGTGT	2100
Db		2041	AATPAAGAATTTACAAAAGAGCTACTCAGAGCAGTGTGTAGAGCTGCTGTGTGTGT	2100
OY		2101	GCTGTGTGTGAGTGTACATGCCAAAGTGTGCTCTCTCTTGACCATTATTTCCAGAC	2160
Db		2101	GCTGTGTGTGAGTGTACATGCCAAAGTGTGCTCTCTCTTGACCATTATTTCCAGAC	2160
OY		2161	TTTAAACACAGCATGTTTCCAATGGCACTAAGAGCTGCAATGTATGCACCAACATAT	2220
Db		2161	TTTAAACACAGCATGTTTCCAATGGCACTAAGAGCTGCAATGTATGCACCAACATAT	2220
OY		2221	CTCATTTATTCGCCAGTAAATGTGATTAATATGTCATCTGTTAACAATAAAAAATTGGAC	2280
Db		2221	CTCATTTATTCGCCAGTAAATGTGATTAATATGTCATCTGTTAACAATAAAAAATTGGAC	2280
OY		2281	TTCACAAAAAGCAGCTGGAATGTGACCAACACCAATATGCATAAATCTTAACCTCTACATCA	2340
Db		2281	TTCACAAAAAGCAGCTGGAATGTGACCAACACCAATATGCATAAATCTTAACCTCTACATCA	2340
OY		2341	GCTACACACCTGTTGACATATATTGTTAAGAACCTGCGCATTTGTGGGTTCTCTTAAGC	2400
Db		2341	GCTACACACCTGTTGACATATATTGTTAAGAACCTGCGCATTTGTGGGTTCTCTTAAGC	2400
OY		2401	AAAATACTCTGATTAGCTCAGCTGGGGCTGTCATCAGAGCGGTTTGAAGAAAATATTCAA	2460
Db		2401	AAAATACTCTGATTAGCTCAGCTGGGGCTGTCATCAGAGCGGTTTGAAGAAAATATTCAA	2460
OY		2461	TTCTCAGCAGAGCCAGAAATTTGAATTCCTCATCTTTTGAAGATCATTTTACCAGGTTTG	2520

Db	2461																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																															
----	------	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--

for use in vaccines -
Claim 1; Page 452-453; 543pp; English.

The present invention describes polynucleotide sequences (I) which encode prostate-specific proteins (II). (I) and (II) have cytosstatic activity, and can be used in vaccine production and gene therapy. (I), (II), antibodies to (II), fusion proteins comprising (II), and isolated T cells prepared using (I) or (II) are used treat cancer in a patient. (I) and the antibodies are also used in the detection of cancer in a patient. The cancer that is diagnosed or treated is particularly prostate cancer. (I) and (II) can be used in vaccines. The antibodies or (I) can be used for monitoring the progression of cancer in a patient. (I) and (II) can also be used to improve diagnostic and therapeutic methods for prostate cancer. They can indicate the level of metastasis as well as the prostate volume. AAH93357 to AAH93944 and AAH01115 to AAH01318 represent polynucleotide and amino acid sequences used in the exemplification of the present invention.

Sequence 3923 BP; 1157 A; 840 C; 740 G; 1186 T; 0 other;

Query Match 84.8%; Score 3036; DB 22; Length 3923;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 3036; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY 1 ACACAGAAATATGCAAGTGCAGAGAGTGCATCAGAAAAACAGAGGGGAGATTGTGT 60
DB 1 ACACAGAAATATGCAAGTGCAGAGAGTGCATCAGAAAAACAGAGGGGAGATTGTGT 60
QY 61 GCGTCAGCGGAGGAGAGACAGAGAAATCTGATGTTGGAGAACCTCGATATACAGAG 120
DB 61 GCGTCAGCGGAGGAGAGACAGAGAAATCTGATGTTGGAGAACCTCGATATACAGAG 120
QY 121 GAATTACAAACATATATCTAGTGTTCATGAACACCAAGATAAATAGTGAAGAGTA 180
DB 121 GAATTACAAACATATATCTAGTGTTCATGAACACCAAGATAAATAGTGAAGAGTA 180
QY 181 GTCCGCTGTGAGTCTCCTCACTGACACAGGGCTGGATCCATCGAGCGCACTTCTGAG 240
DB 181 GTCCGCTGTGAGTCTCCTCACTGACACAGGGCTGGATCCATCGAGCGCACTTCTGAG 240
QY 241 TACTCAGTGCAGAAAGAAAGACATACAGACATCTCAATGAGGAGGGGTGAGAAATAGAAA 300
DB 241 TACTCAGTGCAGAAAGAAAGACATACAGACATCTCAATGAGGAGGGGTGAGAAATAGAAA 300
QY 301 GCGTCTGACTTATCCATCTGAGGCCACACATCTGCTGAATGAGATATTAACATCAC 360
DB 301 GCGTCTGACTTATCCATCTGAGGCCACACATCTGCTGAATGAGATATTAACATCAC 360
QY 361 TAGAAACAGACAGATGACATATATATGTCTAAGTAGTGACATGTTTTCACATTTCCAG 420
DB 361 TAGAAACAGACAGATGACATATATATGTCTAAGTAGTGACATGTTTTCACATTTCCAG 420
QY 421 CCCCTTTAAATATCCACACACAGAGAAACAAAGAACACACAGAGATCCCTGGGAGA 480
DB 421 CCCCTTTAAATATCCACACACAGAGAAACAAAGAACACACAGAGATCCCTGGGAGA 480
QY 481 AATGCCGGCGCCCATCTTGCGTCATCGATGAGCGCTGCGCTGTGCTGCTGCTGCTGT 540
DB 481 AATGCCGGCGCCCATCTTGCGTCATCGATGAGCGCTGCGCTGTGCTGCTGCTGCTGT 540
QY 541 GAGGGAAGGACATTAGAAAATGAAATGATGTGTTCTTAAAGATGGGACAGAAAACAGA 600
DB 541 GAGGGAAGGACATTAGAAAATGAAATGATGTGTTCTTAAAGATGGGACAGAAAACAGA 600
QY 601 TCCCTGTGTGATATTTATTTGAACGGGATACAGATTTGAAATGAAGTCCAAAGTACAG 660
DB 601 TCCCTGTGTGATATTTATTTGAACGGGATACAGATTTGAAATGAAGTCCAAAGTACAG 660
QY 661 CATTAACAATGAGAGAAAACAGACAGAAAATCTTGTGCTTACACAGACATGCAACA 720
DB 661 CATTAACAATGAGAGAAAACAGACAGAAAATCTTGTGCTTACACAGACATGCAACA 720
```

```
QY 721 AACAAATGATACTGTGATGACATGAGGAGCCAGACCTGGGAGGAGATACACGCGG 780
DB 721 AACAAATGATACTGTGATGACATGAGGAGCCAGACCTGGGAGGAGATACACGCGG 780
QY 781 GCAGAGGTCAGAGATTTGCGCCCTGCTGCTTAACATGTGCTTCAATACCAATCATTTTC 840
DB 781 GCAGAGGTCAGAGATTTGCGCCCTGCTGCTTAACATGTGCTTCAATACCAATCATTTTC 840
QY 841 AATATTTCAACCCCAAAACAAAGCTGTTGTAATATATCATCTAGGTTCCCTTGGG 900
DB 841 AATATTTCAACCCCAAAACAAAGCTGTTGTAATATATCATCTAGGTTCCCTTGGG 900
QY 901 CCACACATCTCCATATATACAGCCACACATCATTTTAAATTAATAGTCCAGATCTGTA 960
DB 901 CCACACATCTCCATATATACAGCCACACATCATTTTAAATTAATAGTCCAGATCTGTA 960
QY 961 CTGAGACCTTCTACAGTGAATATACATATACATTTTGTCAAAAGACCTTCGTGTT 1020
DB 961 CTGAGACCTTCTACAGTGAATATACATATACATTTTGTCAAAAGACCTTCGTGTT 1020
QY 1021 GCTGCTTAATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1080
DB 1021 GCTGCTTAATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1080
QY 1081 AACAGGCTGGAAGCATCTCAAGATCTTTCAGAGGATTAATCTACTAGACACAGCATGA 1140
DB 1081 AACAGGCTGGAAGCATCTCAAGATCTTTCAGAGGATTAATCTACTAGACACAGCATGA 1140
QY 1141 TCATTACGAGTGAATATATATATATATATATATATATATATATATATATATATATAT 1200
DB 1141 TCATTACGAGTGAATATATATATATATATATATATATATATATATATATATATATAT 1200
QY 1201 TCATTCCCATTTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1260
DB 1201 TCATTCCCATTTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1260
QY 1261 GATTTTCCCATTTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1320
DB 1261 GATTTTCCCATTTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1320
QY 1321 ATTAACATATTTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1380
DB 1321 ATTAACATATTTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1380
QY 1381 GATTTTCCCATTTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1440
DB 1381 GATTTTCCCATTTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1440
QY 1441 AGCCTCTCCCATTTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1500
DB 1441 AGCCTCTCCCATTTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1500
QY 1501 AAACAAATCTAATCTGTAATTTCTGTAACATGTGACAGACATTAATTTCTTGCTGCT 1560
DB 1501 AAACAAATCTAATCTGTAATTTCTGTAACATGTGACAGACATTAATTTCTTGCTGCT 1560
QY 1561 GAGAGGCTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1620
DB 1561 GAGAGGCTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1620
QY 1621 TCTTACTTCATGCAAGAAGGAGACATATGATGATGATGATGATGATGATGATGATGAT 1680
DB 1621 TCTTACTTCATGCAAGAAGGAGACATATGATGATGATGATGATGATGATGATGATGAT 1680
QY 1681 CTAAGAAGTATATTTGATATTAAGATTTAGATTAATATATATATATATATATATATAT 1740
DB 1681 CTAAGAAGTATATTTGATATTAAGATTTAGATTAATATATATATATATATATATATAT 1740
QY 1741 GGAATGTTTATGAGGACGCTTTGTAAGCCGAGGATGGAAGCAAGGACAGGAACTGCA 1800
DB 1741 GGAATGTTTATGAGGACGCTTTGTAAGCCGAGGATGGAAGCAAGGACAGGAACTGCA 1800
QY 1801 TAGTATCTTATATATATATATATATATATATATATATATATATATATATATATATAT 1860
DB 1801 TAGTATCTTATATATATATATATATATATATATATATATATATATATATATATATAT 1860
```


Db	1801	TAGATATCTTATATATATCTTCACTTTCCTATCTCTATCTATCTATCTCAATATCCAAAGCTTTT	1860
Qy	1861	CACGAATTCATGCACTGCAAAATCCCAAAAGTAACCTTATCCATTCATGCTGAGTGC	1920
Db	1861	CACGAAATTCATGCACTGCAAAATCCCAAAAGGTAACTTTATCCATTTTCATGCTGAGTGC	1920
Qy	1921	GCTTTAGAAATTTTGGCAAAATCATCTGCTGCACCTTATCTCAACTTTGGAGATGTGTTGTC	1980
Db	1921	GCTTTAGAAATTTTGGCAAAATCATCTGCTGCACCTTATCTCAACTTTGGAGATGTGTTGTC	1980
Qy	1981	TTGTAGTAAATGTGAAGAAATAGGGCACTGTGTGAGCCACTTTTAGGTTCACCTCGGC	2040
Db	1981	TTGTAGTAAATGTGAAGAAATAGGGCACTGTGTGAGCCACTTTTAGGTTCACCTCGGC	2040
Qy	2041	AATTAAGAAATTTCAAGAGCTACTCTAGAGCACACTTTTAAAGACTCTGTGTGTGTGT	2100
Db	2041	AATTAAGAAATTTCAAGAGCTACTCTAGAGCACACTTTTAAAGACTCTGTGTGTGTGTGT	2100
Qy	2101	GTTGTGTGTGTGAGTGTACATGCCAAAGTGTGCTCTCTCTCTGTGACCACTATTTTTCAGAC	2160
Db	2101	GTTGTGTGTGTGAGTGTACATGCCAAAGTGTGCTCTCTCTCTGTGACCACTATTTTTCAGAC	2160
Qy	2161	TTTAAACAACGAGTCTTCAAAAGGCACTATGAGCTGCCAATGTATGTATCACCACTAT	2220
Db	2161	TTTAAACAACGAGTCTTCAAAAGGCACTATGAGCTGCCAATGTATGTATCACCACTAT	2220
Qy	2221	CTCATATTTTCTCCAGTAAATGTGTATATATGTATCTGTATACATATAAAAGATTTTGAC	2280
Db	2221	CTCATATTTTCTCCAGTAAATGTGTATATATGTATCTGTATACATATAAAAGATTTTGAC	2280
Qy	2281	TTTCAAAAAGCACTGTGAATATGCAACAACCAATATGTCAATTAATCTTAACCTTCACATCA	2340
Db	2281	TTTCAAAAAGCACTGTGAATATGCAACAACCAATATGTCAATTAATCTTAACCTTCACATCA	2340
Qy	2341	GCTACACACGTCTTGAATATATTTGTTAGAAAGCACTCGCATTTGTGGGTTCTTTAAGC	2400
Db	2341	GCTACACACGTCTTGAATATATTTGTTAGAAAGCACTCGCATTTGTGGGTTCTTTAAGC	2400
Qy	2401	AAATTACTTTCATTTAGTCTCAGCTGTGGGCTGTCTCATCAGCGGTTTGAGAAATATTCAA	2460
Db	2401	AAATTACTTTCATTTAGTCTCAGCTGTGGGCTGTCTCATCAGCGGTTTGAGAAATATTCAA	2460
Qy	2461	TTCTCAGCAGAGCCAGCAATTTGAAATTCCTCATCTTTTAGAAATTCATTTACAGAGTTTG	2520
Db	2461	TTCTCAGCAGAGCCAGCAATTTGAAATTCCTCATCTTTTAGAAATTCATTTACAGAGTTTG	2520
Qy	2521	GAGAGGATTCAGACAGCTCAGGTGCTTTCACATAATGTCTGAACTTCTGTCCCTCTTTG	2580
Db	2521	GAGAGGATTCAGACAGCTCAGGTGCTTTCACATAATGTCTGAACTTCTGTCCCTCTTTG	2580
Qy	2581	TGTTCAATGAGATGATGCCAAATTAATGTTTAACTTTGAAAGCATGCTCATAGGAGAGATA	2640
Db	2581	TGTTCAATGAGATGATGCCAAATTAATGTTTAACTTTGAAAGCATGCTCATAGGAGAGATA	2640
Qy	2641	TAAAGAACTCTGAGTATATCAACTTATAGGATTCAAAGAAATATTTAGATTTTAACTTCACA	2700
Db	2641	TAAAGAACTCTGAGTATATCAACTTATAGGATTCAAAGAAATATTTAGATTTTAACTTCACA	2700
Qy	2701	CTGGTCAAAAAGGAACCAAGATATCAAAAGAACTGTAGCTGTATCTGCCATCTCTGTGA	2760
Db	2701	CTGGTCAAAAAGGAACCAAGATATCAAAAGAACTGTAGCTGTATCTGCCATCTCTGTGA	2760
Qy	2761	GCCCAACCAACAGACAGAGCCCAAGGATGCTGAGATCCCTTAATCAAGAAACCAAGTG	2820
Db	2761	GCCCAACCAACAGACAGAGCCCAAGGATGCTGAGATCCCTTAATCAAGAAACCAAGTG	2820
Qy	2821	TCATGAGTTGAATTTCTCTATTTATGATGTAGCTTGTGGCCATCTGTGGCTCTCTCTT	2880
Db	2821	TCATGAGTTGAATTTCTCTATTTATGATGTAGCTTGTGGCCATCTGTGGCTCTCTCTT	2880
Qy	2881	GACCAATTAATGCTTACGCTTGTGCTTCCACGACTTTTATCTTTTCCAAACACATGCG	2940
Db	2881	GACCAATTAATGCTTACGCTTGTGCTTCCACGACTTTTATCTTTTCCAAACACATGCG	2940

Db	2881	GACACATATTAGCTTCTAGCCTTTGCTCCACGACTTTATCTTTCTCCACACATCGC	2940
Qy	2941	TTACCAATCCTCTCTGCTGCTGTGCTTTGGACTTCCCAAGAAATTTCAAGACTCT	3000
Db	2941	TTACCAATCCTCTCTGCTGCTGTGCTTTGGACTTCCCAAGAAATTTCAAGACTCT	3000
Qy	3001	CAAGCTTTTCTCTCATCTCCACACACTTAACTGAAT	3036
Db	3001	CAAGCTTTTCTCTCATCTCCACACACTTAACTGAAT	3036
RESULT 4			
ID	ABK92196	standard; DNA; 3923 BP.	
AC	ABK92196;		
DT	15-AUG-2002	(first entry)	
DE	Prostate cancer-associated DNA sequence #82.		
KW	Prostate cancer; prostate tumour tissue; human; mammal; cytostatic;		
KW	gene therapy; gene; ds.		
OS	Mammalia.		
PN	WO200230268-A2.		
PD	18-APR-2002.		
PF	12-OCT-2001; 2001WO-US32045.		
PR	13-OCT-2000; 2000US-0687576.		
PR	08-DEC-2000; 2000US-0733288.		
PR	08-DEC-2000; 2000US-0733742.		
PR	24-JAN-2001; 2001US-263857P.		
PR	16-MAR-2001; 2001US-276791P.		
PR	16-MAR-2001; 2001US-276888P.		
PR	06-APR-2001; 2001US-281922P.		
PR	24-APR-2001; 2001US-286214P.		
PR	30-APR-2001; 2001US-084704P.		
PR	04-MAY-2001; 2001US-288589P.		
PA	(EOSB-) EOS BIOTECHNOLOGY INC.		
PI	Gish KC, Mack DH, Wilson KE, Afar D, Hevezl P;		
DR	WPI, 2002-471335/50.		
PT	Detecting a prostate cancer-associated transcript in a cell in a		
PT	patient, useful for diagnosing prostate cancer (PC) or screening		
PT	modulators of PC, by determining if prostate cancer-associated genes		
PT	are expressed in a prostate tissue		
PS	Claim 22; Page 365-366; 436pp; English.		
CC	The present invention relates to methods of detecting a prostate		
CC	cancer-associated transcript in a cell from a patient. The method		
CC	comprises contacting a biological sample from the patient with		
CC	prostate cancer-associated polynucleotides (designated PC genes) that		
CC	selectively hybridize to a sequence that is at least 80% identical		
CC	to them. The prostate cancer-associated polynucleotide sequences		
CC	are differentially expressed in prostate tumour tissue or in		
CC	prostate cancer and are derived from the tissues of various		
CC	organisms such as humans or other mammals (e.g. mice, sheep and dogs).		
CC	The methods of the invention are useful for diagnosing and treating		
CC	prostate cancer in mammals. The prostate cancer-associated genes are		
CC	useful for diagnosing or treating prostate cancer, as well as for		
CC	identifying modulators of prostate cancer or agents that inhibit		
CC	prostate cancer. The nucleic acid sequences are particularly useful		
CC	in gene therapy, as a vaccine or in antisense applications.		
CC	ABK92115-ABK92263 represent prostate cancer-associated polynucleotide		
CC	sequences.		

XX	Sequence	3923 BP; 1157 A; 840 C; 740 G; 1186 T; 0 other;			
SQL	Query Match	84.8%; Score 3036; DB 24; Length 3923;			
	Best Local Similarity	100.0%; Pred. No. 0;			
	Matches 3036;	Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
OY	1	ACAGAGAAATAGCAAGTGGCCGAGAGAGCTGGCATCAGAAAAACAGAGGGGAGATTGTTGT	60		
DB	1	ACAGAGAAATAGCAAGTGGCCGAGAGAGCTGGCATCAGAAAAACAGAGGGGAGATTGTTGT	60		
OY	61	GGCTGCACCGGAGGAGACAGAGAGATCTGATGGGAAAGAGCCGTGATGATACAG	120		
DB	61	GGCTGCACCGGAGGAGACAGAGAGATCTGATGGGAAAGAGCCGTGATGATACAG	120		
OY	121	GAATTACACACATATACTAGTGTGTTCAATGAACACCAAGATAAATAGTGAAGAGCTA	180		
DB	121	GAATTACACACATATACTAGTGTGTTCAATGAACACCAAGATAAATAGTGAAGAGCTA	180		
OY	181	GTCGGCTGTAGTCTCTCACTGACACAGGGCTGGATCCACATCGACGGCACTTTCTGAG	240		
DB	181	GTCGGCTGTAGTCTCTCACTGACACAGGGCTGGATCCACATCGACGGCACTTTCTGAG	240		
OY	241	TACTCAGTGCAGCAAGAAAGACATACAGACATCTCAATGCGAGGGGTGAGAAATAGAAA	300		
DB	241	TACTCAGTGCAGCAAGAAAGACATACAGACATCTCAATGCGAGGGGTGAGAAATAGAAA	300		
OY	301	GGCTGCACCTTACCATCTGAGGCGCACACATCTGCTGAATGGAATTAACATCAC	360		
DB	301	GGCTGCACCTTACCATCTGAGGCGCACACATCTGCTGAATGGAATTAACATCAC	360		
OY	361	TAGAAACAGCAAGATGACAAATATATATGTCTAAGTAGTACATGTTTTGACATTTCCAG	420		
DB	361	TAGAAACAGCAAGATGACAAATATATATGTCTAAGTAGTACATGTTTTGACATTTCCAG	420		
OY	421	CCCCCTTAAATATCCACACACAGGAAGCAAAAGAAAGAACACAGAGATCCCTGGGAGA	480		
DB	421	CCCCCTTAAATATCCACACACAGGAAGCAAAAGAAAGAACACAGAGATCCCTGGGAGA	480		
OY	481	AATGCCGGCCGATCTTGGGTGATCGATGAGCCCTGCCCTGGCTGGTCCCGCTTGT	540		
DB	481	AATGCCGGCCGATCTTGGGTGATCGATGAGCCCTGCCCTGGCTGGTCCCGCTTGT	540		
OY	541	GAGGAGAGACATTAAGAAATGAATGTGTTCTTAAAGATGGGACAGAAAAACA	600		
DB	541	GAGGAGAGACATTAAGAAATGAATGTGTTCTTAAAGATGGGACAGAAAAACA	600		
OY	601	TCTGTGTGATATTTATTTGAACGGGATTAACAGATTTGAAATGAAGTCCAAAGTCAG	660		
DB	601	TCTGTGTGATATTTATTTGAACGGGATTAACAGATTTGAAATGAAGTCCAAAGTCAG	660		
OY	661	CATTACCAATGAGAGAAACAGACGAGAAATCTTGATGCTTACAAAGACATGCAACA	720		
DB	661	CATTACCAATGAGAGAAACAGACGAGAAATCTTGATGCTTACAAAGACATGCAACA	720		
OY	721	AACAAATGCAATCTGTGATGACATGAGCGCAAGCTGGGAGAGATTAACACAGGG	780		
DB	721	AACAAATGCAATCTGTGATGACATGAGCGCAAGCTGGGAGAGATTAACACAGGG	780		
OY	781	GCAGAGGATCAGAGTTGTGGCCCTGTCCTAAACTGCTGCTATAAACCAATCATTTTC	840		
DB	781	GCAGAGGATCAGAGTTGTGGCCCTGTCCTAAACTGCTGCTATAAACCAATCATTTTC	840		
OY	841	ATATTTCTAACCCCTCAAAACAAAGCTTTGTAATATGATCTCTACGGTCTCTTGGG	900		
DB	841	ATATTTCTAACCCCTCAAAACAAAGCTTTGTAATATGATCTCTACGGTCTCTTGGG	900		
OY	901	CCCAACATTTCTCATATATTCACGCGACACTCATATTTTAATATTTAGTTCCAGATCTGTA	960		
DB	901	CCCAACATTTCTCATATATTCACGCGACACTCATATTTTAATATTTAGTTCCAGATCTGTA	960		
OY	961	CTGAGACCTTCTACACTGTAGATTAACATTTACTCATTTTGTCTAAAGACCCCTTGCTT	1020		
DB	961	CTGAGACCTTCTACACTGTAGATTAACATTTACTCATTTTGTCTAAAGACCCCTTGCTT	1020		
OY	1021	GCTGCCATATATGTAGTGCAGCTGTTTTTCTTAAGGAGTGTCTGGCCAGGGGATCTGTG	1080		
DB	1021	GCTGCCATATATGTAGTGCAGCTGTTTTTCTTAAGGAGTGTCTGGCCAGGGGATCTGTG	1080		
OY	1081	AACAGCTGGGAGACATCTCAAGATCTTTCAGAGGTTTACTTACTACACACAGCATGA	1140		
DB	1081	AACAGCTGGGAGACATCTCAAGATCTTTCAGAGGTTTACTTACTACACACAGCATGA	1140		
OY	1141	TCATTACGAGATGAAATTTCTTAATCAATATATCTCTAGTGTCTTGGCCATGAGAAAT	1200		
DB	1141	TCATTACGAGATGAAATTTCTTAATCAATATATCTCTAGTGTCTTGGCCATGAGAAAT	1200		
OY	1201	TCATTTCCACTTTTGTGCCATCTCTCAAGACCTCAAAATGTCATTCATTAATATCA	1260		
DB	1201	TCATTTCCACTTTTGTGCCATCTCTCAAGACCTCAAAATGTCATTCATTAATATCA	1260		
OY	1261	GGATTAACCTTTTAAAAATTTCAATGCTTAATGCGAGCTATGGAATTTA	1320		
DB	1261	GGATTAACCTTTTAAAAATTTCAATGCTTAATGCGAGCTATGGAATTTA	1320		
OY	1321	ATTACATATTTTGTTCAGATGCAAGATGACTAATGCTTTATCCCTCCCTTGTGT	1380		
DB	1321	ATTACATATTTTGTTCAGATGCAAGATGACTAATGCTTTATCCCTCCCTTGTGT	1380		
OY	1381	GATTTTCTCCAGTAAATGTTAAATGCTTAGCGCTGTACTGAGGCTGTATACAGAC	1440		
DB	1381	GATTTTCTCCAGTAAATGTTAAATGCTTAGCGCTGTACTGAGGCTGTATACAGAC	1440		
OY	1441	AGCCTCTCCCATCCCTCCAGCTTATCTGTCATCCACATCAACCCCTCCATACACCT	1500		
DB	1441	AGCCTCTCCCATCCCTCCAGCTTATCTGTCATCCACATCAACCCCTCCATACACCT	1500		
OY	1501	AAACAAATCTTAATCTGTAATCTCTGAACATGTCAGAGACTAATATTCTCTGCT	1560		
DB	1501	AAACAAATCTTAATCTGTAATCTCTGAACATGTCAGAGACTAATATTCTCTGCT	1560		
OY	1561	GAGAGGCTCTCTGTCCTTAATCTAGATGATGAAAGTTTGAATGAATTTGACTA	1620		
DB	1561	GAGAGGCTCTCTGTCCTTAATCTAGATGATGAAAGTTTGAATGAATTTGACTA	1620		
OY	1621	TCTTACTTCAATGCAAGAGGAGACATATGAGATTCATCTACATGAGACACAATA	1680		
DB	1621	TCTTACTTCAATGCAAGAGGAGACATATGAGATTCATCTACATGAGACACAATA	1680		
OY	1681	CTAAAGGTATTTGATTAATAGATTTTAAATTAATTAATGAATGCAAGAGCCACAGA	1740		
DB	1681	CTAAAGGTATTTGATTAATAGATTTTAAATTAATTAATGAATGCAAGAGCCACAGA	1740		
OY	1741	GGGAAATGTTATGAGGACGTTTGTAAAGCTGGGATGTGAAGCAAGGACGAACTCA	1800		
DB	1741	GGGAAATGTTATGAGGACGTTTGTAAAGCTGGGATGTGAAGCAAGGACGAACTCA	1800		
OY	1801	TAGTATCTTATATATATATCTTCAATTCCTATCTATCTATCAATATCCAAACAGCTTTT	1860		
DB	1801	TAGTATCTTATATATATATCTTCAATTCCTATCTATCTATCAATATCCAAACAGCTTTT	1860		
OY	1861	CACAGATTCATGAGAGCAAAATCCCAAGGTAACTTTATTCATTTTCAATGAGTATGC	1920		
DB	1861	CACAGATTCATGAGAGCAAAATCCCAAGGTAACTTTATTCATTTTCAATGAGTATGC	1920		
OY	1921	GCTTTAAATTTTGGCAAAATCATCTGCTCACTATATCAACTTGAAGTGTGTTTCC	1980		
DB	1921	GCTTTAAATTTTGGCAAAATCATCTGCTCACTATATCAACTTGAAGTGTGTTTCC	1980		
OY	1981	TTGTAGTTAATGAAAGAAATAGGGCACTTTGTGAGCCACTTTAGGGTTCACCTGCG	2040		
DB	1981	TTGTAGTTAATGAAAGAAATAGGGCACTTTGTGAGCCACTTTAGGGTTCACCTGCG	2040		
OY	2041	AATTAAGAAATTTACAAAGAGCTACTCAGAGACAGTGTTTAAGAGCTGTGTGTGTGT	2100		
DB	2041	AATTAAGAAATTTACAAAGAGCTACTCAGAGACAGTGTGTGTGTGTGTGTGTGTGT	2100		

OY 2101 GTGTGTTGAGTGTACATGCCAAAGTGTGCTCTCTCTTGAACCATTAATTGAGAC 2160
|||||
DB 2101 GTGTGTGTGTGAGTGTACATGCCAAAGTGTGCTCTCTCTTGAACCATTAATTGAGAC 2160
2161 TTTAAACAGACATGTTTTCAAAATGGCACTATGAGTGCCTCAATGATGATATCACCACCATAT 2220
|||||
DB 2161 TTTAAACAGACATGTTTTCAAAATGGCACTATGAGTGCCTCAATGATGATATCACCACCATAT 2220
2221 CTCATTATTTCTCCATTAATGTGATATATGTCTTATGATATTAATAAAGTTTGAC 2280
|||||
DB 2221 CTCATTATTTCTCCATTAATGTGATATATGTCTTATGATATTAATAAAGTTTGAC 2280
2281 TTCACAAAAGACGTGAAATGAGACACACATATGCAATTAATGCACTCCACCATCA 2340
|||||
DB 2281 TTCACAAAAGACGTGAAATGAGACACACATATGCAATTAATGCACTCCACCATCA 2340
2341 GCTACACACTGCTTGAATATATTTAGAACACCTCGCATTTGTGGTCTCTTAAGC 2400
|||||
DB 2341 GCTACACACTGCTTGAATATATTTAGAACACCTCGCATTTGTGGTCTCTTAAGC 2400
2401 AAAATACCTTGATTTAGTCTGAGTGGGCTGTGCATCGAGGGGTTGAGAAATATTCAA 2460
|||||
DB 2401 AAAATACCTTGATTTAGTCTGAGTGGGCTGTGCATCGAGGGGTTGAGAAATATTCAA 2460
2461 TTCTCAGCAGAGCCAGAAATTTGAATTCCTCATCTTTAGGAATCATTTACAGGTTTG 2520
|||||
DB 2461 TTCTCAGCAGAGCCAGAAATTTGAATTCCTCATCTTTAGGAATCATTTACAGGTTTG 2520
2521 GAGAGGATTCAGACAGCTCAGGTGCTTCTACTAATGTCCTGAACCTTGTCCCTCTTTG 2580
|||||
DB 2521 GAGAGGATTCAGACAGCTCAGGTGCTTCTACTAATGTCCTGAACCTTGTCCCTCTTTG 2580
2581 TGTTCATGATAGTCCCAATTAATGTATCTTTGAACTGATGCTCATAGAGAGAAATA 2640
|||||
DB 2581 TGTTCATGATAGTCCCAATTAATGTATCTTTGAACTGATGCTCATAGAGAGAAATA 2640
2641 TTAGAACTCTGAGTGTATCAACATTAGGATTTCAAGAAATATTAGATTAAAGTCACA 2700
|||||
DB 2641 TTAGAACTCTGAGTGTATCAACATTAGGATTTCAAGAAATATTAGATTAAAGTCACA 2700
2701 CTGGTCAAAAGAACCAAGATACAAAGAACTGTGAGCTGCACTGCCATCTCTGTGA 2760
|||||
DB 2701 CTGGTCAAAAGAACCAAGATACAAAGAACTGTGAGCTGCACTGCCATCTCTGTGA 2760
2761 GCCACAAACCAAGAGAGACCCACAGCATGTCTGAGATCTTAAATCAAGAAACAGATG 2820
|||||
DB 2761 GCCACAAACCAAGAGAGACCCACAGCATGTCTGAGATCTTAAATCAAGAAACAGATG 2820
2821 TCATGAGTTGAATTCCTCTATTAATGATGATGCTGAGCTTCTGCGCTCTCTCTT 2880
|||||
DB 2821 TCATGAGTTGAATTCCTCTATTAATGATGATGCTGAGCTTCTGCGCTCTCTCTT 2880
2881 GACACATATTAAGCTTCTAGCTTTGCTTCACAGACTTTATCTTTTCTCCACACATGCC 2940
|||||
DB 2881 GACACATATTAAGCTTCTAGCTTTGCTTCACAGACTTTATCTTTTCTCCACACATGCC 2940
2941 TTACCAATCTCTCTCTGCTGTGCTTGTGCTTTGGACTTCCCAACAGATTTCAACGACTCT 3000
|||||
DB 2941 TTACCAATCTCTCTCTGCTGTGCTTGTGCTTTGGACTTCCCAACAGATTTCAACGACTCT 3000
3001 CAAGTCTTTTCTTCCATCCCAACCACTAAGCTGAAT 3036
|||||
DB 3001 CAAGTCTTTTCTTCCATCCCAACCACTAAGCTGAAT 3036

RESULT 5
ABL95397
ID ABL95397 standard; cDNA: 3923 BP.
XX ABL95397;
AC
CC
DT 19-JUL-2002 (first entry)

XX Human DD3 cDNA sequence SEQ ID NO 690.
DE Human; cancer; prostate cancer; vaccine; cytostatic; immunostimulant;
KW gene therapy; gene; ss.
XX Homo sapiens.
OS
XX US2002022248-A1.
PN
XX 21-FEB-2002.
PD
XX 12-JAN-2001; 2001US-0759143.
PF
XX 25-FEB-1997; 97US-0806099.
PR 01-AUG-1997; 97US-0904804.
PR 09-FEB-1998; 98US-0020956.
PR 25-FEB-1998; 98US-0030607.
PR 14-JUL-1998; 98US-0115453.
PR 23-SEP-1998; 98US-0159812.
PR 15-JAN-1999; 99US-0232149.
PR 09-APR-1999; 99US-0288946.
PR 13-JUL-1999; 99US-0352616.
PR 12-NOV-1999; 99US-0439313.
PR 18-NOV-1999; 99US-0443686.
PR 14-JAN-2000; 2000US-0483672.
PR 27-MAR-2000; 2000US-0536857.
PR 09-MAY-2000; 2000US-0568100.
PR 12-MAY-2000; 2000US-0570737.
PR 13-JUN-2000; 2000US-0593793.
PR 27-AUG-2000; 2000US-0605783.
PR 10-AUG-2000; 2000US-0636215.
PR 29-AUG-2000; 2000US-0651236.
PR 06-SEP-2000; 2000US-0657279.
PR 02-OCT-2000; 2000US-0679426.
PR 10-OCT-2000; 2000US-0685166.
XX
XX (XUJ/) XU J.
PA (DIIL/) DILLON D. C.
PA (MITC/) MITCHAM J. L.
PA (HARL/) HARLOCKER S. L.
PA (JIAN/) JIANG Y.
PA (KALO/) KALOS M. D.
PA (FANG/) FANGER G. R.
PA (RETT/) RETTER M. W.
PA (STOL/) STOLK J. A.
PA (DAYC/) DAY C. H.
PA (VEDV/) VEDVICK T. S.
PA (CART/) CARTER D.
PA (LISX/) LI S. X.
PA (WANG/) WANG A.
PA (SKEL/) SKEIKY Y. A. W.
PA (HEPL/) HEPLER W. T.
PA (HEND/) HENDERSON R. A.
XX
PI Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Kalos MD;
PI Fanger GR, Retter MW, Stolk JA, Day CH, Vedvick TS, Carter D;
PI Li SX, Wang A, Skelky YAW, Hepler WT, Henderson RA;
XX WPI: 2002-255649/30.
PT New prostate-specific polynucleotides for diagnosing and treating
PT diseases, in particular prostate cancer, and as markers for the
PT progression of cancer
PS
PS Claim 1, SEQ ID NO 690; 87bp; English.
XX
XX The present invention provides prostate-specific coding sequences and
CC their encoded proteins. These can be used in the diagnosis and treatment
CC of cancers, particularly prostate cancer. The present sequence is a cDNA
CC described in the invention.
XX
XX Sequence 3923 BP; 1157 A; 840 C; 740 G; 1186 T; 0 other;

Dp	2101	GTGTGTGTGTGAGTGTACATGTCACAAAGTGTGCTCTCTCTCTTGTACCCATTATTTTCAGAC	2160
Qy	2161	TTAAACACAGCATGTTTTTCAATGGCACATGAGCTGGCCAAATGATATCACACACCATAT	2220
Dp	2161	TTAAACACAGCATGTTTTTCAATGGCACATGAGCTGGCCAAATGATATCACACACCATAT	2220
Qy	2221	CTCATTTTATTCGCCAGTAAATGTGATTAATATGTCATGTTGAACATATAAAAAAGTTTGAC	2280
Dp	2221	CTCATTTTATTCGCCAGTAAATGTGATTAATATGTCATGTTGAACATATAAAAAAGTTTGAC	2280
Qy	2281	TTCCAAACAGCAGCTGGAAATGTGACCAACACACATATGCATTAATCTAACCTCCACATCA	2340
Dp	2281	TTCCAAACAGCAGCTGGAAATGTGACCAACACACATATGCATTAATCTAACCTCCACATCA	2340
Qy	2341	GCTACACACGTGCTTGACATATATTGTTTAGAAGCACCTGGCATTGTTGGGTTCTCTTAAGC	2400
Dp	2341	GCTACACACGTGCTTGACATATATTGTTTAGAAGCACCTGGCATTGTTGGGTTCTCTTAAGC	2400
Qy	2401	AAATTAAGTTCGATTAGGTCTCAGCTGGGGGCTGTCATCAGCAGGCGGTTTGAGAAATATCAA	2460
Dp	2401	AAATTAAGTTCGATTAGGTCTCAGCTGGGGGCTGTCATCAGCAGGCGGTTTGAGAAATATCAA	2460
Qy	2461	TTCTCAGCAGACGCCAGCAATTTGAATTCCTCATCTTTTAGAATTCATTTACAGAGTTTG	2520
Dp	2461	TTCTCAGCAGACGCCAGCAATTTGAATTCCTCATCTTTTAGAATTCATTTACAGAGTTTG	2520
Qy	2521	GAGGAGATTCAGACAGCTCAGGTGCTTCCACTATATGTCTCGAACCTCTGCCCCCTTTTG	2580
Dp	2521	GAGGAGATTCAGACAGCTCAGGTGCTTCCACTATATGTCTCGAACCTCTGCCCCCTTTTG	2580
Qy	2581	TGTTTCATGATAGTATGTCCAATTAATTAATTTATCTTTGAACTGATGCTCATAGAGAGATA	2640
Dp	2581	TGTTTCATGATAGTATGTCCAATTAATTAATTTATCTTTGAACTGATGCTCATAGAGAGATA	2640
Qy	2641	TAAAGACTCTGAGTATATCAACTTTAGGGATTCAAGAAATATTAGATTTAAGCTCACA	2700
Dp	2641	TAAAGACTCTGAGTATATCAACTTTAGGGATTCAAGAAATATTAGATTTAAGCTCACA	2700
Qy	2701	CTGGTCCAAAAGGAGCAACAAGATACAAAGAACTCTGAGCTGTCATGCTGCCCATCTCTGGA	2760
Dp	2701	CTGGTCCAAAAGGAGCAACAAGATACAAAGAACTCTGAGCTGTCATGCTGCCCATCTCTGGA	2760
Qy	2761	GCCACAAACCAACAGACGAGACCCACACGATGCTGAGATCTTAAATCAAGGAACCAAGTG	2820
Dp	2761	GCCACAAACCAACAGACGAGACCCACACGATGCTGAGATCTTAAATCAAGGAACCAAGTG	2820
Qy	2821	TCATGAGTGTGAATTCCTCTATTAATAGATGCTAGTCTTGCGCATCTCTGGCTCTCCCTT	2880
Dp	2821	TCATGAGTGTGAATTCCTCTATTAATAGATGCTAGTCTTGCGCATCTCTGGCTCTCCCTT	2880
Qy	2881	GACACATATTAAGCTTTAGAGCTTTGCTCCACGACTTTTATCTTTCTCCAAACATATGC	2940
Dp	2881	GACACATATTAAGCTTTAGAGCTTTGCTCCACGACTTTTATCTTTCTCCAAACATATGC	2940
Qy	2941	TTACCAATTCCTCTCTGCTCTGTGCTTTGACTTCCCAAGAATTTCAAGACTCT	3000
Dp	2941	TTACCAATTCCTCTCTGCTCTGTGCTTTGACTTCCCAAGAATTTCAAGACTCT	3000
Qy	3001	CAAGTCTTTTCTTCATCCCCACACATCAACTGTAAT	3036
Dp	3001	CAAGTCTTTTCTTCATCCCCACACATCAACTGTAAT	3036
RESULT 6			
ACAS9834			
ID	ACAS9834	standard; cdna: 3923 BP.	
XX	ACAS9834;		
XX			
XX	10-JUN-2003	(first entry)	
DE	Prostate cancer therapy associated cdna #545.		

XX		Prostate cancer; vaccine; gene therapy; cytostatic; fusion protein;
KM		Immunogen; cancer; prostate specific antigen; PSA;
KW		prostatic acid phosphatase; PAP; prostate specific membrane antigen;
KX		PSMA; gene; ss.
OS		Homo sapiens.
XX		
PN	US2002192763-A1.	
PD	19-DEC-2002.	
XX		
PE	29-JUN-2001; 2001US-0895793.	
XX		
PR	17-APR-2000; 2000US-157455P.	
PR	04-OCT-2000; 2000US-0679272.	
PK	28-MAR-2001; 2001US-0822827.	
XX		
PA	(XUJ/) XU J.	
PA	(DILL/) DILLON D C.	
PA	(MITC/) MITCHAM J L.	
PA	(HARL/) HARLOCKER S L.	
PA	(JIAN/) JIANG Y.	
PA	(KALO/) KALOS M D.	
PA	(FANG/) FANGER G R.	
PA	(RETT/) RETTER M W.	
PA	(STOL/) STOLK J A.	
PA	(DAYC/) DAY C H.	
PA	(VEDV/) VEDVICK T S.	
PA	(CART/) CARTER D.	
PA	(LISX/) LI S X.	
PA	(WANG/) WANG A.	
PA	(SKEI/) SKEIKY Y A W.	
PA	(HEPL/) HEPLER W T.	
PA	(HEND/) HENDERSON R A.	
PA	(HURA/) HURAI J.	
PA	(MCNE/) MCNEILL P D.	
PA	(HOUG/) HOUGHTON R L.	
PA	(DBAS/) Y DE BASSOLS C V.	
PA	(FOYT/) FOY T M.	
XX		
XX	Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Kalos MD;	
P1	Fanger GR, Retter MW, Stolk JA, Day CH, Vedvick TS, Carter D;	
P1	Li SX, Wang A, Skeiky YAW, Hepler WT, Henderson RA, Hurai J;	
P1	McNeill PD, Houghton RL, Y De Bassols CV, Foy TM;	
DR	WPI: 2003-352711/33.	
XX		
PT	New fusion protein comprising prostate-specific polypeptides, or its	
PT	immunogenic portions, useful for diagnosing, preventing and/or treating	
PT	cancer, particularly prostate cancer -	
XX		
PS	Example 16; SEQ ID NO 690; 85pp; English.	
XX		
CC	The invention describes a fusion protein comprising at least one amino	
CC	acid sequence of immunogenic portions of any of the 3 sequences not	
CC	defined in the specification, or sequences having at least 70 or 90 %	
CC	sequence identity to any one of the 35 sequences defined in the USPO	
CC	web site, which is encoded by any of the 4 nucleotide sequences not	
CC	defined in the specification. The fusion protein, composition and	
CC	methods are useful for diagnosing, preventing and/or treating cancer,	
CC	particularly prostate cancer. The proteins are useful as markers to	
CC	indicate the presence or absence of cancer. This sequence	
CC	Note: The sequence data for this patent did not form part of the	
CC	printed specification, but was obtained in electronic format directly	
CC	from the US patent office at	
CC	seqdata.uspto.gov/sequence.html?docID=US20020192763.	
XX		
SQ	Sequence 3923 BP; 1157 A; 840 C; 740 G; 1186 T; 0 other;	

Query Match 84.8%; Score 3036; DB 25; Length 3923;
 Best Local Similarity 100.0%; Pred. No. 0;

Matches 3036: Conservative 0; Mismatches 0; Indels 0; Gaps 0;				
Qy	1	ACAGAGAAATAGCAAGTGGCGAGAGCTGGCATCAGAAAAACAGAGGGGAGATTGTGT	60	
Db	1	ACAGAGAAATAGCAAGTGGCGAGAGCTGGCATCAGAAAAACAGAGGGGAGATTGTGT	60	
Qy	61	GGCTGACGCCAGGGAGACCAAGAAATCTGCATGTGGGAAGGACCTGATGATACAGAG	120	
Db	61	GGCTGACGCCAGGGAGACCAAGAAATCTGCATGTGGGAAGGACCTGATGATACAGAG	120	
Qy	121	GAATTACAAACATATCTAGTGTTCATGAACACCAATAAATTAAGTAAGAGCTA	180	
Db	121	GAATTACAAACATATCTAGTGTTCATGAACACCAATAAATTAAGTAAGAGCTA	180	
Qy	181	GTCCGCTGTGAGTCTCTCAGTGCACACAGGGCTGGATCACCATGCAGGGCACTTCTGAG	240	
Db	181	GTCCGCTGTGAGTCTCTCAGTGCACACAGGGCTGGATCACCATGCAGGGCACTTCTGAG	240	
Qy	241	TACTCAGTGCAGCAAGAAAGACTACAGACATCTCAATGCGAGGGGTGAGAAATTAAGAA	300	
Db	241	TACTCAGTGCAGCAAGAAAGACTACAGACATCTCAATGCGAGGGGTGAGAAATTAAGAA	300	
Qy	301	GGCTGCTGACTTTTACATCTGAGGGCACATCTGCTGAANTGGAGTAATTAACATCAC	360	
Db	301	GGCTGCTGACTTTTACATCTGAGGGCACATCTGCTGAANTGGAGTAATTAACATCAC	360	
Qy	361	TAGAAGACGACAGATGACAAATATATGTCTAAGTAGACATGTTTTGCACTTTCCAG	420	
Db	361	TAGAAGACGACAGATGACAAATATATGTCTAAGTAGACATGTTTTGCACTTTCCAG	420	
Qy	421	CCCCCTTAAATATCCACACACAGAAAGCAAAAGAACACAGAGATCCCTGGGAGA	480	
Db	421	CCCCCTTAAATATCCACACACAGAAAGCAAAAGAACACAGAGATCCCTGGGAGA	480	
Qy	481	AATGCCGCCGCCATCTTGGGTGATGATGAGCTGCCCTGTGCTGCTGCCGCTGT	540	
Db	481	AATGCCGCCGCCATCTTGGGTGATGATGAGCTGCCCTGTGCTGCTGCCGCTGT	540	
Qy	541	GAGGGAAGGACATTAGAAATGAATTGATGTCTTAAAGATGGGACAGAAACAGA	600	
Db	541	GAGGGAAGGACATTAGAAATGAATTGATGTCTTAAAGATGGGACAGAAACAGA	600	
Qy	601	TCCGTGTGTGATTTTATTTGAACGGGATTACAGATTGGAATGAAGTCCAAAGTCAG	660	
Db	601	TCCGTGTGTGATTTTATTTGAACGGGATTACAGATTGGAATGAAGTCCAAAGTCAG	660	
Qy	661	CATTACCAATGAGAGGAAAACAGAGAAAATCTTGTGCTTACAAAGACATGCAACA	720	
Db	661	CATTACCAATGAGAGGAAAACAGAGAAAATCTTGTGCTTACAAAGACATGCAACA	720	
Qy	721	AACAAATGGAATACTGTGATGACATGAGGACGCCAAGCTGGGAGAGATTAACGACGG	780	
Db	721	AACAAATGGAATACTGTGATGACATGAGGACGCCAAGCTGGGAGAGATTAACGACGG	780	
Qy	781	GCAGAGGTCAGAGATTGCGGCCCTGTCCTTAACCTGCGGTATTAACCAATCATTTTC	840	
Db	781	GCAGAGGTCAGAGATTGCGGCCCTGTCCTTAACCTGCGGTATTAACCAATCATTTTC	840	
Qy	841	ATAATTTTAAACCTCAAAACAAAGCTGTGTAATATGATCTACGCTTCTTGGG	900	
Db	841	ATAATTTTAAACCTCAAAACAAAGCTGTGTAATATGATCTACGCTTCTTGGG	900	
Qy	901	CCCAACATTTCTCCATATATCCAGCACACATCTTTTAAATTAATTTCCAGATCTGTA	960	
Db	901	CCCAACATTTCTCCATATATCCAGCACACATCTTTTAAATTAATTTCCAGATCTGTA	960	
Qy	961	CTGAGACCTTTCTACCTGTAGATTAACATTTACTCATTTTGTCAAAGACCTTCGTGT	1020	
Db	961	CTGAGACCTTTCTACCTGTAGATTAACATTTACTCATTTTGTCAAAGACCTTCGTGT	1020	
Qy	1021	GCTGCTAATATATGAGTGAATGTTTTTCCCTAAGAGAGTGTCTGGCCAGGGGATCTGTG	1080	
Db	1021	GCTGCTAATATATGAGTGAATGTTTTTCCCTAAGAGAGTGTCTGGCCAGGGGATCTGTG	1080	

Qy	1081	AACAGCTGGGAGCATCTCAAGATCTTCCAGGGTATTAATCTACTACACAGACATGA	1140	
Db	1081	AACAGCTGGGAGCATCTCAAGATCTTCCAGGGTATTAATCTACTACACAGACATGA	1140	
Qy	1141	TCATTACGAGAGTGAATTAATCAATCAATCATCTCAGTGTCTTGGCCATCTGAAT	1200	
Db	1141	TCATTACGAGAGTGAATTAATCAATCAATCATCTCAGTGTCTTGGCCATCTGAAT	1200	
Qy	1201	TCATTGCCACTTTTGTGCCATCTCTCAAGACCTCAAAATGTCAATTCATTAATATCA	1260	
Db	1201	TCATTGCCACTTTTGTGCCATCTCTCAAGACCTCAAAATGTCAATTCATTAATATCA	1260	
Qy	1261	GGATTAACCTTTTAACTGGAAGAAATTCATATGTAATGCAGCTATGGGAATTTA	1320	
Db	1261	GGATTAACCTTTTAACTGGAAGAAATTCATATGTAATGCAGCTATGGGAATTTA	1320	
Qy	1321	ATTAACATATTTTGTTCACAGTGCAGAAAGATGACTAAGTCTTTATCCCTCCCTTGT	1380	
Db	1321	ATTAACATATTTTGTTCACAGTGCAGAAAGATGACTAAGTCTTTATCCCTCCCTTGT	1380	
Qy	1381	GATTTTTCACAGATTAAGTAAATGCTTAGCTGTGAGGCTGTATACAGAC	1440	
Db	1381	GATTTTTCACAGATTAAGTAAATGCTTAGCTGTGAGGCTGTATACAGAC	1440	
Qy	1441	AGCCTCTCCCATCCCTCCAGCCTTATCTGTCATACACATCAACCCCTCCATACACCT	1500	
Db	1441	AGCCTCTCCCATCCCTCCAGCCTTATCTGTCATACACATCAACCCCTCCATACACCT	1500	
Qy	1501	AAACAAATCTTAATCTGTAATCTCTGTAACATGTCAGACATTAATTTCTCTGCT	1560	
Db	1501	AAACAAATCTTAATCTGTAATCTCTGTAACATGTCAGACATTAATTTCTCTGCT	1560	
Qy	1561	GAGAGAGCTCTCTTGTCTCTTAATCTAGAAATATGTAAGTTTGAATAGTTGACTA	1620	
Db	1561	GAGAGAGCTCTCTTGTCTCTTAATCTAGAAATATGTAAGTTTGAATAGTTGACTA	1620	
Qy	1621	TCTTACTTCATGCAAGAGGACACATATGAGATTCATCATGACAGACAAATA	1680	
Db	1621	TCTTACTTCATGCAAGAGGACACATATGAGATTCATCATGACAGACAAATA	1680	
Qy	1681	CTAAAGGTATATTTGATTAAGATTTTAAATTAATTAATTAATTAATTAATTAATTA	1740	
Db	1681	CTAAAGGTATATTTGATTAAGATTTTAAATTAATTAATTAATTAATTAATTAATTA	1740	
Qy	1741	GGGAATGTTTATGGGGACGTTTGTAAAGCCCTGGGATGTGAAGCAAGGACAGACCTCA	1800	
Db	1741	GGGAATGTTTATGGGGACGTTTGTAAAGCCCTGGGATGTGAAGCAAGGACAGACCTCA	1800	
Qy	1801	TAGTATCTTATATATATACTTCAATTTCTATCTATCTATCAATATCAAGACTTTT	1860	
Db	1801	TAGTATCTTATATATATACTTCAATTTCTATCTATCTATCAATATCAAGACTTTT	1860	
Qy	1861	CACGAATTCATGAGAGGCAAAATCCCAAGGTAACTTTATCCATTTCAATGGAGATGC	1920	
Db	1861	CACGAATTCATGAGAGGCAAAATCCCAAGGTAACTTTATCCATTTCAATGGAGATGC	1920	
Qy	1921	GCTTTAGAAATTTTGGCAAAATCATCTGTCTATCTATCTCAACTTTGAGATGTGTTGCC	1980	
Db	1921	GCTTTAGAAATTTTGGCAAAATCATCTGTCTATCTATCTCAACTTTGAGATGTGTTGCC	1980	
Qy	1981	TTGTAGTTAATTTGAAGAAATAGGGCACTCTTGTGAGCCCACTTTAGGGTTCACCTCGGC	2040	
Db	1981	TTGTAGTTAATTTGAAGAAATAGGGCACTCTTGTGAGCCCACTTTAGGGTTCACCTCGGC	2040	
Qy	2041	AATTAAGAAATTTACAAAGAGTACTCAGAGCACTTGTTAAGAGCTCTGTGTGTGTGT	2100	
Db	2041	AATTAAGAAATTTACAAAGAGTACTCAGAGCACTTGTTAAGAGCTCTGTGTGTGTGT	2100	
Qy	2101	GTTGTGTGTGAGAGTGCATGCCAAAGTGTGACCTCTCTCTTACCCATTAATTTTCAGAC	2160	
Db	2101	GTTGTGTGTGAGAGTGCATGCCAAAGTGTGACCTCTCTCTTACCCATTAATTTTCAGAC	2160	

QY	2161	TTAAACAAGACATCTTTTCCAATGGCACTATGAGCTGGCATGATGATATCACCAACCATAT	2220
Db	2161	TTAAAAACAAGCATCTTTTCCAATGGCACTATGAGCTGGCATGATGATATCACCAACCATAT	2220
QY	2221	CTCATTTATTCGCCAGTAAATGTGATTAATTAATGTCATCGTTAAATATAAAAAAGTTTGAC	2280
Db	2221	CTCATTTATTCGCCAGTAAATGTGATTAATTAATGTCATCTGTTAAATATAAAAAAGTTTGAC	2280
QY	2281	TTCCAAAAGACGCTGGAAATGAGCAACACACAAATATGATATTAATCTTAACCTCTACATCA	2340
Db	2281	TTCCAAAAGACGCTGGAAATGAGCAACACACAAATATGATATTAATCTTAACCTCTACATCA	2340
QY	2341	GCTACACACCTGCTTGACATATATTGTTAGAAAGCACTCGCATTTTGCGGGTCTCTTAAGC	2400
Db	2341	GCTACACACCTGCTTGACATATATTGTTAGAAAGCACTCGCATTTTGCGGGTCTCTTAAGC	2400
QY	2401	AAATTACTTGATTAAGCTTCAGCTGGGGGCTGTCATACAGCGGGTTGAGAAATATTCAA	2460
Db	2401	AAATTACTTGATTAAGCTTCAGCTGGGGGCTGTCATACAGCGGGTTGAGAAATATTCAA	2460
QY	2461	TTCTCAGCAGAGACAGAAATTTGAATTCCTCATCTTTTAGAATCAATTTACAGAGTTTG	2520
Db	2461	TTCTCAGCAGAGACAGCAATTTGAATTCCTCATCTTTTAGAATCAATTTACAGAGTTTG	2520
QY	2521	GAGAGGATTCAGACAGCTCAGCTGCTTTCACATTAATGCTCTGAACCTTCTGTCCTCTTG	2580
Db	2521	GAGAGGATTCAGACAGCTCAGGTCCTTTCACATTAATGCTCTGAACCTTCTGTCCTCTTG	2580
QY	2581	TGTTTCATGAGTATGTCCAATTAATTAATGTTATCTTTGAACCTGATCTCATATAGAGAAATA	2640
Db	2581	TGTTTCATGAGTATGTCCAATTAATTAATGTTATCTTTGAACCTGATCTCATATAGAGAAATA	2640
QY	2641	TAAAGACTCTGAGTATATCAACATTTTGGGGTTCAAAAGAAATTTAGATTTAACTCACA	2700
Db	2641	TAAAGACTCTGAGTATATCAACATTTTGGGGTTCAAAAGAAATTTAGATTTAACTCACA	2700
QY	2701	CTGGTCAAAAGGAACAACAATATCAAGAACCTGAGCTGTCATGCTGCCATCTCTGTGA	2760
Db	2701	CTGGTCAAAAGGAACAACAATATCAAGAACCTGAGCTGTCATGCTGCCATCTCTGTGA	2760
QY	2761	GCCACAAACACACAGAGACCCCAACGCGATGCTAGATCCTTAATCAAGAAACCACTG	2820
Db	2761	GCCACAAACACACAGAGACCCCAACGCGATGCTAGATCCTTAATCAAGAAACCACTG	2820
QY	2821	TCATGAGTGAATCTCTCTATTTATGATAGTACGTCTGGGCATCTGCGCTCTCCCTTT	2880
Db	2821	TCATGAGTGAATCTCTCTATTTATGATAGTACGTCTCTGGCCATCTCTGCTCTCTTT	2880
QY	2881	GACACATATTAGCTTCTAGCCCTTGCTTCCACGACTTTATCTTTTCTCCAAACATATCG	2940
Db	2881	GACACATATTAGCTTCTAGCCCTTGCTTCCACGACTTTATCTTTTCTCCAAACATATCG	2940
QY	2941	TTACCAATCTCTCTCTGCTCTGTGGCTTTGGAATTTCCCAAGAATTTACAGACTCT	3000
Db	2941	TTACCAATCTCTCTCTGCTCTGTGGCTTTGGAATTTCCCAAGAATTTCAAGACTCT	3000
QY	3001	CAAGCTTTTCTCTCCATCCCAACACTTAACCTGAAT	3036
Db	3001	CAAGCTTTTCTCTCCATCCCAACACTTAACCTGAAT	3036
RESULT 7			
AAV62427			
XX	AAV62427	standard; cDNA: 2037 BP.	
XX	AAV62427:		
XX	30-DEC-1998	(first entry)	
XX	Prostate cancer antigen (PCA3)	cDNA splice variant 1.	
XX	Prostate cancer antigen cDNA splice variant 1; PCA3; prostatic cancer;		
XX	PC; ds.		

XX	Homo sapiens.
OS	Location/Qualifiers
XX	Key CDS
FH	379..534
FT	/tag= "a"
FT	/product= "PCa3 protein variant 1"
FT	2019..2024
FT	/ <tag= b<="" td=""></tag=>
XX	
PN	M09845420-A1.
XX	
PD	15-OCT-1998.
XX	
PF	09-APR-1998; 98WO-CA00346.
PR	10-APR-1997; 97US-0041836.
XX	(DIAG-) DIAGNOCLURE INC.
PA	
PI	Busemakers MJG;
XI	
DR	WPI: 1998-568347/48.
DR	P-PADB: AAM79736.
XX	New nucleic acid encoding prostate cancer antigen 3 - for diagnosis, prevention and treatment of prostatic cancer
PT	
PS	Claim 3; Fig 2B-2J; 11pp; English.
XX	The present sequence represents the prostate cancer antigen (PCA3) cDNA splice variant 1 sequence comprising of exons 1, 2, 3, 4a and 4b of the PCA3 gene. The PCA3 cDNA splice variant 1 sequence, isolated from a human primary prostatic tumour tissue cDNA library, was found in approximately 5% of the cDNA clones isolated. The invention claims for PCA3 cDNA variants and the proteins they encode. The invention also claims for antibodies against PCA3 protein. The antibodies are claimed to be useful for detecting PCA3 protein in immunossay tests, for diagnosing, assessing and prognosting of prostatic cancer (PC). Antibodies, optionally coupled to a cytotoxin or radiolotope, and nucleic acids antisense to PCA3 cDNA are claimed to be useful for treating PC, while determining elevated levels of PCA3 (as RNA or protein) is useful for detecting a predisposition to development of PC, e.g. in prenatal tests. Detecting PCA3 protein allows differentiation between malignant and benign prostatic disease, and the level of PCA3 expression allows correlation with the grade of tumour. PCA3 protein and its fragments are also claimed to be useful in vaccines for preventing PC; in drug screens for identifying specific (antiagonists (potentially useful therapeutically)) and for studying protein-DNA interactions.
SX	Sequence 2037 BP; 622 A; 426 C; 406 G; 575 T; 8 other:
Query Match	45.5%; Score 1629; DB 19; Length 2037; Best Local Similarity 99.6%; Pred. No. 0;
Matches 2029; Conservative	0; Mismatches 8; Indels 0; Gaps 0
OY	23 AGAAGCTGGCATCAGAAAAACAGAAGGGAGATTTGTGGCGTCGCAGCCGAGGAACAACCAG 82
Dd	1 AGAAAGCTGGCATCAGAAAAACAGAAGGGAGATTTGTGGCGTCGCAGCCGAGGAACAACCAG 60
OY	83 GAACATCTGCATGGTGGAAGAGACTGTAAGATCACAGAGAATAATPACAAACATATACTTAG 142
Dd	61 GAAATCTGCCATGGTGGGAAGSAGACTGATGATACAGAGAGAATAATCAAACACATATACTTAG 120
OY	143 TGTTTTCAATGAACAACCAAGATPAATTAAGTGAAGAGCTAGTCCGCTGTGAGTCCTCACT 202
Dd	121 TGTTCATATGAACACCAAGATAAATTAATGTGAAGAGCTAGTCCGCTGTGAGTCCTCACT 180
OY	203 GACACAGGCGCTGAGAACCATCGACGCACTTTCTGCATACATCACTGACGAAAGAAGA 262
Dd	181 GACACAGGCGCTGAGATCACCATCGAGGAGCACTTTCTGCATACATCACTGACGAAAGAAGA 240

QY	263	CTACGACATCTCCANTGGCAGGGGAGAAATAAAGAAAGCGTGCATCTTACCATCTGA	322
Db	241	CTACGACATCTCTCAATGGCAGGGGAGAAATAAAGAAAGCGTGCATCTTACCATCTGA	300
QY	323	GGCCACACATCTGCTGAAATGAGATTAATTAATCATCTACATAGAACAGCAATGACAAATA	382
Db	301	GGCCACACATCTGCTGAAATGAGATTAATTAATCATCTACATAGAACAGCAATGACAAATA	360
QY	383	TAAATGCTAAGTAGAGATGTTTTGGACATTTTCACAGCCCTTTAAATATCCACACACA	442
Db	361	TAAATGCTAAGTAGAGATGTTTTGGACATTTTCACAGCCCTTTAAATATCCACACACA	420
QY	443	CAGGAAGCAAAAGGAAGCACAGAGATCCCTGGGAGAAATCCCGCCGCATTTGGG	502
Db	421	CAGGAAGCAAAAGGAAGCACAGAGATCCCTGGGAGAAATCCCGCCGCATTTGGG	480
QY	503	TCATGATGAGGCTCGCCCTGTGCTGCCCTGTGGAGGGAAGGACATTAGAAATG	562
Db	481	TCATGATGAGGCTCGCCCTGTGCTGCCCTGTGGAGGGAAGGACATTAGAAATG	540
QY	563	AATTGATGTTCTCTTAAAGATGGGACAGAAACAGATCCGTTGTGGATTAATTAATYG	622
Db	541	AATTGATGTTCTCTTAAAGATGGGACAGAAACAGATCCGTTGTGGATTAATTAATYG	600
QY	623	AACGGGATTTACGATTTGAAAAGAGTCACAAAGTACAGATTTACAAATGAGAGAAACA	682
Db	601	AACGGGATTTACGATTTGAAAAGAGTCACAAAGTACAGATTTACAAATGAGAGAAACA	660
QY	683	GACGAGAAATCTTGTATGGCTTCACAAACATGCACAAACAAATGGAATCTGTGATG	742
Db	661	GACGAGAAATCTTGTATGGCTTCACAAACATGCACAAACAAATGGAATCTGTGATG	720
QY	743	ACATGAGGACGCAAGCTGGGGAGAGATTAACACAGGGGACAGAGGTCAGATTTGGCC	802
Db	721	ACATGAGGACGCAAGCTGGGGAGAGATTAACACAGGGGACAGAGGTCAGATTTGGCC	780
QY	803	CTGCGCCCTAAACCTGGGCTTCATACCAATCATTTATATTTTAAACCTCMAAACAA	862
Db	781	CTGCGCCCTAAACCTGGGCTTCATACCAATCATTTATATTTTAAACCTCMAAACAA	840
QY	863	AGCTTTTAAATATGTGATCTCTACGGTTCCTTCGGGCCCAACATTCCTCATATATCCA	922
Db	841	AGCTTTTAAATATGTGATCTCTACGGTTCCTTCGGGCCCAACATTCCTCATATATCCA	900
QY	923	GCCACACTCATTTTAAATATTTAGTTCACAGATCTGTACTGTGACCTTTTACACTGTAG	982
Db	901	GCCACACTCATTTTAAATATTTAGTTCACAGATCTGTACTGTGACCTTTTACACTGTAG	960
QY	983	AATAACATTTACTCATTTTGTTCMAAGACCCTTCGTGTGCTGCTTAATATGAGCTGACT	1042
Db	961	AATAACATTTACTCATTTTGTTCMAAGACCCTTCGTGTGCTGCTTAATATGAGCTGACT	1020
QY	1043	GTTTTTCTAAGGAGTGTCTTGCGCCACAGGGGATCTGTAAACAGGCTGGGAAGCATCTCAA	1102
Db	1021	GTTTTTCTAAGGAGTGTCTTGCGCCACAGGGGATCTGTAAACAGGCTGGGAAGCATCTCAA	1080
QY	1103	GATCTTTCACAGGTTATCTACTACTAGACACAGCATGTACTTAACGAGGTAAATATCTA	1162
Db	1081	GATCTTTCACAGGTTATCTACTACTAGACACAGCATGTACTTAACGAGGTAAATATCTA	1140
QY	1163	ATCAACATCATCTCTCAGTGTCTTGCCCATCTAGAAATTCATTTCCACTTTGTGCCCA	1222
Db	1141	ATCAACATCATCTCTCAGTGTCTTGCCCATCTAGAAATTCATTTCCACTTTGTGCCCA	1200
QY	1223	TTCTCACAACCTGCAAAATGTCAATTCATTAATATCACAGGATTAACCTTTTTTTTAAAC	1282
Db	1201	TTCTCACAACCTGCAAAATGTCAATTCATTAATATCACAGGATTAACCTTTTTTTTAAAC	1260
QY	1283	TGGAAGATTTCAATTTTACATGACAGCTATGGGAATTAATTAACATATTTGTTTTCCAGT	1342
Db	1261	TGGAAGATTTCAATTTTACATGACAGCTATGGGAATTAATTAACATATTTGTTTTCCAGT	1320
QY	1343	GCAAAAGATGACTAAGTCCCTTAATCCCTCCCTTGTGTTGATTTTTTTTCCAGTATTAAGT	1402

[illegible]

PI Bussemakers MJG;
XX
DX MPI; 1998-568347/48.
XX
PT New nucleic acid encoding prostate cancer antigen 3 - for diagnosis,
XX prevention and treatment of prostatic cancer
PS
XX Claim 4: Pages 76-77; 111pp; English.
XX
CC The present sequence represents the prostate cancer antigen (PCA3)
CC cDNA splice variant 2 sequence comprising of exons 1, 3, 4a and
CC 4b of the PCA3 gene. The PCA3 cDNA splice variant 2 sequence,
CC isolated from a human primary prostatic tumour tissue cDNA library,
CC was found in approximately 65% of the cDNA clones isolated. The
CC invention claims for PCA3 cDNA variants and the proteins they encode.
CC The invention also claims for antibodies against PCA3 protein. The
CC antibodies are claimed to be useful for detecting PCA3 protein in
CC immunosay tests, for diagnosing, assessing and prognosing of
CC prostatic cancer (PC). Antibodies, optionally coupled to a cytotoxin
CC or radioisotope, and nucleic acids antisense to PCA3 cDNA are claimed
CC to be useful for treating PC, while determining elevated levels of
CC PCA3 (as RNA or protein) is useful for detecting a predisposition
CC to development of PC, e.g. in prenatal tests. Detecting PCA3 protein
CC allows differentiation between malignant and benign prostatic disease,
CC and the level of PCA3 expression allows correlation with the grade of
CC tumour. PCA3 protein and its fragments are also claimed to be useful
CC in vaccines for preventing PC; in drug screens for identifying
CC specific (ant)agonists (potentially useful therapeutically) and for
CC studying protein-DNA interactions.
XX
SQ Sequence 1872 BP; 567 A; 389 C; 369 G; 539 T; 8 other;
Query Match 38.2%; Score 1367; DB 19; Length 1872;
Best Local Similarity 99.5%; Pred. No. 0;
Matches 1/67; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
QY 285 GGTGAGAAATTAAGAAAGGCTGCTGACTTACATCTGAGGCCACATCTGCTGAATG 344
DB 98 GGTGAGAAATTAAGAAAGGCTGCTGACTTACATCTGAGGCCACATCTGCTGAATG 157
QY 345 AGATATTAACTACTAGAAACAGCAAGTGCATATATATCTAAGTAGACATGT 404
DB 158 AGATATTAACTACTAGAAACAGCAAGTGCATATATATCTAAGTAGACATGT 217
QY 405 TTTTGACATTTTCACGCCCTTTAAATATCCACACACAGCAAGCAAAAGAAAGCAC 464
DB 218 TTTTGACATTTTCACGCCCTTTAAATATCCACACACAGCAAGCAAAAGAAAGCAC 277
QY 465 AGAGATCCCTGGGAGAAATGCCCGGCCCATCTTGGGTATCGATGAGCCCTG 524
DB 278 AGAGATCCCTGGGAGAAATGCCCGGCCCATCTTGGGTATCGATGAGCCCTG 337
QY 525 GCCTGGTCCCGCTTGGAGGAAAGACATTAGAAATGAATTGATGTCTTAAAGCA 584
DB 338 GCCTGGTCCCGCTTGGAGGAAAGACATTAGAAATGAATTGATGTCTTAAAGCA 397
QY 585 TGGCGAGGAAACAGATCCGTGTGTGATTTATTTGAACGGGATTAAGATTTGAAT 644
DB 398 TGGCGAGGAAACAGATCCGTGTGTGATTTATTTGAACGGGATTAAGATTTGAAT 457
QY 645 GAAGTCACAAAGTAGACATTACCAATGAGAGGAAACAGACGAGAAATCTTGATGCTT 704
DB 458 GAAGTCACAAAGTAGACATTACCAATGAGAGGAAACAGACGAGAAATCTTGATGCTT 517
QY 705 CACAGACATGCAACAAACAAATGAATATCTGTGATGATGAGCAGCAAGCTGGGG 764
DB 518 CACAGACATGCAACAAACAAATGAATATCTGTGATGATGAGCAGCAAGCTGGGG 577
QY 765 AGGAGATTACCAAGGGGAGAGGATTTGCGCCGTGCTTAAACGTGGCTTC 824
DB 578 AGGAGATTACCAAGGGGAGAGGATTTGCGCCGTGCTTAAACGTGGCTTC 637
QY 825 ATAAACCAATTCATTCTATTTCTAACCTCAAAACAAAGCTGTGTAAATATCTGATCTC 884

DB 638 ATAAACCAATTCATTCTATTTCTAACCCCAAAACAAAGCTGTGTAAATCTGATCTC 697
QY 885 TACGGTTCCTTGGGGCCCAACATTTCTCCATATATCCAGCCACATCTTTTAATATT 944
DB 698 TACGGTTCCTTGGGGCCCAACATTTCTCCATATATCCAGCCACATCTTTTAATATT 757
QY 945 AGTTCCAGATCTGTACTGTGACCTTCTACACTGTAGATAATACATCTATCTTGTTC 1004
DB 758 AGTTCCAGATCTGTACTGTGACCTTCTACACTGTAGATAATACATCTATCTTGTTC 817
QY 1005 AAAGACCTTTCGTGTGCTGCCATATATGAGCTGACTGTTTCTTAAGAGACTTCTG 1064
DB 818 AAAGACCTTTCGTGTGCTGCCATATATGAGCTGACTGTTTCTTAAGAGACTTCTG 877
QY 1065 GCCCAGGGATCTGTAAACAGCTGGGAAACATCTCAAGATCTTCCAGGATTAATCTTA 1124
DB 878 GCCCAGGGATCTGTAAACAGCTGGGAAACATCTCAAGATCTTCCAGGATTAATCTTA 937
QY 1125 CTAGCACAGCATGATTCATTACGAGTGAATATCTAATCAACATCATCTCCAGTGTCT 1184
DB 938 CTAGCACAGCATGATTCATTACGAGTGAATATCTAATCAACATCATCTCCAGTGTCT 997
QY 1185 TTGCCCATCTGAATTCATTTTCCACTTTTGTGCCATTTCTCAAGACCTCAAAATGTCA 1244
DB 998 TTGCCCATCTGAATTCATTTTCCACTTTTGTGCCATTTCTCAAGACCTCAAAATGTCA 1057
QY 1245 TTCCATTAATATACAGAGATTAACCTTTTAACTTTTAACTTTTAACTTTTAACTTT 1304
DB 1058 TTCCATTAATATACAGAGATTAACCTTTTAACTTTTAACTTTTAACTTTTAACTTT 1117
QY 1305 CAGCTATGGAATTAATTAATACATATTTGTTTCCAGTCAAGATGACATAGCTCTTA 1364
DB 1118 CAGCTATGGAATTAATTAATACATATTTGTTTCCAGTCAAGATGACATAGCTCTTA 1177
QY 1365 TTCCCTCCCTTTGTTGATTTTTCAGATATAAAGTTAAAGTCTTACCTGTACTG 1424
DB 1178 TTCCCTCCCTTTGTTGATTTTTCAGATATAAAGTTAAAGTCTTACCTGTACTG 1237
QY 1425 AGGCTATATACAGCAAGCTCCGCCATCCCGCCGCTTATCTGTCATCCACATCAAC 1484
DB 1238 AGGCTATATACAGCAAGCTCCGCCATCCCGCCGCTTATCTGTCATCCACATCAAC 1297
QY 1485 CCCTCCCATATCCACTTAACAAATCTAATCTTAATCTTGAATGTCAGAGACATAC 1544
DB 1298 CCCTCCCATATCCACTTAACAAATCTAATCTTGAATGTCAGAGACATAC 1357
QY 1545 ATTATTCCTTTCGCTGAGAAAGCTTCTTGTCTTAAATCTGAATGATGAAGTT 1604
DB 1358 ATTATTCCTTTCGCTGAGAAAGCTTCTTGTCTTAAATCTGAATGATGAAGTT 1417
QY 1605 TTGAATTAAGTGCATCTTACTTTCATGCAAAAGAGGACATATGACATTCATCATCA 1664
DB 1418 TTGAATTAAGTGCATCTTACTTTCATGCAAAAGAGGACATATGACATTCATCATCA 1477
QY 1665 CATGAGACAGCAATCTAATAAGTGAATTTGATTTAAGAGTTAGATTAATATATGA 1724
DB 1478 CATGAGACAGCAATCTAATAAGTGAATTTGATTTAAGAGTTAGATTAATATATGA 1537
QY 1725 ATGCAAGACCCACAGAGGAAAGTTATGGGGCAGCTTTGTAAGCCTGGAGTGAAGCA 1784
DB 1538 ATGCAAGACCCACAGAGGAAAGTTATGGGGCAGCTTTGTAAGCCTGGAGTGAAGCA 1597
QY 1785 AAGGACGAGAACTCTAGATCTTATATATATATCTTACTTCTATCTCTATATACAA 1844
DB 1598 AAGGACGAGAACTCTAGATCTTATATATATATATCTTACTTCTATATACAA 1657
QY 1845 TATCAACAAGCTTTTCAAGATTCATGCAAGTCAAAATCCCAAGAGTAACCTTATATCC 1904
DB 1658 TATCAACAAGCTTTTCAAGATTCATGCAAGTCAAAATCCCAAGAGTAACCTTATATCC 1717
QY 1905 ATTTTCTGAGTGGCTTTTGAATTTTGGCAAAATCATATGCTGATCTTATCTCAACTT 1964

Db	1718	ATTTCATGCTAGTGCCTCGCTTTAGAATTTTGCCAAATCATACTGCTACTTAATCACTT	1777
Qy	1965	TGAGATGTGTTTGTCTCCTTAGTAAATGAAGAAATAGGGACACTTGTAGCCACTTT	2024
Db	1778	TCAGATGTGTTTGTCTCCTTAGTAAATGAAGAAATAGGGACACTTGTAGCCACTTT	1837
Qy	2025	AGGTTTCACTCTCGCAATTAANGAATTTACAAGA	2059
Db	1838	AGGTTTCACTCTCGCAATTAANGAATTTACAAGA	1872
Result 9			
ID	AAA06687		
XX	AAA06687	standard; cDNA; 3112 BP.	
AC	AAA06687;		
XX			
DT	13-JUN-2000	(first entry)	
XX			
DE	Human immunogenic prostate tumour protein cDNA sequence SEQ ID NO.468.		
XX			
KW	Human; prostate cancer; diagnosis; tumour; gene therapy; detection;		
XX	immunogenic; cytostatic; vaccine; ss.		
OS	Homo sapiens.		
PN	WO200004149-A2.		
PD	27-JAN-2000.		
XX			
PF	14-JUL-1999;	99WO-US15838.	
XX			
PR	14-JUL-1998;	98US-0115453.	
PR	14-JUL-1998;	98US-0116134.	
PR	23-SEP-1998;	98US-0159812.	
PR	23-SEP-1998;	98US-0159822.	
PR	15-JAN-1999;	99US-0232149.	
PR	15-JAN-1999;	99US-0232880.	
XX	09-APR-1999;	99US-0288946.	
PA	(CORI-) CORIXA CORP.		
XX			
PI	Dillon DC, Harlocker SL, Yugiu J, Xu J, Mitcham JL;		
DR	WPI; 2000-171268/15.		
XX			
PT	New polypeptide useful for treating and diagnosing prostate cancer		
PT	comprises an immunogenic portion of prostate tumor protein -		
XX			
PS	Claim 1; Page 259-260; 263pp; English.		
XX			
CC	The present invention describes isolated polypeptides, comprising an		
CC	immunogenic portion of a prostate tumor protein (PTP). The polypeptides		
CC	and polynucleotides encoding them have cytostatic activity and can be		
CC	used in vaccines and in gene therapy. The polypeptides and		
CC	polynucleotides encoding them, antigen presenting cells which express		
CC	the polypeptides, antibodies against the polypeptides and vaccines		
CC	comprising them can be used for inhibiting the development of prostate		
CC	cancer in a patient. The polypeptides can be used to generate antibodies		
CC	or anti-idiotypic antibodies for passive immuno therapy. A portion of		
CC	the polynucleotide encoding the polypeptides can be used as a probe or		
CC	to modulate the expression of the polypeptides. AAA066241 to AAA06691 and		
CC	AAV82000 to AAV82020 represent sequences used in the exemplification of		
CC	the present invention.		
XX			
SQ	Sequence 3112 BP; 975 A; 587 C; 624 G; 926 T; 0 other;		
Query Match	38.1%; Score 1364; DB 21; Length 3112;		
Best Local Similarity	99.8%; Pred. No. 0;		
Matches 1774; Conservative	0; Mismatches 1; Indels 3; Gaps 3;		
Yy	285 GGTCAGAAATAGAAAGGCTGCTGACATTACCATCTGAGGCCACACATCTGCGAAATGG	344	

Db	1313	GGTGAAGAATTAAGAAAGCGCTGCTGACTTTTACCATTCTGAGGCGACACACTGCTGTAATATG	1372
QY	345	AGATTAATTAACATCTACTAGAAACACCAAGATGACAAATATATGTGTAGTGTGACATGT	404
Db	1373	AGATTAATTAACATCTACTAGAAACACCAAGATGACAAATATATGTGTAGTGTGACATGT	1432
QY	405	TTTTCGACATTTCCAGCCCCCTTTTAATATTCACACACACAGAGAAGCACAAAAGAAAGACAC	464
Db	1433	TTTTTCACATTTTCCAGCCCCCTTTTAATATTCACACACACAGAGAAGCACAAAAGAAAGACAC	1492
QY	465	AGAGATCCCTGGGAGAAATGCCCGCGCCCATCTTGGGTCAATCGATGAGCTCGCCCTGT	524
Db	1493	AGAGATCCCTGGGAGAAATGCCCGCGCCCATCTTGGGTCAATCGATGAGCTCGCCCTGT	1552
QY	525	GCGTGTCCCGCTGTGAGGGAGAGACATTGAAAATGAATGATGTGTCCTCTTAAGAGA	584
Db	1553	GCGTGTCCCGCTGTGTGAGGGAGAGACATTGAAAATGAATGATGTGTCCTCTTAAGAGA	1612
QY	585	TGGGAGAGAAAACAGATCCTGTGTGGAGATTTATTTTAAGGGGATTACAGATTTGGAAT	644
Db	1613	TGGGAGAGAAAACAGATCCTGTGTGGAGATTTATTTTAAGGGGATTACAGATTTGGAAT	1672
QY	645	GAAGTACACAAAGTAGACATTACCAATGAGAGAAAACAGACGAGAAAATCTGTATGGCTT	704
Db	1673	GAAGTACACAAAGTAGACATTACCAATGAGAGAAAACAGACGAGAAAATCTGTATGGCTT	1732
QY	705	CACAAAGCATGCAACAAACAAATGGAATACTGTGATGACATGTAGGCGCCCAACTGGGG	764
Db	1733	CACAAAGCATGCAACAAACAAATGGAATACTGTGATGACATGTAGGCGCCCAACTGGGG	1792
QY	765	AGGAGATTAACACGGGGGAGAGGGTTCAGAGATTTGGCCCTCTCTCTTAACGTGAGCTTC	824
Db	1793	AGGAGATTAACACGGGGGAGAGGGTTCAGAGATTTGGCCCTCTCTCTTAACGTGAGCTTC	1852
QY	825	ATTAACCAATCTTTCATATTTCTAACCCTCAAAAACAAAGCTGTGTATATCTGATCTC	884
Db	1853	ATTAACCAATCTTTCATATTTCTAACCCTCAAAAACAAAGCTGTGTATATCTGATCTC	1912
QY	885	TACGGTTCCTTCTGGGCCCAACATTTCTGCATATATCCAGCCACACTATTTTAAATATT	944
Db	1913	TACGGTTCCTTCTGGGCCCAACATTTCTGCATATATCCAGCCACACTATTTTAAATATT	1972
QY	945	AGTTCCCGATCTCTACTGTGACCTTCTACAGTGTAGAAATACATTAACATCTTGTTC	1004
Db	1973	AGTTCCCGATCTCTACTGTGACCTTCTACAGTGTAGAAATACATTAACATCTTGTTC	2032
QY	1005	AAAGACCCCTTCTGTGCTGCCCTAATATATGATGATGACTGTTTTCCTAAGAGATGTTCTG	1064
Db	2033	AAAGACCCCTTCTGTGCTGCCCTAATATATGATGATGACTGTTTTCCTAAGAGATGTTCTG	2092
QY	1065	GCCGAGGGGATCTGTGAACAGGCTGGGAAGGATCTCAAGATCTTCCAGGGTTATACTTA	1124
Db	2093	GCCGAGGGGATCTGTGTGAACAGGCTGGGAAGGATCTCAAGATCTTCCAGGGTTATACTTA	2152
QY	1125	CTACACACACAGCATGATCATTAACGAGATGATTTATCAATCAACATCATCTCGAGTCT	1184
Db	2153	CTACACACACAGCATGATCATTAACGAGATGATTTATCAATCAACATCATCTCGAGTCT	2212
QY	1185	TTGGCCCACTACTGAATAATTCATTTCCCACTTTTGTGCCCCATCTCAAGACTCAAAATGTCA	1244
Db	2213	TTGGCCCACTACTGAATAATTCATTTCCCACTTTTGTGCCCCATCTCAAGACTCAAAATGTCA	2272
QY	1245	TTTCATTAATATATCAGAGATTAACCTTTTTTTTTTAACCTGGAGAATTTCAATGTATCATG	1304
Db	2273	TTTCATTAATATATCAGAGATTAACCTTTTTTTTTTAACCTGGAGAATTTCAATGTATCATG	2332
QY	1305	CAGCTATGGGAATTTAATTAACATTTTGTTTTCCAGTGGCAAGATATAGTAAGCTTTTA	1364
Db	2333	CAGCTATGGGAATTTAATTAACATTTTGTTTTCCAGTGGCAAGATATAGTAAGCTTTTA	2392
QY	1365	TCCCTCCCTTGTGTGATTTTTTTTCCAGATATAAATGATGCTTAGCCTGTATCTG	1424
Db	2393	TCCCTCCCTTGTGTGATTTTTTTTCCAGATATAAATGATGCTTAGCCTGTATCTG	2452

QY 825 ATACCAATCATTTTCATATTTCTAACCTCAAAAACAAGCTGTGTAATATCTGATCTC 884
Db 1853 ATAACCAATCATTTTCATATTTCTAACCTCAAAAACAAGCTGTGTAATATCTGATCTC 1912
QY 885 TAGGTCCTCTGGGCCCAACATCTCCATATATCCAGCCACACTCTTTTAATATT 944
Db 1913 TAGGTCCTCTGGGCCCAACATCTCCATATATCCAGCCACACTCTTTTAATATT 1972
QY 945 AGTCCCAAGATCTGACTGTGACCTTTCTACACTGTAGAAATACATTTCTATTTGTTTC 1004
Db 1973 AGTCCCAAGATCTGACTGTGACCTTTCTACACTGTAGAAATACATTTCTATTTGTTTC 2032
QY 1005 AAAGACCCCTGTGCTGTGCTGCTTAATATGATGACTGACTGTTTCTTAAGAGTGTCTG 1064
Db 2033 AAAGACCCCTGTGCTGTGCTGCTTAATATGATGACTGACTGTTTCTTAAGAGTGTCTG 2092
QY 1065 GCCCAGGGGATCTGTGAACAGGCTGGGAAGCATCTCAAGATCTTCCAGGGTATATCTTA 1124
Db 2093 GCCCAGGGGATCTGTGAACAGGCTGGGAAGCATCTCAAGATCTTCCAGGGTATATCTTA 2152
QY 1125 CTAGCACACAGCANGATCATTAAGGAGTGAATTTATCTATCAACATCATCTCAGTGTCT 1184
Db 2153 CTAGCACACAGCANGATCATTAAGGAGTGAATTTATCTATCAACATCATCTCAGTGTCT 2212
QY 1185 TTGCCCATACAGAAATTTATTTCCACTTTGTGCCCATCTCTCAAGACTCTCAAAATGTCA 1244
Db 2213 TTGCCCATACAGAAATTTATTTCCACTTTGTGCCCATCTCTCAAGACTCTCAAAATGTCA 2272
QY 1245 TTCCATTAATATCAAGAGTAACTTTTCTTAACTGGGAAGATTCATGTAACATG 1304
Db 2273 TTCCATTAATATCAAGAGTAACTTTTCTTAACTGGGAAGATTCATGTAACATG 2332
QY 1305 CAGCTATGGAATTTAATTAACATATTTTGTTCAGTGAAGATGAATGACTTCTTA 1364
Db 2333 CAGCTATGGAATTTAATTAACATATTTTGTTCAGTGAAGATGAATGACTTCTTA 2392
QY 1365 TCCCTCCCTCTGTTGATTTTTTTTCCAGATATAAGTTAAATGCTTACGTTACTG 1424
Db 2393 TCCCTCCCTCTGTTGATTTTTTTTCCAGATATAAGTTAAATGCTTACGTTACTG 2452
QY 1425 AGGCTGTATACAG-CACAGCCTCTCCCATCCCTCCAGCCTTATGTCATCACCATAA 1483
Db 2453 AGGCTGTATACAGCAGCAGCCTCTCCCATCCCTCCAGCCTTATGTCATCACCATAA 2512
QY 1484 CCCCTCCCATACCACTTAACAAAATCTAAGTTGTAATCTTGAACATGTCAGACATA 1543
Db 2513 CCCCTCCCAT-GCACCTTAACAAAATCTAAGTTGTAATCTTGAACATGTCAGAG-CATA 2570
QY 1544 CATTAATCCCTCTGCTGAGAAAGCTCTCTCTCTTAATCTAGAATGATGAAGT 1603
Db 2571 CATTAATCCCTCTGCTGAGAAAGCTCTCTCTCTTAATCTAGAATGATGAAGT 2630
QY 1604 TTGTAATAGTGTGACTATCTTACTTCATGCAAGAGGAGACATATGAGATTCTATC 1663
Db 2631 TTGTAATAGTGTGACTATCTTACTTCATGCAAGAGGAGACATATGAGATTCTATC 2690
QY 1664 ACATGAGACAGCAAAATCTAAAGTGTATTTGATTAATGAAGTTTGAATATATATGA 1723
Db 2691 ACATGAGACAGCAAAATCTAAAGTGTATTTGATTAATGAAGTTTGAATATATATGA 2750
QY 1724 AATCAAGAGCCACAGAGGAGATGTTATGGGACGCTTTTAAGCCCTGGAGATGGAAGC 1783
Db 2751 AATCAAGAGCCACAGAGGAGATGTTATGGGACGCTTTTAAGCCCTGGAGATGGAAGC 2810
QY 1784 AAAGCAGGAGAACTCATAGTATCTTATATATATATCTTACTTCTATCTATCTACA 1843
Db 2811 AAAGCAGGAGAACTCATAGTATCTTATATATATATCTTACTTCTATCTATCTACA 2870
QY 1844 ATATCCAAAGCTTTTACAGAAATTCATGCAAGTCAAAATCCCAAGAGTAACTTTATC 1903
Db 2871 ATATCCAAAGCTTTTACAGAAATTCATGCAAGTCAAAATCCCAAGAGTAACTTTATC 2930
QY 1904 CATTCAATGATGAGCTTGAAGTTTGGCAAAATCATACTGTACTTATCTCAACT 1963

Db 2931 CATTCAATGATGAGCTTGAAGTTTGGCAAAATCATACTGTCACTTATCTCAACT 2990
QY 1964 TTGAGATGATGTTGCTCTGTGATTAATTTGAAGAAATAGGCACTCTGTAGCACTT 2023
Db 2991 TTGAGATGATGTTGCTCTGTGATTAATTTGAAGAAATAGGCACTCTGTAGCACTT 3050
QY 2024 TAGGTCATCTCTGCAATTAAGAAATTTTACAAAGAGC 2061
Db 3051 TAGGTCATCTCTGCAATTAAGAAATTTTACAAAGAGC 3088

RESULT 11
AAH93803
ID AAH93803 standard; cDNA; 3112 BP.
XX
AC AAH93803;
XX
DT 04-OCT-2001 (first entry)
XX
DE Human prostate-specific cDNA sequence P710P #1.
XX
KW Human; prostate cancer; prostate-specific; diagnosis; vaccine;
KW cytostatic; gene therapy; metastasis; ss.
XX
OS Homo sapiens.
XX
PN WO200151633-A2.
XX
PD 19-JUL-2001.
XX
PF 16-JAN-2001; 2001WO-US01574.
XX
PR 14-JAN-2000; 2000US-0483672.
XX
PA (CORI-) CORIXA CORP.
XX
PI Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Reed SG;
PI Kalos MD, Fanger GR, Day CH, Retter MW, Stolk JA, Skelky YAW;
PI Wang A, Meagher MJ;
XX
DR WPI: 2001-425873/45.
XX
PT New polynucleotide encoding a prostate-specific protein, for
PT diagnosing, monitoring and treating prostate cancer in a patient and
PT for use in vaccines -
XX
PS Claim 1; Page 382-383; 543pp; English.
XX
CC The present invention describes polynucleotide sequences (I) which encode
CC prostate-specific proteins (II). (I) and (II) have cytostatic activity,
CC and can be used in vaccine production and gene therapy. (I), (II),
CC antibodies to (II), fusion proteins comprising (II), and isolated
CC T cells prepared using (I) or (II) are used treat cancer in a patient.
CC (I) and the antibodies are also used in the detection of cancer in a
CC patient. The cancer that is diagnosed or treated is particularly
CC prostate cancer. (I) and (II) can be used in vaccines. The antibodies or
CC (I) can be used for monitoring the progression of cancer in a patient.
CC (I) and (II) can also be used to improve diagnostic and therapeutic
CC methods for prostate cancer. They can indicate the level of metastasis
CC as well as the prostate volume. AAH93357 to AAH93944 and AAH01115 to
CC AAH01318 represent polynucleotide and amino acid sequences used in the
CC exemplification of the present invention.
XX
SQ Sequence 3112 BP; 975 A; 587 C; 624 G; 926 T; 0 other;

Query Match 38.1%; Score 1364; DB 22; Length 3112;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1774; Conservative 0; Mismatches 1; Indels 3; Gaps 3;

QY 285 GGTGAGAAATTAAGAAAGGCTCTGACTTTTACATCTGAGGCCACACATCTGCAATGG 344
Db 1313 GGTGAGAAATTAAGAAAGGCTCTGACTTTTACATCTGAGGCCACACATCTGCAATGG 1372

PI Kalos MD, Retter MW, Stolk JA, Day CH, Skelky YAW, Wang A;
XX WPI: 2001-308785/32.
XX
XX Isolated polypeptide comprising at least an immunogenic portion of a
PT prostate-specific protein, useful in the diagnosis and therapy of
PT prostate cancer -
XX
XX Claim 5; Page 282-283; 325pp; English.
XX
XX The present invention describes an isolated polypeptide (P1) comprising
CC at least an immunogenic portion of a prostate-specific protein, or its
CC variant. Also described are polynucleotides (N1) encoding (P1), or its
CC (N1) have cytostatic activity and can be used in vaccine production.
CC The polypeptides, nucleic acids and antibodies from the present
CC invention are useful in the diagnosis and therapy of prostate cancer.
CC Prostate specific genes P704P, P712P, P774P, P775P and B305D are located
CC in a genomic region on chromosome 22q11.2 known as the Cat Eye Syndrome
CC region. Prostate specific antigen (PSA) P501S was located on
CC chromosome 1. AAH84671 to AAH85143 and AAG99000 to AAG99077 represent
CC polynucleotide and polypeptide sequences used in the exemplification
CC of the present invention.
XX
XX Sequence 3112 BP; 975 A; 587 C; 624 G; 926 T; 0 other;

Query Match 38.1%; Score 1364; DB 22; Length 3112;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1774; Conservative 0; Mismatches 1; Indels 3; Gaps 3;

OY 285 GGTGAAATTAAGAAAGCTGCTGACTTACCATCTGAGCCACATCTGCTGAATGG 344
DB 1313 GGTGAAATTAAGAAAGCTGCTGACTTACCATCTGAGCCACATCTGCTGAATGG 1372
OY 345 AGATATTAACATCTCTAGAAACAGCAAGATGACATATATATGTCTAAGTAGTGCATGT 404
DB 1373 AGATATTAACATCTCTAGAAACAGCAAGATGACATATATATGTCTAAGTAGTGCATGT 1432
OY 405 TTTTCACATTTCCAGCCCTTTAAATATCCACACAGCAGAAACCAAAAAAGAGAC 464
DB 1433 TTTTCACATTTCCAGCCCTTTAAATATCCACACAGCAGAAACCAAAAAAGAGAC 1492
OY 465 AGAGATCCCTGGGAAATGCGCGCCGCATCTTGGTCAATCGATGAGCCCTGCGCTGT 524
DB 1493 AGAGATCCCTGGGAAATGCGCGCCGCATCTTGGTCAATCGATGAGCCCTGCGCTGT 1552
OY 525 GCCTGTGCTCCGCTGTGAGGAGAGACATTAAGAAATGAATGATGTCTTCTTAAAGGA 584
DB 1553 GCCTGTGCTCCGCTGTGAGGAGAGACATTAAGAAATGAATGATGTCTTCTTAAAGGA 1612
OY 585 TGGGAGGAAAAAGATCCTGTGTGATATTTATTTGAAGGGGATTCACATTTGAAT 644
DB 1613 TGGGAGGAAAAAGATCCTGTGTGATATTTATTTGAAGGGGATTCACATTTGAAT 1672
OY 645 GAAGTCACAAAGTGAATACCAATGAGAGAAAAAGAGAGAAATCTTGATGCTT 704
DB 1673 GAAGTCACAAAGTGAATACCAATGAGAGAAAAAGAGAGAAATCTTGATGCTT 1732
OY 705 CACAAGACATCAACAAACAAATGAATACTGTGATGACATGAGCGACCAAGCTGGGG 764
DB 1733 CACAAGACATCAACAAACAAATGAATACTGTGATGACATGAGCGACCAAGCTGGGG 1792
OY 765 AGGAGATTAACACGGGGGAGAGGGGTCAGAGATTTGCGCCCTGCTAAACTGTGCTTC 824
DB 1793 AGGAGATTAACACGGGGGAGAGGGGTCAGAGATTTGCGCCCTGCTAAACTGTGCTTC 1852
OY 825 ATAACCAATCATTTATATTTCTAACCCCTCAAAACAAAGCTGTGTAATTCGATGTC 884
DB 1853 ATAACCAATCATTTATATTTCTAACCCCTCAAAACAAAGCTGTGTAATTCGATGTC 1912
OY 885 TAGGGTCTCTTGCGGCCAACATTCATATATTCAGCCACACTCTTTTATATATTT 944
DB 1913 TAGGGTCTCTTGCGGCCAACATTCATATATTCAGCCACACTCTTTTATATATTT 1972

OY 945 AGTCCAGAGATCTGATCTGATGACCTTTCTACACTGTAGAAATTAATCAATTTGCTTC 1004
DB 1973 AGTCCAGAGATCTGATCTGATGACCTTTCTACACTGTAGAAATTAATCAATTTGCTTC 2032
OY 1005 AAGAGCCCTTGCTGTGCTGCTTATATGCTACTGATCTTTTCTTAAGAGTGTCTG 1064
DB 2033 AAGAGCCCTTGCTGTGCTGCTTATATGCTACTGATCTTTTCTTAAGAGTGTCTG 2092
OY 1065 GCCCAGGGGATCTGAAACAGAGCTGGGAAGCATCTCAAGATCTTCCAGGGTATACTTA 1124
DB 2093 GCCCAGGGGATCTGAAACAGAGCTGGGAAGCATCTCAAGATCTTCCAGGGTATACTTA 2152
OY 1125 CTAGCACACAGCATGATCATTAAGAGATTAATCTAATCAATCATCTGCTGCT 1184
DB 2153 CTAGCACACAGCATGATCATTAAGAGATTAATCTAATCAATCATCTGCTGCT 2212
OY 1185 TTGCCATACGAAATTAATTTCCAGCTTTTGGCCATCTTCAGAGCTCAAAATGTCA 1244
DB 2213 TTGCCATACGAAATTAATTTCCAGCTTTTGGCCATCTTCAGAGCTCAAAATGTCA 2272
OY 1245 TTCCATTAATATCACAGATTAATCTTTTAACTGAGAGAAATTAATGTTACATG 1304
DB 2273 TTCCATTAATATCACAGATTAATCTTTTAACTGAGAGAAATTAATGTTACATG 2332
OY 1305 CAGCTATGAGGAATTAATTAATATTTGTTTCCAGTGCAGAAAGATGACTAAGTCTTA 1364
DB 2333 CAGCTATGAGGAATTAATTAATATTTGTTTCCAGTGCAGAAAGATGACTAAGTCTTA 2392
OY 1365 TCCTCCCTCTGTTGTTGATTTTTCAGATAAAGTAAATTAATCTTACCTGTTACTG 1424
DB 2393 TCCTCCCTCTGTTGTTGATTTTTCAGATAAAGTAAATTAATCTTACCTGTTACTG 2452
OY 1425 AGGCTGATATACG-CACAGCCTTCCCATCCCTCCACCTTATCTGTCATCACATCAA 1483
DB 2453 AGGCTGATATACGACACAGCCTTCCCATCCCTCCACCTTATCTGTCATCACATCAA 2512
OY 1484 CCCCTCCATACACACTTAAACAAATCTAATCTGTAATCTCTGTAACATGTCAGACATA 1543
DB 2513 CCCCTCCAT-GCACCTTAAACAAATCTAATCTGTAATCTCTGTAACATGTCAGAG-CATA 2570
OY 1544 CATTAATCTCTGCTGCTGAGAGAGCTCTCTCTGCTCTTAATCTAGAAATGATGAAGT 1603
DB 2571 CATTAATCTCTGCTGCTGAGAGAGCTCTCTCTGCTCTTAATCTAGAAATGATGAAGT 2630
OY 1604 TTGAATTAAGTTGATCTTACTTATGTCGAAAGAGGACATATGAGATTCATCATC 1663
DB 2631 TTGAATTAAGTTGATCTTACTTATGTCGAAAGAGGACATATGAGATTCATCATC 2690
OY 1664 ACATGAGACAGCAAAATCTAAGAGTATTTGAATTAAGTATTAAGTATTAATATGA 1723
DB 2691 ACATGAGACAGCAAAATCTAAGAGTATTTGAATTAAGTATTAAGTATTAATATGA 2750
OY 1724 AATGCAAGAGCCACAGAGGAATGTTATGAGGACGTTTGAAGCTGGAGTGAAGC 1783
DB 2751 AATGCAAGAGCCACAGAGGAATGTTATGAGGACGTTTGAAGCTGGAGTGAAGC 2810
OY 1784 AAGGCAAGGAACTCATATGATCTTATATATTAATCTTCAATCTCATCTATCA 1843
DB 2811 AAGGCAAGGAACTCATATGATCTTATATATTAATCTTCAATCTCATCTATCA 2870
OY 1844 ATATCCAAACAGCTTTTACAGAAATTCATGAGAGTCAATCCCAAGAGTAACTTTATC 1903
DB 2871 ATATCCAAACAGCTTTTACAGAAATTCATGAGAGTCAATCCCAAGAGTAACTTTATC 2930
OY 1904 CATTTCAATGATGAGGCTTTAGAAATTTGGCAAAATCATCTGCTCATATCTCAACT 1963
DB 2931 CATTTCAATGATGAGGCTTTAGAAATTTGGCAAAATCATCTGCTCATATCTCAACT 2990
OY 1964 TTGAGATGTGTTGCTCTTGTAGTAAATGGAAGAAATAGGGCACTCTTGAGCCACTT 2023
DB 2991 TTGAGATGTGTTGCTCTTGTAGTAAATGGAAGAAATAGGGCACTCTTGAGCCACTT 3050
OY 2024 TAGGGTCACTCTGCGCAATTAAGAAATTTACAAAGAGC 2061

OY 1245 TTCCATTATATACAGAGATTAACCTTTTAAACCTGGAAGATTCATGTTACATG 1304
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 2273 TTCCATTATATACAGAGATTAACCTTTTAAACCTGGAAGATTAACGTTACATG 2332
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 OY 1305 CAGCATATGGGAATTAATACATATTTTGTTCAGTCAAGATGATGATGCTTTA 1364
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 2333 CAGCATATGGGAATTAATACATATTTTGTTCAGTCAAGATGATGATGCTTTA 2392
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 OY 1365 TCCCTCCCTTTGTTGATTTTTCAGTATAAAGTTAAATGCTTAGCTTGATG 1424
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 2393 TCCCTCCCTTTGTTGATTTTTCAGTATAAAGTTAAATGCTTAGCTTGATG 2452
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 OY 1425 AGGCTGTATACAG-CACAGCCTTCCTCCATCCCTCCAGCTTATCTGTATACCATCA 1483
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 2453 AGGCTGTATACAGC-CACAGCCTTCCTCCATCCCTCCAGCTTATCTGTATACCATCA 2512
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 OY 1484 CCCCTCCCTACCATCAACAAATCTAATCTTGAATCTTGAACATGTCAGACATA 1543
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 2513 CCCCTCCCTACCATCAACAAATCTAATCTTGAATCTTGAACATGTCAGACATA 2570
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 OY 1544 CATTTATCTTCTGCTGAGAAAGCTTCCTTGTCTCTTAAATCTAGAAATGATGAACT 1603
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 2571 CATTTATCTTCTGCTGAGAAAGCTTCCTTGTCTCTTAAATCTAGAAATGATGAACT 2630
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 OY 1604 TTTGATATAGTACTATCTTCTGATGCAAGGAGGACATATGATGATTCATCATC 1663
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 2631 TTTGATATAGTACTATCTTCTGATGCAAGGAGGACATATGATGATTCATCATC 2690
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 OY 1664 ACATGAGACAGCAAAATCTAATAAGTATTTGATTTAGAGTTAGATTAATATATGA 1723
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 2691 ACATGAGACAGCAAAATCTAATAAGTATTTGATTTAGAGTTAGATTAATATATGA 2750
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 OY 1724 AATGCAAGGCCACAGAGGGAATGTTATGAGGACGCTTGTAGCCTGGATGTAAC 1783
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 2751 AATGCAAGGCCACAGAGGGAATGTTATGAGGACGCTTGTAGCCTGGATGTAAC 2810
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 OY 1784 AAGGAGGAGGACCTCATGATCTATCTATATATATCTTCTATCTATCTATACATA 1843
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 2811 AAGGAGGAGGACCTCATGATCTATCTATATATCTTCTATCTATCTATACATA 2870
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 OY 1844 ATATCCCAACAGCTTTTCACAGATTCATGACAGTGAATCCCAAGGTAAACCTTATC 1903
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 2871 ATATCCCAACAGCTTTTCACAGATTCATGACAGTGAATCCCAAGGTAAACCTTATC 2930
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 OY 1904 CATTTATGCTGAGTGCCTTTAGAAATTTGGCAATCATACTGCTTATCTCACT 1963
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 2931 CATTTATGCTGAGTGCCTTTAGAAATTTGGCAATCATACTGCTTATCTCACT 2990
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 OY 1964 TTGAGATGCTTTGCTGCTGATGTTAATGAAAGAAATAGGCGACCTGTGAGCCACT 2023
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 2991 TTGAGATGCTTTGCTGCTGATGTTAATGAAAGAAATAGGCGACCTGTGAGCCACT 3050
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 OY 2024 TAGGCTTCACTCTGCAATTAAGATTTACAAAGAGC 2061
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 3051 TAGGCTTCACTCTGCAATTAAGATTTACAAAGAGC 3088
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

RESULT 15

ABL95267
 ID ABL95267 standard; cDNA: 3112 BP.

AC ABL95267;

DT 19-JUL-2002 (first entry)

DE Human P710P cDNA sequence SEQ ID NO 468.

KW Human: cancer; prostate cancer; vaccine; cytostatic; immunostimulant;
 KW gene therapy; gene; ss.
 OS Homo sapiens.

XX

PN US200202248-A1.
 PD 21-FEB-2002.
 XX
 XX
 PF 12-JAN-2001; 2001US-0759143.
 XX
 PR 25-FEB-1997; 97US-0806099.
 PR 01-AUG-1997; 97US-0904804.
 PR 09-FEB-1998; 98US-0020956.
 PR 25-FEB-1998; 98US-0030607.
 PR 14-JUL-1998; 98US-0115453.
 PR 23-SEP-1998; 98US-0159812.
 PR 15-JAN-1999; 98US-0232149.
 PR 09-APR-1999; 99US-0288946.
 PR 13-JUL-1999; 99US-0352616.
 PR 12-NOV-1999; 99US-0439313.
 PR 18-NOV-1999; 99US-0483686.
 PR 14-JAN-2000; 2000US-0483672.
 PR 27-MAR-2000; 2000US-0536857.
 PR 09-MAY-2000; 2000US-0568100.
 PR 12-MAY-2000; 2000US-0570737.
 PR 13-JUN-2000; 2000US-0593793.
 PR 27-JUN-2000; 2000US-0605783.
 PR 10-AUG-2000; 2000US-0636215.
 PR 29-AUG-2000; 2000US-0651236.
 PR 06-SEP-2000; 2000US-0657279.
 PR 02-OCT-2000; 2000US-0679426.
 PR 10-OCT-2000; 2000US-0685166.
 XX
 PA (XUJ/) XU J.
 PA (DILL/) DILLON D. C.
 PA (MITC/) MITCHAM J. L.
 PA (HARL/) HARLOCKER S. L.
 PA (JIAN/) JIANG Y.
 PA (KALO/) KALOS M. D.
 PA (FANG/) FANGER G. R.
 PA (RETT/) RETTER M. W.
 PA (STOL/) STOLK J. A.
 PA (DAYC/) DAY C. H.
 PA (VEDV/) VEDVICK T. S.
 PA (CART/) CARTER D.
 PA (LISX/) LI S. X.
 PA (WANG/) WANG A.
 PA (SKEL/) SKELKY Y. A. W.
 PA (HEPL/) HEPLER W. T.
 PA (HEND/) HENDERSON R. A.
 XX
 PI Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Kalos MD;
 PI Fanger GR, Retter MW, Stolk JA, Day CH, Vedvick TS, Carter D;
 PI Li SX, Wang A, Skelky YAW, Hepler WT, Henderson RA;
 XX
 DR WPI: 2002-255649/30.
 XX
 PT New prostate-specific polynucleotides for diagnosing and treating
 PT diseases, in particular prostate cancer, and as markers for the
 PT progression of cancer
 PT
 PS Claim 1: SEQ ID NO 468; 87pp; English.
 PS
 XX The present invention provides prostate-specific coding sequences and
 XX CC their encoded proteins. These can be used in the diagnosis and treatment
 XX CC of cancers, particularly prostate cancer. The present sequence is a cDNA
 XX CC described in the invention.
 XX
 SQ Sequence 3112 BP; 975 A; 587 C; 624 G; 926 T; 0 other;
 XX
 XX
 Query Match 38.1%; Score 1364; DB 24; Length 3112;
 Best local similarity 99.8%; Pred. No. 0;
 Matches 1774; Conservative 0; Mismatches 1; Indels 3; Gaps 3;
 OY 285 GGTGAGAAATTAAGAAAGGCTGCTGACTTTACATCTGAGGCCACACATCTGCTGAATGG 344
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 1313 GGTGAGAAATTAAGAAAGGCTGCTGACTTTACATCTGAGGCCACACATCTGCTGAATGG 1372

QY	345	AGATAAATTAACATCTACTGTAGAAAACACCAAGATGACAACTATTAATGTGTAAAGTAGACATGT	404
Db	1373	AGATAAATTAACATCTACTGTAGAAAACACCAAGATGACAACTATTAATGTGTAAAGTAGACATGT	1432
QY	405	TTTTACATATTTCCAGCCCTTTAAATATATCCACACACACAGAGAAACACAAAAGAAAGCAC	464
Db	1433	TTTTACATATTTCCAGCCCTTTAAATATATCCACACACACAGAGAAACACAAAAGAAAGCAC	1492
QY	465	AGAGATTCCTTGGGAGAAATGCCCGGCGCATCTTGGGTATCGATGAGCTCGCCCTGT	524
Db	1493	AGAGATTCCTTGGGAGAAATGCCCGGCGCATCTTGGGTATCGATGAGCTCGCCCTGT	1552
QY	525	GCCCTGTCCCGCTTGTGAGGGAGAGACATTTGAAAAATGAATGATGCTTCCTTAAGGA	584
Db	1553	GCCCTGTCCCGCTTGTGAGGGAGAGACATTTGAAAAATGAATGATGCTTCCTTAAGGA	1612
QY	585	TGGCGAGGAAAAACAGATCCTGTGTGATATTTATTTGAAGGGATTAACAGATTTGGAAT	644
Db	1613	TGGCGAGGAAAAACAGATCCTGTGTGATATTTATTTGAAGGGATTAACAGATTTGGAAT	1672
QY	645	GAAGTCACAAAAGTGAGCATTTACCAATGAGAGAAAAACAGAGAAAAATCTTGATGCTT	704
Db	1673	GAAGTCACAAAAGTGAGCATTTACCAATGAGAGAAAAACAGAGAAAAATCTTGATGCTT	1732
QY	705	CACAAGACATGCAACAAAACAAAATGATATCTGATACATGAGAGCCGCAAGCTGGGG	764
Db	1733	CACAAGACATGCAACAAAACAAAATGATATCTGATACATGAGAGCCGCAAGCTGGGG	1792
QY	765	AGGAGATPAACAAGGGGAGAGGGTCAGGATTTGCGCCCTGCGCTAACTGTGCTTC	824
Db	1793	AGGAGATPAACAAGGGGAGAGGGTCAGGATTTGCGCCCTGCGCTAACTGTGCTTC	1852
QY	825	ATTAACCAATCATTTCAATATTTCTPAACCTCAAAAACAAAGCTGTGTAAATCTGATGTC	884
Db	1853	ATTAACCAATCATTTCAATATTTCTPAACCTCAAAAACAAAGCTGTGTAAATCTGATGTC	1912
QY	885	TACGGTTCCTTGTGGGCCCAACATTTCCATATATCCAGCCACACTATTTTAAATTT	944
Db	1913	TACGGTTCCTTGTGGGCCCAACATTTCCATATATCCAGCCACACTATTTTAAATTT	1972
QY	945	AGTTCCACGATCTGTACTGTGACCTTTCTACACTGTAGAATPAACATTAATCTATTTGTC	1004
Db	1973	AGTTCCACGATCTGTACTGTGACCTTTCTACACTGTAGAATPAACATTAATCTATTTGTC	2032
QY	1005	AAAGACCTTGTGTGCTGCTCAATATATGAGTACGACGTTTTCCTAAAGAGTGTCTG	1064
Db	2033	AAAGACCTTGTGTGCTGCTCAATATATGAGTACGACGTTTTCCTAAAGAGTGTCTG	2092
QY	1065	GCCACAGGGGATCTGTGAACAGGCTGGGAGACATCTCAAGATCTTCCAGGGTATACTTA	1124
Db	2093	GCCACAGGGGATCTGTGAACAGGCTGGGAGACATCTCAAGATCTTCCAGGGTATACTTA	2152
QY	1125	CTAGACACACACATGATCATTAACGAGAGGATTTATCTPAATACATACATCCTCAGTGTCT	1184
Db	2153	CTAGACACACACATGATCATTAACGAGAGGATTTATCTPAATACATACATCCTCAGTGTCT	2212
QY	1185	TTGGCCCATACTGAATTCATTTCCCACTTTGTGCCAATTCCTCAAGACCTCAAAATGTCA	1244
Db	2213	TTGGCCCATACTGAATTCATTTCCCACTTTGTGCCAATTCCTCAAGACCTCAAAATGTCA	2272
QY	1245	TTCCATTAATATCCACAGATTAATCTTTTTTTTTTAACCTGGAAAGATTCATGTTACATG	1304
Db	2273	TTCCATTAATATCCACAGATTAATCTTTTTTTTTTTTTTAACCTGGAAAGATTCATGTTACATG	2332
QY	1305	CAGCTATGGGATTTAAATACATATTTTGTCTTCAGTGCAAAGATGACTAAGCTCTTA	1364
Db	2333	CAGCTATGGGATTTAAATACATATTTTGTCTTCAGTGCAAAGATGACTAAGCTCTTA	2392
QY	1365	TCCTCCTCCCTTGTGTGATTTTTTTTTTCCAGTATPAAGTAAATGCTTAAGCCTGTACTG	1424
Db	2393	TCCTCCTCCCTTGTGTGATTTTTTTTTTCCAGTATPAAGTAAATGCTTAAGCCTGTACTG	2452

[illegible]

Search completed: September 26, 2003, 22:20:52
Job time : 944.707 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 26, 2003, 21:40:03 : Search time 205.585 Seconds
(without alignments)
7690.430 Million cell updates/sec

Title: US-09-402-713a-6
Perfect score: 3582
Sequence: 1 acagaagaatagcaagtcg.....tgattcttgttaacattt 3582

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 569978 seqs, 220691566 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : Issued_Patents_NA:*
1: /cgn2_6/prodata/1/lna/5A_COMB.seq:*
2: /cgn2_6/prodata/1/lna/5B_COMB.seq:*
3: /cgn2_6/prodata/1/lna/5A_COMB.seq:*
4: /cgn2_6/prodata/1/lna/5B_COMB.seq:*
5: /cgn2_6/prodata/1/lna/5A_COMB.seq:*
6: /cgn2_6/prodata/1/lna/5B_COMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1364	38.1	3112	US-09-439-313-468	Sequence 468, App
2	1364	38.1	3112	US-09-352-616A-468	Sequence 468, App
3	1357	37.9	2426	US-09-439-313-470	Sequence 470, App
4	1357	37.9	2426	US-09-352-616A-470	Sequence 470, App
5	1123	31.4	2229	US-09-439-313-469	Sequence 469, App
6	1123	31.4	2229	US-09-352-616A-469	Sequence 469, App
7	720	20.1	812	US-09-439-313-471	Sequence 471, App
8	720	20.1	812	US-09-352-616A-471	Sequence 471, App
9	201	5.6	718	US-09-439-313-313	Sequence 313, App
10	201	5.6	718	US-09-352-616A-313	Sequence 313, App
11	201	5.6	718	US-09-232-149A-313	Sequence 313, App
12	179	5.0	301	US-09-439-313-287	Sequence 287, App
13	179	5.0	301	US-09-352-616A-287	Sequence 287, App
14	179	5.0	301	US-09-352-616A-287	Sequence 287, App
15	127	3.5	283	US-09-439-313-235	Sequence 235, App
16	127	3.5	283	US-09-352-616A-235	Sequence 235, App
17	127	3.5	283	US-09-232-149A-235	Sequence 235, App
18	29	0.8	540	US-09-220-132-125	Sequence 125, App
19	29	0.8	1867	US-08-607-509-3	Sequence 3, App1
20	29	0.8	1867	US-08-634-642-3	Sequence 3, App1
21	29	0.8	1867	US-08-989-370-3	Sequence 3, App1
22	29	0.8	2169	US-08-806-326-5	Sequence 5, App1
23	29	0.8	3925	US-08-793-044-1	Sequence 1, App1
24	29	0.8	48974	US-08-920-422-17	Sequence 10, App1
25	28	0.8	12141	US-09-488-671-10	Sequence 17, App1
26	27	0.8	65	US-08-222-177A-116	Sequence 116, App
27	27	0.8	65	US-08-222-177A-421	Sequence 421, App

C 28	27	0.8	72	1	US-08-222-177A-131	Sequence 131, App
C 29	27	0.8	72	1	US-08-222-177A-427	Sequence 427, App
C 30	27	0.8	128	4	US-09-354-147C-33	Sequence 33, App1
C 31	27	0.8	194	1	US-08-222-177A-15	Sequence 15, App1
C 32	27	0.8	240	1	US-08-222-177A-30	Sequence 30, App1
C 33	27	0.8	264	1	US-08-222-177A-10	Sequence 10, App1
C 34	27	0.8	298	1	US-08-599-252-88	Sequence 88, App1
C 35	27	0.8	298	5	PCT-US96-06353-88	Sequence 88, App1
C 36	27	0.8	298	5	PCT-US96-06583-88	Sequence 88, App1
C 37	27	0.8	835	4	US-09-171-209-42	Sequence 42, App1
C 38	27	0.8	1325	3	US-08-915-795-6	Sequence 6, App1
C 39	27	0.8	1526	4	US-09-495-050A-293	Sequence 293, App
C 40	27	0.8	1560	2	US-08-907-706-2	Sequence 2, App1
C 41	27	0.8	1803	4	US-09-909-595-3	Sequence 3, App1
C 42	27	0.8	1816	4	US-09-645-926A-5	Sequence 5, App1
C 43	27	0.8	2040	1	US-08-393-985-17	Sequence 17, App1
C 44	27	0.8	3000	1	US-08-393-985-3	Sequence 3, App1
C 45	27	0.8	3001	4	US-09-539-333D-167	Sequence 167, App

ALIGNMENTS

RESULT 1
US-09-439-313-468
; Sequence 468, Application US/09439313
; Patent No. 6329505
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan Louise
; APPLICANT: Jiang Yugu
; APPLICANT: Reed, Steven G.
; APPLICANT: Kalos, Michael
; APPLICANT: Rafter, Gary
; APPLICANT: Retter, Mark
; APPLICANT: Solk, John
; APPLICANT: Day, Craig
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
; FILE REFERENCE: 210121.427C9
; CURRENT APPLICATION NUMBER: US/09/439,313
; CURRENT FILING DATE: 1999-11-12
; NUMBER OF SEQ. ID NOS: 575
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 468
; LENGTH: 3112
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-439-313-468
Query Match 38.1%; Score 1364; DB 4; Length 3112;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1774; Conservative 0; Mismatches 1; Indels 3; Gaps 3;
C 28 27 0.8 72 1 US-08-222-177A-131 Sequence 131, App
C 29 27 0.8 72 1 US-08-222-177A-427 Sequence 427, App
C 30 27 0.8 128 4 US-09-354-147C-33 Sequence 33, App1
C 31 27 0.8 194 1 US-08-222-177A-15 Sequence 15, App1
C 32 27 0.8 240 1 US-08-222-177A-30 Sequence 30, App1
C 33 27 0.8 264 1 US-08-222-177A-10 Sequence 10, App1
C 34 27 0.8 298 1 US-08-599-252-88 Sequence 88, App1
C 35 27 0.8 298 5 PCT-US96-06353-88 Sequence 88, App1
C 36 27 0.8 298 5 PCT-US96-06583-88 Sequence 88, App1
C 37 27 0.8 835 4 US-09-171-209-42 Sequence 42, App1
C 38 27 0.8 1325 3 US-08-915-795-6 Sequence 6, App1
C 39 27 0.8 1526 4 US-09-495-050A-293 Sequence 293, App
C 40 27 0.8 1560 2 US-08-907-706-2 Sequence 2, App1
C 41 27 0.8 1803 4 US-09-909-595-3 Sequence 3, App1
C 42 27 0.8 1816 4 US-09-645-926A-5 Sequence 5, App1
C 43 27 0.8 2040 1 US-08-393-985-17 Sequence 17, App1
C 44 27 0.8 3000 1 US-08-393-985-3 Sequence 3, App1
C 45 27 0.8 3001 4 US-09-539-333D-167 Sequence 167, App
QY 285 GGTGAGAAATTAAGAAAGGCTGCTGACTTTCACATCTGAGCCACACATCTGCGAATG 344
1313 GGTGAGAAATTAAGAAAGGCTGCTGACTTTCACATCTGAGCCACACATCTGCGAATG 1372
QY 345 AGATTAATTAATCACTACAGAAAGCAAGATGACATATATATGCTAAGTAGACATGT 404
1373 AGATTAATTAATCACTACAGAAAGCAAGATGACATATATATGCTAAGTAGACATGT 1432
QY 405 TTTTGCACATTTCCAGCCCTTTAATATTCACACACAGAAAGCAAAAGAGAC 464
1433 TTTTGCACATTTCCAGCCCTTTAATATTCACACACAGAAAGCAAAAGAGAC 1492
QY 465 AGAGATCCCTGGGAGAAATGCCCGCCGCCATTTGGGTCATGATGAGCGCTTCCCTGT 524
1493 AGAGATCCCTGGGAGAAATGCCCGCCGCCATTTGGGTCATGATGAGCGCTTCCCTGT 1552
QY 525 GCCTGATCCCGCTTGTGAGGAGGAGACATTAGAAATGATGATGCTTCTTAAGCA 584

Db 1553 GCGTGGTCCCGCTGTGAGGAGACATTTAGAAATGAATGATGTCTCTTAAGGA 1612
OY TGGGAGGAAAAACAGATCTGTGTGATATTATTTGAACGGGATTACAGTTTGAAT 644
Db 1613 TGGGAGGAAAAACAGATCTGTGTGATATTATTTGAACGGGATTACAGTTTGAAT 1672
OY 645 GAAGTCACAAAGTGAAGCATTTACCAATGAGAGAAAAACAGAGAGAAATCTTGATGGCT 704
Db 1673 GAAGTCACAAAGTGAAGCATTTACCAATGAGAGAAAAACAGAGAGAAATCTTGATGGCT 1732
OY 705 CACAAGACATGCACAAACAAATGGAATACTGTGATGACATGAGGAGCCAGCTGGG 764
Db 1733 CACAAGACATGCACAAACAAATGGAATACTGTGATGACATGAGGAGCCAGCTGGG 1792
OY 765 AGAGATATACACGAGGAGAGAGGATCTGTGGCCCTGCTGCTAACTGCTGCTC 824
Db 1793 AGAGATATACACGAGGAGAGAGGATCTGTGGCCCTGCTGCTAACTGCTGCTC 1852
OY 825 ATAAACCAATCATTTTCAATTTTCTAACCCCTCAAAACAAAGCTGTGTAATATCTGATCTC 884
Db 1853 ATAAACCAATCATTTTCAATTTTCTAACCCCTCAAAACAAAGCTGTGTAATATCTGATCTC 1912
OY 885 TACGGTTCTCTTGGGCCCCAACATTTCTCATATATCCAGCCACTCTATTTTAATTT 944
Db 1913 TACGGTTCTCTTGGGCCCCAACATTTCTCATATATCCAGCCACTCTATTTTAATTT 1972
OY 945 AGTTCCAGATCTGACTGTGACCTTTCTACAGCTAGAAATACATTAATCTATTTGTC 1004
Db 1973 AGTTCCAGATCTGACTGTGACCTTTCTACAGCTAGAAATACATTAATCTATTTGTC 2032
OY 1005 AAAGACCTCTGCTGCTGCTGCTTAATATAGCTGACTGTTTTCCTAAGAGAGTCTG 1064
Db 2033 AAAGACCTCTGCTGCTGCTGCTTAATATAGCTGACTGTTTTCCTAAGAGAGTCTG 2092
OY 1065 GCCCAGGGGATCTGTGAACAGGCTGGGAAGCATCTCAAGATCTTCCAGGGTTACTTA 1124
Db 2093 GCCCAGGGGATCTGTGAACAGGCTGGGAAGCATCTCAAGATCTTCCAGGGTTACTTA 2152
OY 1125 CTAGCACACAGCATGATCATTTAGAGAGATTAATCTAATACATCATCTCAGTCT 1184
Db 2153 CTAGCACACAGCATGATCATTTAGAGAGATTAATCTAATACATCATCTCAGTCT 2212
OY 1185 TTGGCCCATCTGAAATTCATTTCCACTTTTGTGCCATCTCTCAAGACCTCAAAATGTCA 1244
Db 2213 TTGGCCCATCTGAAATTCATTTCCACTTTTGTGCCATCTCTCAAGACCTCAAAATGTCA 2272
OY 1245 TTCCATTAAATCAAGGATTAATCTTTTAACTGGAAGAAATTCATTTACTG 1304
Db 2273 TTCCATTAAATCAAGGATTAATCTTTTAACTGGAAGAAATTCATTTACTG 2332
OY 1305 CAGCTATGGAATTTAATTAATTTTGTTCAGTGAAGATGACTAAGTCTTTA 1364
Db 2333 CAGCTATGGAATTTAATTAATTTTGTTCAGTGAAGATGACTAAGTCTTTA 2392
OY 1365 TCCCTCCCTTTGTTGATTTTTCAGATATAAGTTAAATGCTTACGCTGTACTG 1424
Db 2393 TCCCTCCCTTTGTTGATTTTTCAGATATAAGTTAAATGCTTACGCTGTACTG 2452
OY 1425 AGGCTGATACAG-CACAGGCTGCCCATGCCATGCCCTTATCTGACATCACATCA 1483
Db 2453 AGGCTGATACAGCACAGGCTGCCCATGCCCTTATCTGACATCACATCA 2512
OY 1484 CCCCCTCCATACCACTAAACAAATCTAATTTTCTGAACTGACAGATCA 1543
Db 2513 CCCCCTCCAT-CCACCTAAACAAATCTAATTTTCTGAACTGACAG-CATA 2570
OY 1544 CATTAATCTCTTCTGAGAGCTCTCTGCTCTTAATCTAGAAATGATTAAGT 1603
Db 2571 CATTAATCTCTTCTGAGAGCTCTCTGCTCTTAATCTAGAAATGATTAAGT 2630
OY 1604 TTGAATTAAGTTGACTATCTTACTTCAATGCAAGAGGACATATGAGATTATCATC 1663

Db 2631 TTGAATTAAGTTGACTATCTTACTTCAATGCAAGAGGACATATGAGATTATCATC 2690
OY 1664 ACATGAGACAGCAATTAATTAAGCTTAATTTGATTTATAAGGTTAATTAATTAAGA 1723
Db 2691 ACATGAGACAGCAATTAATTAAGCTTAATTTGATTTATAAGGTTAATTAATTAAGA 2750
OY 1724 AATGAGAGCCACAGAGGAAATGTTTATGGGACGTTTGTAAAGCTGGATGGAAG 1783
Db 2751 AATGAGAGCCACAGAGGAAATGTTTATGGGACGTTTGTAAAGCTGGATGGAAG 2810
OY 1784 AAAGCAGGAACTCATAGTATCTTAATTAATTAATTAATTAATTAATTAATTAATTA 1843
Db 2811 AAAGCAGGAACTCATAGTATCTTAATTAATTAATTAATTAATTAATTAATTAATTA 2870
OY 1844 ATATCCAAACGCTTTTACAGAAATTCATGAGTGCATAATCCCAAGTAACCTTTATC 1903
Db 2871 ATATCCAAACGCTTTTACAGAAATTCATGAGTGCATAATCCCAAGTAACCTTTATC 2930
OY 1904 CATTTCAATGAGTGGCTTTAGAAATTTTGGCAATCATCTGCTACTATATCTCACT 1963
Db 2931 CATTTCAATGAGTGGCTTTAGAAATTTTGGCAATCATCTGCTACTATATCTCACT 2990
OY 1964 TTGAGATGTGTTGCTCTTGTAGTTAATTTGAAGAAATAGGCACTCTTGAGCCACT 2023
Db 2991 TTGAGATGTGTTGCTCTTGTAGTTAATTTGAAGAAATAGGCACTCTTGAGCCACT 3050
OY 2024 TAGGGTTCACCTCGCAATTAAGAAATTTACAAGAGC 2061
Db 3051 TAGGGTTCACCTCGCAATTAAGAAATTTACAAGAGC 3088

RESULT 2

US-09-352-616A-468
: Sequence 468, Application US/09352616A
: Patent No. 6395278
: GENERAL INFORMATION:
: APPLICANT: Dillon, Davin C.
: APPLICANT: Harlocker, Susan Louise
: APPLICANT: Jiang, Yugu
: APPLICANT: Xu, Jiaogchun
: TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
: FILE REFERENCE: 210121.427C8
: CURRENT APPLICATION NUMBER: US/09/352.616A
: NUMBER OF SEQ ID NOS: 472
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 468
: LENGTH: 3112
: TYPE: DNA
: ORGANISM: Homo sapiens
US-09-352-616A-468

Query Match 38.1%, Score 1364, DB 4, Length 3112;
Best Local Similarity 99.8%, Pred. No. 0;
Matches 1774, Conservative 0, Mismatches 1, Indels 3, Gaps 3;

OY 285 GGTGAGAAATTAAGAAAGGCTGCTGACTTTACCATCTGAGGCAACATCTCTGAATG 344
Db 1313 GGTGAGAAATTAAGAAAGGCTGCTGACTTTACCATCTGAGGCAACATCTCTGAATG 1372
OY 345 AGATAATTAACATCTAGTAAGAACGCAAGATGACAATTAATGCTAAGTGAACATGT 404
Db 1373 AGATAATTAACATCTAGTAAGAACGCAAGATGACAATTAATGCTAAGTGAACATGT 1432
OY 405 TTTTGACATTTTCCAGCCCTTTAATTAATTCACACACACAGAGACAAAGAGAACAC 464
Db 1433 TTTTGACATTTTCCAGCCCTTTAATTAATTCACACACACAGAGACAAAGAGAACAC 1492
OY 465 AGAATCCCTGAGGAAATGCGCGCGCATCTTGGGTATCATGATAGCTCGCCCTGT 524
Db 1493 AGAATCCCTGAGGAAATGCGCGCGCATCTTGGGTATCATGATAGCTCGCCCTGT 1552

OY	1604	TTTGAAATTAAGTGGACACTATCTTACTTCAATGCAAAAGAGGACACATTAAGATTGATCATCTC	1663
Db	2631	TTTTAAATTAAGTTGACTATCTTACTTCAATGCAAAAGAGGACACATTAAGATTGATCATCTC	2690
OY	1664	ACATGAGACACCAATATCTAAAGTGTAAATTGATTAAAGATTAGATTAATATATGA	1723
Db	2661	ACATGAGACACCAATATCTAAAGTGTAAATTGATTAAAGATTAGATTAATATATGA	2750
OY	1724	AATGCAAGAGCCACAGAGGGAATGTTATGCGGACGTTTGTAAGCCTGGGATGTGAAGC	1783
Db	2751	AATGCAAGAGCCACAGAGGGAATGTTATGCGGACGTTTGTAAGCCTGGGATGTGAAGC	2810
OY	1784	AAAGCGAGGGAACCTCATAGTATCTTATATATATCTTCAATTTCTATCTATCA	1843
Db	2811	AAAGCGAGGGAACCTCATAGTATCTTATATATATCTTCAATTTCTATCTATCA	2870
OY	1844	ATATCCAAACAAGCTTTTTCACAGAAATTCATGAGTGCACAAATCCCAAGAGTAACCTTATC	1903
Db	2871	ATATCCAAACAAGCTTTTTCACAGAAATTCATGAGTGCACAAATCCCAAGAGTAACCTTATC	2930
OY	1904	CATTTCATGATGATGCGCCTTTAGAAATTTTGGCAAAATCATCTGTCATTATCTCAACT	1963
Db	2931	CATTTCATGATGATGCGCCTTTAGAAATTTTGGCAAAATCATCTGTCATTATCTCAACT	2990
OY	1964	TTTGAGATGTGTTTGTCTCTGTAGTTAATTTGAAAGAAATAGGCGACTTGTGAGCCACTT	2022
Db	2991	TTTGAGATGTGTTTGTCTCTGTAGTTAATTTGAAAGAAATAGGCGACTTGTGAGCCACTT	3050
OY	2024	TAGGGTTCACCTCTGCGCAATTAAGATTATTAACAAGAGC	2061
Db	3051	TAGGGTTCACCTCTGCGCAATTAAGATTATTAACAAGAGC	3088
RESULT 3			
US-09-439-313-470/c			
; Sequence 470, Application US/09439313			
; Patent No. 6329505			
; GENERAL INFORMATION:			
; APPLICANT: Xu, Jiangchun			
; APPLICANT: Dillon, David C.			
; APPLICANT: Mitcham, Jennifer L.			
; APPLICANT: Harlocker, Susan Louise			
; APPLICANT: Jiang Yuqul			
; APPLICANT: Reed, Steven G.			
; APPLICANT: Kalos, Michael			
; APPLICANT: Fanger, Gary			
; APPLICANT: Retter, Mark			
; APPLICANT: Solk, John			
; APPLICANT: Day, Craig			
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND			
; FILE REFERENCE: 210121.427C9			
; CURRENT APPLICATION NUMBER: US/09/439,313			
; CURRENT FILING DATE: 1999-11-12			
; NUMBER OF SEQ ID NOS: 575			
; SOFTWARE: FastSeq for Windows Version 3.0			
; SEQ ID NO 470			
; LENGTH: 2426			
; TYPE: DNA			
; ORGANISM: Homo sapiens			
US-09-439-313-470			
Query Match			
Best Local Similarity 99.8%, Pred. No. 0;			
Matches 1767; Conservative 0; Mismatches 1; Indels 3; Gaps 3;			
OY	285	GGTGAGAATAAGAAAGGCTGCTGACTTTACCATCTGAGGCCACACATCTGCTGAATGG	344
Db	1769	GGTGAGAATAAGAAAGGCTGCTGACTTTACCATCTGAGGCCACACATCTGCTGAATGG	1710
OY	345	AGATTAATTAACATCTAGAAACAGCAAGATGACAAATTAATGTCTAAGTAGACATGT	404
Db	1709	AGATTAATTAACATCTAGAAACAGCAAGATGACAAATTAATGTCTAAGTAGACATGT	1650

405 TTTTGCACATTTCCAGCCCTTTAAATATCCACACACAGGAGACACAAAAGAGCAC 464
1649 TTTTGCACATTTCCAGCCCTTTAAATATCCACACACAGGAGACACAAAAGAGCAC 1590
465 AGAGATCCCTGGGAGAAATGCCCCGCCCATCTTGGGTCATGATGAGCCTGCCCTGT 524
1589 AGAGATCCCTGGGAGAAATGCCCCGCCCATCTTGGGTCATGATGAGCCTGCCCTGT 1530
525 GCTTGTCCTCCCTTGTGAGGAGAGACATTTAGAAATGAATGATGTCTCTTAAGGA 584
1529 GCTTGTCCTCCCTTGTGAGGAGAGACATTTAGAAATGAATGATGTCTCTTAAGGA 1470
585 TGGGAGAGAAAACAGATCCTGTGTGATATTATTTGAACGCGATTACAGATTTGAAT 644
1469 TGGGAGAGAAAACAGATCCTGTGTGATATTATTTGAACGCGATTACAGATTTGAAT 1410
645 GAAGTCACAAAGTGAGCATTTACCATGAGAGAAAACAGAGAAAATCTTGATGGCT 704
1409 GAAGTCACAAAGTGAGCATTTACCAATGAGAGAAAACAGAGAAAATCTTGATGGCT 1350
705 CACAAGACATGCAACAAACAAATGGAATAGTGTGATGATGATGAGCAGCCAGCTGGG 764
1349 CACAAGACATGCAACAAACAAATGGAATAGTGTGATGATGATGAGCAGCCAGCTGGG 1290
765 AGGAGATACCAAGGGGAGAGGGTCAGGATTTGGCCCTGCTTAACCTGTGCTTC 824
1289 AGGAGATACCAAGGGGAGAGGGTCAGGATTTGGCCCTGCTTAACCTGTGCTTC 1230
825 ATAACCAATCATTTTCATATTCTTAACCTCAAAACAAAGGCTGTGAATATCTGATC 884
1229 ATAACCAATCATTTTCATATTCTTAACCTCAAAACAAAGGCTGTGTGAATATCTGATC 1170
885 TAGGTTCTCTTGCGGCCAACATCTTCATATATCCAGCACACTCATTTTAAATATT 944
1169 TAGGTTCTCTTGCGGCCAACATCTTCATATATCCAGCACACTCATTTTAAATATT 1110
945 AGTTCCCGATCTGTACTGTACCTTTTACACCTAGAAATACATTTCTCATTTTGTTC 1004
1109 AGTTCCCGATCTGTACTGTACCTTTTACACCTAGAAATACATTTCTCATTTTGTTC 1050
1005 AAAGACCTTCTGTGCTGCTTAATATGAGCTGACTGTTTCTTAAGGAGTGTCTG 1064
1049 AAAGACCTTCTGTGCTGCTTAATATGAGCTGACTGTTTCTTAAGGAGTGTCTG 990
1065 GCCCAGGGGATCTGTGAACAGGCTGGGAAGCATCTCAAGATCTTCCAGGGTTATCTTA 1124
989 GCCCAGGGGATCTGTGAACAGGCTGGGAAGCATCTCAAGATCTTCCAGGGTTATCTTA 930
1125 CTACGACACAGCATGATCATAGGAGATATCTAATCAACATCATCTCTCACTGTCT 1184
929 CTACGACACAGCATGATCATAGGAGATATCTAATCAACATCATCTCTCACTGTCT 870
1185 TTGGCCATACGAAATCATTTCCACTTTTGCCCATCTTCTCAAGACCTCAAAATGCA 1244
869 TTGGCCATACGAAATCATTTCCACTTTTGCCCATCTTCTCAAGACCTCAAAATGCA 810
1245 TTCCATTAATATCACAGGATTAACCTTTTAACTGGAAGAAATTCATGTTATCATG 1304
809 TTCCATTAATATCACAGGATTAACCTTTTAACTGGAAGAAATTCATGTTATCATG 750
1305 CAGCTATAGGAAATTAATTAATTTTGTCTTCCAGTGAAGTGAATGCTAAGTCTTTA 1364
749 CAGCTATAGGAAATTAATTAATTTTGTCTTCCAGTGAAGTGAATGCTAAGTCTTTA 690
1365 TCCCTCCCTTTGTTGATTTTCTTCCAGTGAAGTGAATGCTAAGTCTTTA 1424
689 TCCCTCCCTTTGTTGATTTTCTTCCAGTGAAGTGAATGCTAAGTCTTTA 630
1425 AGGCTGTATACAG-CACAGCCTCTCCCATCTTCAAGCCTTATCTGTATCAGCATCA 1483
629 AGGCTGTATACAGCAGCCTCTCCCATCTTCAAGCCTTATCTGTATCAGCATCA 570

1484 CCCCTCCATACCACTAACAACAAATCTAATCTGTAATCTTGAACATGTCAGACATA 1543
569 CCCCTCCAT-CCACTAACAACAAATCTAATCTGTAATCTTGAACATGTCAGG-CATA 512
1544 CATTAATCTTCTGCTGGAAGGCTCTCTCTCTCTTAATCTGAATGATGTAAGT 1603
511 CATTAATCTTCTGCTGGAAGGCTCTCTCTCTCTCTTAATCTGAATGATGTAAGT 452
1604 TTTGAATAGTGTGATATCTTCTTCAAGCAAGAGGAGACATATGATGATTCATC 1663
451 TTTGAATAGTGTGATATCTTCTTCAAGCAAGAGGAGACATATGATGATTCATC 392
1664 ACATGAGACGCAATTAATAAGTGTATTTGATTAATAGAGTTAGATTAATATATGA 1723
391 ACATGAGACGCAATTAATAAGTGTATTTGATTAATAGAGTTAGATTAATATATGA 332
1724 AATGCAAGGACACAGAGGAAATGTTTATGGGACGTTTGAACCTGGGATGGAAGC 1783
331 AATGCAAGGACACAGAGGAAATGTTTATGGGACGTTTGAACCTGGGATGGAAGC 272
1784 AAAGCAGGAACTCATAGTATCTTATATATATATCTTCTATCTATCTATCA 1843
271 AAAGCAGGAACTCATAGTATCTTATATATATATCTTCTATCTATCTATCA 212
1844 ATATCAACAAGCTTTTACAGATTCATGCAAGTCAAAATCCCAAGGTAACCTTATC 1903
211 ATATCAACAAGCTTTTACAGATTCATGCAAGTCAAAATCCCAAGGTAACCTTATC 152
1904 CATTCAGTGTAGAGGCTTTAGATTTTGGCAATATATCTGCTATCTATCACT 1963
151 CATTCAGTGTAGAGGCTTTAGATTTTGGCAATATATCTGCTATCTATCACT 92
1964 TTGAGATGTGTTGCTTGTAGTAAATTTGAAGAAATAGGAGACTTGTGAGGCACT 2023
91 TTGAGATGTGTTGCTTGTAGTAAATTTGAAGAAATAGGAGACTTGTGAGGCACT 32
2024 TAGGTTCTCTTGCGGCCAACATCTTCATATATCCAGCACACTCATTTTAAATATT 2054
31 TAGGTTCTCTTGCGGCCAACATCTTCATATATCCAGCACACTCATTTTAAATATT 1

RESULT 4
US-09-352-616A-470/C
; Sequence 470, Application US/09352616A
; Patent No. 6395278
; GENERAL INFORMATION:
; APPLICANT: Dillon, Davin C.
; APPLICANT: Harlocker, Susan Louise
; APPLICANT: Jiang, Yuqi
; APPLICANT: Xu, Jianshun
; TITLE OF INVENTION: MITCHEM, JENNIFER LYNN
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
; FILE REFERENCE: 210121.427C8
; CURRENT FILING DATE: 1999-07-13
; NUMBER OF SEQ ID NOS: 472
; SOFTWARE: FASTSEQ for Windows Version 3.0
; LENGTH: 2426
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-352-616A-470

Query Match 37.9%; Score 1357; DB 4; Length 2426;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1767; Conservative 0; Mismatches 1; Indels 3; Gaps 3;

285 GGTGAGAAATTAAGAAAGGCTCTGACTTTTACATCTGAGGACACATCTGTAAGTGG 344
1769 GGTGAGAAATTAAGAAAGGCTCTGACTTTTACATCTGAGGACACATCTGTAAGTGG 1770
345 AGATTAATTAACATCACTAGAAACAGCAAGATGACAAATATATATGTTAAGTAGTACATGT 404

1709 AGATATATTAACATCTAGTAAACAGACAAATGACATATATATGCTAAAGTAGACATGT 1650
405 TTTTGCACATTTCCAGCCCCCTTTAAATATCCACACACAGAGACACAAAAGAGACAC 464
1649 TTTTTCACATTTTCCAGCCCCCTTTAAATATCCACACACAGAGACACAAAAGAGACAC 1590
465 AGAGATCCCTGGGAGAAATGCCGGCCGATCTTGGTGCATCGATGAGACCTGCCCCCT 524
1589 AGAGATCCCTGGGAGAAATGCCGGCCGATCTTGGTGCATCGATGAGACCTGCCCCCT 1530
525 GCCTGGCCCCCTTGTGAGGAGAGACATTTAGAAAATGAATTGATGTTCTTTAAAGA 584
1529 GCCTGGCCCCCTTGTGAGGAGAGACATTTAGAAAATGAATTGATGTTCTTTAAAGA 1470
585 TGGGACGAGAAAACAGATCCTGTGTGGATATTTATTTGAACGGGATTAAGATTTAAAT 644
1469 TGGGACGAGAAAACAGATCCTGTGTGGATATTTATTTGAACGGGATTAAGATTTAAAT 1410
645 GAAGTCACAAATGAGCATTTACCAATGAGAGAAAACAGACGAGAAAATCTTGATGGCT 704
1409 GAAGTCACAAATGAGCATTTACCAATGAGAGAAAACAGACGAGAAAATCTTGATGGCT 1350
705 CACAAGACATGCAACAAACAAATGGAATCTGTGATGACATGAGGACCAAGCTGGGG 764
1349 CACAAGACATGCAACAAACAAATGGAATCTGTGATGACATGAGGACCAAGCTGGGG 1290
765 AGAGATTAACACAGGGGAGAGGGTGCAGATTTGCCCCCTGCTTAACCTGTGGCTTC 824
1289 AGAGATTAACACAGGGGAGAGGGTGCAGATTTGCCCCCTGCTTAACCTGTGGCTTC 1230
825 ATACCAATCATTTTATATTTCTAACCTCAACAAAGCTTGTAAATATGATCTC 884
1229 ATACCAATCATTTTATATTTCTAACCTCAACAAAGCTTGTAAATATGATCTC 1170
885 TAGGTTCTTGTGGGCCCAACATTTCTCATATATCCACACACATCTTTTAAATATTT 944
1169 TAGGTTCTTGTGGGCCCAACATTTCTCATATATCCACACACATCTTTTAAATATTT 1110
945 AGTTCACATCTGTATCTGTGACCTTTCTACACTGTAGATTAACATCTTCTTGTTC 1004
1109 AGTTCACATCTGTATCTGTGACCTTTCTACACTGTAGATTAACATCTTCTTGTTC 1050
1005 AAGACCTTCTGATGCTGCTTAATATGATGATGATGATGATGATGATGATGATGATG 1064
1049 AAGACCTTCTGATGCTGCTTAATATGATGATGATGATGATGATGATGATGATGATG 990
989 GCCCAGGGGATCTGTGAACAGGCTGGGAGCATCTCAAGATCTTTCAGGGTATACCTTA 930
1125 CTAGCACACAGCATGATCTTACGAGGTGAATATATTAATCAACATCTCTGATGCTC 1184
929 CTAGCACACAGCATGATCTTACGAGGTGAATATATTAATCAACATCTCTGATGCTC 870
1185 TTGGCCATCTGAAATCTTCCCTTTGCTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTG 1244
869 TTGGCCATCTGAAATCTTCCCTTTGCTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTG 810
1245 TTCCATTAATATCACAGATTAACCTTTTAACTGGAAGATTAAGATTAAGATTAAGAT 1304
809 TTCCATTAATATCACAGATTAACCTTTTAACTGGAAGATTAAGATTAAGATTAAGAT 750
1305 CAGCTATGGGAATTAATATCATATTTTGTTCGAGTCAAGAAAGATTAAGATTAAGAT 1364
749 CAGCTATGGGAATTAATATCATATTTTGTTCGAGTCAAGAAAGATTAAGATTAAGAT 690
1365 TCCCTCCCTTTGTTGATTTTTCAGATTAAGATTAAGATTAAGATTAAGATTAAGAT 1424
689 TCCCTCCCTTTGTTGATTTTTCAGATTAAGATTAAGATTAAGATTAAGATTAAGAT 630
1425 AGGCTGTATACAG-CACAGCCCTTCCCATCCCTCAGGCTTATCTGATCAACATCA 1483

629 AGGCTGTATACAGCCACAGCCCTTCCCATCCCTCAGGCTTATCTGATCAACATCA 570
1484 CCCCCTCCAC 1543
569 CCCCCTCCAC 512
1544 CATATTCCTTCTGCTGAGAGACCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1603
511 CATATTCCTTCTGCTGAGAGACCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 452
1604 TTTGAATTAAGTTGACATCTTCTTCTCATGCAAGAGAGACACATATGATTCATCTC 1663
451 TTTGAATTAAGTTGACATCTTCTTCTCATGCAAGAGAGACACATATGATTCATCTC 392
1664 ACATGACAGCAAAATCTAATTAAGTTGATTTGATTTGATTTGATTTGATTTGATTT 1723
391 ACATGACAGCAAAATCTAATTAAGTTGATTTGATTTGATTTGATTTGATTTGATTT 332
1724 AATGCAAGAGCCACAGAGGAAATGTTTATGGGACAGCTTGTAAAGCTGGATGTAAC 1783
331 AATGCAAGAGCCACAGAGGAAATGTTTATGGGACAGCTTGTAAAGCTGGATGTAAC 272
1784 AAGGACAGGAACTCATATATCTTATATATATATCTTCTATCTCTATCTATCA 1843
271 AAGGACAGGAACTCATATATCTTATATATATATCTTCTATCTCTATCTATCA 212
1844 ATATCCAAAGTTTTCACAGATTCATGCAATGCAATCCCAAGGTAACCTTATC 1903
211 ATATCCAAAGTTTTCACAGATTCATGCAATGCAATCCCAAGGTAACCTTATC 152
1904 CATTCATGCTGATGCTGCTTATGATTTTGGCAATCATAGCTTATCTATCTCACT 1963
151 CATTCATGCTGATGCTGCTTATGATTTTGGCAATCATAGCTTATCTATCTCACT 92
1964 TTGAGATGTTGTTGCTCTTGTAGTAAATGAAGAAATAGGACACTTGTGAGCCACT 2023
91 TTGAGATGTTGTTGCTCTTGTAGTAAATGAAGAAATAGGACACTTGTGAGCCACT 32
2024 TAGGTTCACTCCTGGCAATTAAGATTTAC 2054
31 TAGGTTCACTCCTGGCAATTAAGATTTAC 1

RESULT 5
US-09-439-313-469/C
; Sequence 469, Application US/09439313
; Patent No. 6329505
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan Louise
; APPLICANT: Jiang Yugu
; APPLICANT: Reed, Steven G.
; APPLICANT: Kalos, Michael
; APPLICANT: Fanger, Gary
; APPLICANT: Retter, Mark
; APPLICANT: Solk, John
; APPLICANT: Day, Craig
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
; FILE REFERENCE: 210121.427C9
; CURRENT FILING DATE: US/09/439,313
; NUMBER OF SEQ ID NOS: 575
; SOFTWARE: FastSeq for windows Version 3.0
; LENGTH: 2229
; SEQ ID NO 469
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-439-313-469

Query Match 31.4%; Score 1123; DB 4; Length 2229;

Best Local Similarity 99.7%; Pred. No. 0;
Matches 1773: Conservative 0; Mismatches 1; Indels 5; Gaps 5;

OY	285	GGTGAATAATGAAGAGCTGCTGACCTTACCATGTGAGGCACACATCTGCTGAAAAGG	344
Db	1775	GGTGAATAATGAAGAGCTGCTGACCTTACCATGTGAGGCACACATCTGCTGAAAAGG	1716
OY	345	AGATTAATTAACATCACTAGAAACAGACAGATGACATATTAATGTCTAAGTAGTACATGT	404
Db	1715	AGATTAATTAACATCACTAGAAACAGACAGATGACATATTAATGTCTAAGTAGTACATGT	1656
OY	405	TTTGGACATTTCCAGCCCCCTTTAAATATCCACACACACAGAGACACAAAAGAGACAC	464
Db	1655	TTTGGACATTTCCAGCCCCCTTTAAATATCCACACACACAGAGACACAAAAGAGACAC	1596
OY	465	AGAGATCCCTGGGAGAAATGCCGCGCCCATCTTGGGTCATCGATGAGCCCTGCGCTGT	524
Db	1595	AGAGATCCCTGGGAGAAATGCCGCGCCCATCTTGGGTCATCGATGAGCCCTGCGCTGT	1536
OY	525	GCTGTGTCCTGCTGTGAGGAGAGACATTAAGAAAATGAATGATGTCTCTTAAAGGA	584
Db	1535	GCTGTGTCCTGCTGTGAGGAGAGACATTAAGAAAATGAATGATGTCTCTTAAAGGA	1476
OY	585	TGGGAGGAGAAACAGATCTGTGTGATTTATTTGAAGGGATTCACATTTGAAT	644
Db	1475	TGGGAGGAGAAACAGATCTGTGTGATTTATTTGAAGGGATTCACATTTGAAT	1416
OY	645	GAATGACAAAGTACATTAACATGAGAGAAACAGAGAGAAATCTTGATGCTT	704
Db	1415	GAATGACAAAGTACATTAACATGAGAGAAACAGAGAGAAATCTTGATGCTT	1356
OY	705	CACAAGACATGCAACAAACAAATGGAATFACTGTGATGACATGAGCGACCAAGCTGGGG	764
Db	1355	CACAAGACATGCAACAAACAAATGGAATFACTGTGATGACATGAGCGACCAAGCTGGGG	1296
OY	765	AGAGATTAACACGAGGAGAGGTCAGAGATTTGGCCCTGCTGCTAAGCTGGCGTTC	824
Db	1295	AGAGATTAACACGAGGAGAGGTCAGAGATTTGGCCCTGCTGCTAAGCTGGCGTTC	1236
OY	825	ATAACCAATGATTTCAATATTTCTAAACCTCAAAACAAAGCTGTTGAATATCTGATCTC	884
Db	1235	ATAACCAATGATTTCAATATTTCTAAACCTCAAAACAAAGCTGTTGAATATCTGATCTC	1176
OY	885	TACGGTTCCTTCTGGGCCCAACATTTCTCAATATCCAGCACACTCAATTTTAATATTT	944
Db	1175	TACGGTTCCTTCTGGGCCCAACATTTCTCAATATCCAGCACACTCAATTTTAATATTT	1116
OY	945	AGTTCACGATCTGACTGTGACCTTTCTACAGCTAGATTAACATTCATTTTGTTC	1004
Db	1115	AGTTCACGATCTGACTGTGACCTTTCTACAGCTAGATTAACATTCATTTTGTTC	1056
OY	1005	AAAGACCTTTCGTGTGCTGCTTAATATAGTACTGACTGTTTTCTTAAGAGAGTGTCTG	1064
Db	1055	AAAGACCTTTCGTGTGCTGCTTAATATAGTACTGACTGTTTTCTTAAGAGAGTGTCTG	996
OY	1065	GCCACGAGGATCTGTGAACAGGCTGGGAGACATCTCAAGATCTTCCAGGTTATACTTA	1124
Db	995	GCCACGAGGATCTGTGAACAGGCTGGGAGACATCTCAAGATCTTCCAGGTTATACTTA	936
OY	1125	CTACACACAGACATGATTAAGGAGATTAATCTAATTAACATCTCTCTGCTGCT	1184
Db	935	CTACACACAGACATGATTAAGGAGATTAATCTAATTAACATCTCTCTGCTGCT	876
OY	1185	TTGGCCACTACTGAATTCATTTCCACTTTTGTGCCCATCTCAAGAGCTCAAAATGTCA	1244
Db	875	TTGGCCACTACTGAATTCATTTCCACTTTTGTGCCCATCTCAAGAGCTCAAAATGTCA	816
OY	1245	TTTCATTAAATATCAGAGATTAATCTTTTAACTTGAAGAGAAATTCATGTTACATG	1304
Db	815	TTTCATTAAATATCAGAGATTAAC-TTTTAACTTGAAGAGAAATTCATGTTACATG	757
OY	1305	CAGCTATGGGAATTAATTAATTTTGTCTTCCAGTGGCAAAATGACTAAGTCTTTA	1364

Db	756	CAGCTATGGGAATTAATTAATTAATTTGTTTCCAGTGCAAAAGATGACTAAGTCTTTA	697
OY	1365	TCCCTCCCTCTGTTGATTTTTCAGTATTAAGTTAAATAGCTTACGCTTACTG	1424
Db	696	TCCCTCCCTCTGTTGATTTTTCAGTATTAAGTTAAATAGCTTACGCTTACTG	637
OY	1425	AGGCTATTAACAG-CACAGCCTTCCCATCCCTCCACACCTTATCTCATCACCATCA	1483
Db	636	AGGCTATTAACAGCAGCAGCCTCCCATCCCTCCACACCTTATCTCATCACCATCA	577
OY	1484	CCCCCTCCATACACACTTAAACAAATCTAATCTTGAATCTTGAACATGTACAGACTA	1543
Db	576	CCCCCTCCAT-GCACCTTAAACAAATCTAATCTTGAATCTTGAACATGTACAG-CTA	519
OY	1544	CATTATTCCTCTGCTGAGAGGCTCTCTCTGCTCTTAAATCTAGATATGTAATG	1603
Db	518	CATTATTCCTCTGCTGAGAGGCTCTCTCTGCTCTTAAATCTAGATATGTAATG	459
OY	1604	TTTGAATTAAGTGAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATGA	1663
Db	458	TTTGAATTAAGTGAATTAATTAATTAATTAATTAATTAATTAATTAATTAATGA	399
OY	1664	ACATGAGACAGCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATGA	1723
Db	398	ACATGAGACAGCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATGA	340
OY	1724	AATGCAAGAGCCACAGAGGAGATTTATGGGGCAGCTTTGTAAGCCTGGAGTGAAGC	1783
Db	339	AATGCAAGAGCCACAGAGGAGATTTATGGGGCAGCTTTGTAAGCCTGGAGTGAAGC	280
OY	1784	AAAGCAGGAGACCTCATATGATCTTAATTAATTAATTAATTAATTAATTAATTAATTA	1843
Db	279	AAAGCAGGAGACCTCATATGATCTTAATTAATTAATTAATTAATTAATTAATTAATTA	220
OY	1844	ATATCCAAACAGCTTTTACAGAAATTCATGAGTGAAGTGAAGTGAAGTGAAGTGAAGT	1903
Db	219	ATATCCAAACAGCTTTTACAGAAATTCATGAGTGAAGTGAAGTGAAGTGAAGTGAAGT	160
OY	1904	CATTTCATGATGAGTGCCTTTAGAAATTTTGGCAATCATCTGCTCACTTATGCAACT	1963
Db	159	CATTTCATGATGAGTGCCTTTAGAAATTTTGGCAATCATCTGCTCACTTATGCAACT	100
OY	1964	TTGAGATGTGTTTGTCTTGTAGTTAATTAAGAAATAGGGCACTGTGTGAGCCACTT	2023
Db	99	TTGAGATGTGTTTGTCTTGTAGTTAATTAAGAAATAGGGCACTGTGTGAGCCACTT	40
OY	2024	TAGGTTCACTCTCGGCAATTAAGAAATTAAGAAAGCT 2062	
Db	39	TAGGTTCACTCTCGGCAATTAAGAAATTAAGAAAGCT 1	

RESULT 6
US-09-352-616A-469/C
; Sequence 469, Application US/09352616A
; Patent No. 6395278
; GENERAL INFORMATION:
; APPLICANT: Dillon, Davin C.
; APPLICANT: Harlocker, Susan Louise
; APPLICANT: Jiang, Yuhui
; APPLICANT: Xu, Jianshun
; APPLICANT: Mitcham, Jennifer Lynn
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
; FILE REFERENCE: 210121.427C8
; CURRENT APPLICATION NUMBER: US/09/352.616A
; CURRENT FILING DATE: 1999-07-13
; NUMBER OF SEQ ID NOS: 472
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 469
; LENGTH: 2229
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-352-616A-469

Query Match 31.4%; Score 1123; DB 4; Length 2229;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 1773; Conservative 0; Mismatches 1; Indels 5; Gaps 5;

```

OY 285 GGTGAGAAATAAGAAAGGCTGCTGACTTACATCTGAGGCCACACATCTGCTGAAATG 344
    |||||||
Db 1775 GGTGAGAAATAAGAAAGGCTGCTGACTTACATCTGAGGCCACACATCTGCTGAAATG 1716

OY 345 AATATATTAACATCTACTAGAAAACAGACATGACATATATATGTCTAAGTAGTACATGT 404
    |||||||
Db 1715 AATATATTAACATCTACTAGAAAACAGACATGACATATATATGTCTAAGTAGTACATGT 1656

OY 405 TTTTGACATTTCCAGCCCCCTTTAAATATCCACACACAGAGAAAGACAAAAGAGACAC 464
    |||||||
Db 1655 TTTTGACATTTCCAGCCCCCTTTAAATATCCACACACAGAGAAAGACAAAAGAGACAC 1596

OY 465 AGAGATCCCTGGGAGAAATGCCGGCCCATCTTGAGTATCGATGAGCCCTGCGCTGT 524
    |||||||
Db 1595 AGAGATCCCTGGGAGAAATGCCGGCCCATCTTGAGTATCGATGAGCCCTGCGCTGT 1536

OY 525 GCCTGGTCCCGCTGTGTGAGGAGAGACATTAAGAAATGATATGATGTCTCTTAAAGA 584
    |||||||
Db 1535 GCCTGGTCCCGCTGTGTGAGGAGAGACATTAAGAAATGATATGATGTCTCTTAAAGA 1476

OY 585 TGGGCGAGAAACAGATCCCTGTGTGATATTATTTGAACGGGATTAAGATTTGAAT 644
    |||||||
Db 1475 TGGGCGAGAAACAGATCCCTGTGTGATATTATTTGAACGGGATTAAGATTTGAAT 1416

OY 645 GAATGCACAAATGAGCATTTACCAATGAGAGAAAACAGACAGAAATCTTGATGGCTT 704
    |||||||
Db 1415 GAATGCACAAATGAGCATTTACCAATGAGAGAAAACAGACAGAAATCTTGATGGCTT 1356

OY 705 CACAAGACATGCAACAAATAATGAAATGAACTGTGATGATGAGGACAGCCAGCTGGGG 764
    |||||||
Db 1355 CACAAGACATGCAACAAATAATGAAATGAACTGTGATGATGAGGACAGCCAGCTGGGG 1296

OY 765 AAGAGATTAACACAGGGGCGAGAGGTCAGAGATTCTGGCCCTGCTTAAACTGTGGTTC 824
    |||||||
Db 1295 AAGAGATTAACACAGGGGCGAGAGGTCAGAGATTCTGGCCCTGCTTAAACTGTGGTTC 1236

OY 825 ATTAACCAATTCATTTCAATATTTCTAACCTCAAAACAAAGCTGTGTAAATATCTGATCTC 884
    |||||||
Db 1235 ATTAACCAATTCATTTCAATATTTCTAACCTCAAAACAAAGCTGTGTAAATATCTGATCTC 1176

OY 885 TAGGGTCCCTGTGGGCCCAACATCTCCATATATCCAGCCACATCTTTTAAATATT 944
    |||||||
Db 1175 TAGGGTCCCTGTGGGCCCAACATCTCCATATATCCAGCCACATCTTTTAAATATT 1116

OY 945 AGTTCCAGATCTGTACTGTGACCTTTCTACACTGTAGAAATAACATTAATCTATTGTTTC 1004
    |||||||
Db 1115 AGTTCCAGATCTGTACTGTGACCTTTCTACACTGTAGAAATAACATTAATCTATTGTTTC 1056

OY 1005 AAGAGCCCTTGTGTGCTGCTATATGTAGCTGACTGTCTTTCTTAAAGAGTGTCTG 1064
    |||||||
Db 1055 AAGAGCCCTTGTGTGCTGCTATATATGTAGCTGACTGTCTTTCTTAAAGAGTGTCTG 996

OY 1065 GCCCAGGGGATCTGTGAACAGCTGGGAGCAATCTCAAGATCTTCCAGGGTATATCTTA 1124
    |||||||
Db 995 GCCCAGGGGATCTGTGAACAGCTGGGAGCAATCTCAAGATCTTCCAGGGTATATCTTA 936

OY 1125 CTAGCACACAGATGATCTATTACGAGAGTAATATATCAACATCAATCTCAGCTGT 1184
    |||||||
Db 935 CTAGCACACAGATGATCTATTACGAGAGTAATATATCAACATCAATCTCAGCTGT 876

OY 1185 TTGCCCATCTGAAATTCATTTCCACTTTTGTGCCATCTTCACAGACTCAAAATGTCA 1244
    |||||||
Db 875 TTGCCCATCTGAAATTCATTTCCACTTTTGTGCCATCTTCACAGACTCAAAATGTCA 816

OY 1245 TTCCATTAATACACAGATTAACCTTTTAACTGGAAGAAATCAATGTTCATG 1304
    |||||||
Db 815 TTCCATTAATACACAGATTAAC-TTTTTTTTTAACTGGAAGAAATCAATGTTCATG 757
```

```

OY 1305 CAGCTATGGGAATTTAATTAACATATTTGTTTCCAGTGCAAAAGATAGTAACTCTTTA 1364
    |||||||
Db 756 CAGCTATGGGAATTTAATTAACATATTTGTTTCCAGTGCAAAAGATAGTAACTCTTTA 697

OY 1365 TCCCTCCCTTGTGTGATTTTTCAGATATAAAGTTAAATGCTTACCTTGTACG 1424
    |||||||
Db 696 TCCCTCCCTTGTGTGATTTTTCAGATATAAAGTTAAATGCTTACCTTGTACG 637

OY 1425 AGGCTATATACAG-CACAGCCTCTCCCATCTCCATGAGCTTATCTGTATCATCCATCA 1483
    |||||||
Db 636 AGGCTATATACAGC-CACAGCCTCTCCCATCTCCATGAGCTTATCTGTATCATCCATCA 577

OY 1484 CCCCCTCCATACACCTTAACAAATCTAATCTGTATTCCTTGAACATGTGAGACATA 1543
    |||||||
Db 576 CCCCCTCCAT-GCACCTAAACAAATCTAATCTGTATTCCTTGAACATGTGAGACATA 519

OY 1544 CATTAATTCCTTGTGCTGTGAAGACCTCTCTGTCTCTTAAATCTAAGATGTAAAGT 1603
    |||||||
Db 518 CATTAATTCCTTGTGCTGTGAAGACCTCTCTGTCTCTTAAATCTAAGATGTAAAGT 459

OY 1604 TTTGAATTAAGTACATATCTTACTTCATGCAAAAGAGGACACATATGATGATCATTC 1663
    |||||||
Db 458 TTTGAATTAAGTACATATCTTACTTCATGCAAAAGAGGACACATATGATGATCATTC 399

OY 1664 ACATGAGACAGCAAAATCTAAAGTGAATTTGATTAAGATTTAGATTAATATATGA 1723
    |||||||
Db 398 ACATGAGACAGCAAAATCTAATAAGTGT-ATTTGATTAATAAGATTTAGATTAATATATGA 340

OY 1724 AATGCAAGGCCACAGAGGGAATGTTTATGAGGCGACGTTTGTAAGCCTGGAGTGAAGC 1783
    |||||||
Db 339 AATGCAAGGACACACAGAGGGAATGTTTATGAGGCGACGTTTGTAAGCCTGGAGTGAAGC 280

OY 1784 AAAAGGAGGGAACCCATATGATATCTTAAATATATCTTCAATCTCTATCTATACCA 1843
    |||||||
Db 279 AAAAGGAGGGAACCCATATGATATCTTAAATATATCTTCAATCTCTATCTATACCA 220

OY 1844 ATATCCAAAGGCTTTTCAAGAAATTCAGATGCAAGTATCCCAAGGATTAACCTTTATC 1903
    |||||||
Db 219 ATATCCAAAGGCTTTTCAAGAAATTCAGATGCAAGTATCCCAAGGATTAACCTTTATC 160

OY 1904 CATTTATGTGTAGTCCGCTTTTGAATTTTGGCAATCATCTGTGACTTATCTCAACT 1963
    |||||||
Db 159 CATTTATGTGTAGTCCGCTTTTGAATTTTGGCAATCATCTGTGACTTATCTCAACT 100

OY 1964 TTGAGATGTGTTTGCTTGTGATTAATGAAGAAATAGGGACATCTGTGAGCCACTT 2023
    |||||||
Db 99 TTGAGATGTGTTTGCTTGTGATTAATGAAGAAATAGGGACATCTGTGAGCCACTT 40

OY 2024 TAGGGTTCACTCCTGGCAATTAAGAAATTTACAAGAGCT 2062
    |||||||
Db 39 TAGGGTTCACTCCTGGCAATTAAGAAATTTACAAGAGCT 1

RESULT 7
US-09-439-313-471/c
; Sequence 471, Application US/09439313
; Patent No. 6329505
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan Louise
; APPLICANT: Jiang Yugu
; APPLICANT: Reed, Steven G.
; APPLICANT: Kalos, Michael
; APPLICANT: Fanger, Gary
; APPLICANT: Retter, Mark
; APPLICANT: Solk, John
; APPLICANT: Day, Craig
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
; FILE REFERENCE: 210121.427C9
; CURRENT APPLICATION NUMBER: US/09/439, 313
```

;; CURRENT FILING DATE: 1999-11-12
;; NUMBER OF SEQ ID NOS: 575
;; SOFTWARE: FASTSEQ for Windows Version 3.0
;; SEQ ID NO 471
;; LENGTH: 812
;; TYPE: DNA
;; ORGANISM: Homo sapiens
US-09-439-313-471

Query Match 20.1%; Score 720; DB 4; Length 812;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 720; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 285 GGTGGAATTAAGAAAGGCTGCTGCTTACCATCTGAGGCCACACATCTGCTGAATGG 344
DB 720 GGTGGAATTAAGAAAGGCTGCTGCTTACCATCTGAGGCCACACATCTGCTGAATGG 661
QY 345 AGATTAATTAACATCTGAGAAACAGCAAGATGACATTAATGTCTAAGTAGTGACATGT 404
DB 660 AGATTAATTAACATCTGAGAAACAGCAAGATGACATTAATGTCTAAGTAGTGACATGT 601
QY 405 TTTTGACATTTCCAGCCCTTTTAATATCCACACACAGAGAGCACAAGAAAGAACAC 464
DB 600 TTTTGACATTTCCAGCCCTTTTAATATCCACACACAGAGAGCACAAGAAAGAACAC 541
QY 465 AGAGATCCCTGGGAGAAATGCCCCGCCCATCTTGGGTATCATGATGAGCCCTGCCCTGT 524
DB 540 AGAGATCCCTGGGAGAAATGCCCCGCCCATCTTGGGTATCATGATGAGCCCTGCCCTGT 481
QY 525 GCTGTGTCCTGCTGAGGAGAGACATTAAGAAATGAATGATGTCTTAAAGGA 584
DB 480 GCTGTGTCCTGCTGAGGAGAGACATTAAGAAATGAATGATGTCTTAAAGGA 421
QY 585 TGGGAGGAGAAACAGATCTGTGTGATATTTTGAACGGGATTCAGATTGGAAT 644
DB 420 TGGGAGGAGAAACAGATCTGTGTGATATTTTGAACGGGATTCAGATTGGAAT 361
QY 645 GAAGTCACAAAGTGACCTTACCAATGAGAGAGAAACAGAGAGAAATCTTGATGCTT 704
DB 360 GAAGTCACAAAGTGACCTTACCAATGAGAGAGAAACAGAGAGAAATCTTGATGCTT 301
QY 705 CACAAGACATGCAACAAACAAATGAGATAGTGTGATGACATGAGGAGCCACAGCTGGG 764
DB 300 CACAAGACATGCAACAAACAAATGAGATAGTGTGATGACATGAGGAGCCACAGCTGGG 241
QY 765 AGGAGATTAACCAAGGGGAGAGGGTCAAGATTTGGCCCTGCTGCTAACTGTGCTTC 824
DB 240 AGGAGATTAACCAAGGGGAGAGGGTCAAGATTTGGCCCTGCTGCTAACTGTGCTTC 181
QY 825 ATAACCAAAATATTCTATTTCTAACCCTCAAAACAAAGCTGTTGTAATCTGATCTC 884
DB 180 ATAACCAAAATATTCTATTTCTAACCCTCAAAACAAAGCTGTTGTAATCTGATCTC 121
QY 885 TACGGTTCCTTCTGGGCCCAACATTTCCATATATCCAGCCACACTCTTTTAAATATT 944
DB 120 TACGGTTCCTTCTGGGCCCAACATTTCCATATATCCAGCCACACTCTTTTAAATATT 61
QY 945 AGTTCCAGATCTGATGACCTTCTACACTGTAGAAATACATTACTATTTGTTTC 1004
DB 60 AGTTCCAGATCTGATGACCTTCTACACTGTAGAAATACATTACTATTTGTTTC 1

RESULT 8
US-09-352-616A-471/c
; Sequence 471, Application US/09352616A
; Patent No. 6395278
; GENERAL INFORMATION:
; APPLICANT: Dillon, Davin C.
; APPLICANT: Harlocker, Susan Louise
; APPLICANT: Jiang, Yugu
; APPLICANT: Xu, Jianshun
; APPLICANT: Mitcham, Jennifer Lynn
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS

;; TITLE OF INVENTION: OF PROSTATE CANCER AND METHODS FOR THEIR USE
;; FILE REFERENCE: 210121.427C8
;; CURRENT APPLICATION NUMBER: US/09/352,616A
;; CURRENT FILING DATE: 1999-07-13
;; NUMBER OF SEQ ID NOS: 472
;; SOFTWARE: FASTSEQ for Windows Version 3.0
;; SEQ ID NO 471
;; LENGTH: 812
;; TYPE: DNA
;; ORGANISM: Homo sapiens
US-09-352-616A-471

Query Match 20.1%; Score 720; DB 4; Length 812;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 720; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 285 GGTGGAATTAAGAAAGGCTGCTGCTTACCATCTGAGGCCACACATCTGCTGAATGG 344
DB 720 GGTGGAATTAAGAAAGGCTGCTGCTTACCATCTGAGGCCACACATCTGCTGAATGG 661
QY 345 AGATTAATTAACATCTGAGAAACAGCAAGATGACATTAATGTCTAAGTAGTGACATGT 404
DB 660 AGATTAATTAACATCTGAGAAACAGCAAGATGACATTAATGTCTAAGTAGTGACATGT 601
QY 405 TTTTGACATTTCCAGCCCTTTTAATATCCACACACAGAGAGCACAAGAAAGAACAC 464
DB 600 TTTTGACATTTCCAGCCCTTTTAATATCCACACACAGAGAGCACAAGAAAGAACAC 541
QY 465 AGAGATCCCTGGGAGAAATGCCCCGCCCATCTTGGGTATCATGATGAGCCCTGCCCTGT 524
DB 540 AGAGATCCCTGGGAGAAATGCCCCGCCCATCTTGGGTATCATGATGAGCCCTGCCCTGT 481
QY 525 GCTGTGTCCTGCTGAGGAGAGACATTAAGAAATGAATGATGTCTTAAAGGA 584
DB 480 GCTGTGTCCTGCTGAGGAGAGACATTAAGAAATGAATGATGTCTTAAAGGA 421
QY 585 TGGGAGGAGAAACAGATCTGTGTGATATTTTGAACGGGATTCAGATTGGAAT 644
DB 420 TGGGAGGAGAAACAGATCTGTGTGATATTTTGAACGGGATTCAGATTGGAAT 361
QY 645 GAAGTCACAAAGTGACCTTACCAATGAGAGAGAAACAGAGAGAAATCTTGATGCTT 704
DB 360 GAAGTCACAAAGTGACCTTACCAATGAGAGAGAAACAGAGAGAAATCTTGATGCTT 301
QY 705 CACAAGACATGCAACAAACAAATGAGATAGTGTGATGACATGAGGAGCCACAGCTGGG 764
DB 300 CACAAGACATGCAACAAACAAATGAGATAGTGTGATGACATGAGGAGCCACAGCTGGG 241
QY 765 AGGAGATTAACCAAGGGGAGAGGGTCAAGATTTGGCCCTGCTGCTAACTGTGCTTC 824
DB 240 AGGAGATTAACCAAGGGGAGAGGGTCAAGATTTGGCCCTGCTGCTAACTGTGCTTC 181
QY 825 ATAACCAAAATATTCTATTTCTAACCCTCAAAACAAAGCTGTTGTAATCTGATCTC 884
DB 180 ATAACCAAAATATTCTATTTCTAACCCTCAAAACAAAGCTGTTGTAATCTGATCTC 121
QY 885 TACGGTTCCTTCTGGGCCCAACATTTCCATATATCCAGCCACACTCTTTTAAATATT 944
DB 120 TACGGTTCCTTCTGGGCCCAACATTTCCATATATCCAGCCACACTCTTTTAAATATT 61
QY 945 AGTTCCAGATCTGATGACCTTCTACACTGTAGAAATACATTACTATTTGTTTC 1004
DB 60 AGTTCCAGATCTGATGACCTTCTACACTGTAGAAATACATTACTATTTGTTTC 1

RESULT 9
US-09-439-313-313
; Sequence 313, Application US/09439313
; Patent No. 6329505
; GENERAL INFORMATION:
; APPLICANT: Xu, Jianshun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.


```
APPLICANT: Harlocker, Susan Louise
APPLICANT: Jiang Yugu
APPLICANT: Reed, Steven G.
APPLICANT: Kalos, Michael
APPLICANT: Fanger, Gary
APPLICANT: Retter, Mark
APPLICANT: Solk, John
APPLICANT: Day, Craig
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427C9
CURRENT APPLICATION NUMBER: US/09/439,313
CURRENT FILING DATE: 1999-11-12
NUMBER OF SEQ ID NOS: 575
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 313
LENGTH: 718
TYPE: DNA
ORGANISM: Homo sapien
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(718)
OTHER INFORMATION: n = A,T,C or G
US-09-439-313-313
```

```
Query Match
Best Local Similarity 99.38; Score 201; DB 4; Length 718;
Matches 301; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY 285 GGTGAGAAATTAAGAAAGGCTGCTGACTTACATCTGAGGCCACACATCTGCTGAATGG 344
DB 73 GGTGAGAAATTAAGAAAGGCTGCTGACTTACATCTGAGGCCACACATCTGCTGAATGG 132
QY 345 AGATTAATTAACATCACTAGAAACAGCAAGATGACATATATATCTTAAGTAGACATGT 404
DB 133 AGATTAATTAACATCACTAGAAACAGCAAGATGACATATATATCTTAAGTAGACATGT 192
QY 405 TTTTGACATTTCCAGCCCTTTAAATATCCACACACAGAGACAAAAGAGACAC 464
DB 193 TTTTGACATTTCCAGCCCTTTAAATATCCACACACAGAGACAAAAGAGACAC 252
QY 465 AGAGATCCCTGGGAGAAATGCCCGGCCCATCTTGCGTATCGATGAGCCTGCGCTGT 524
DB 253 AGAGATCCCTGGGAGAAATGCCCGGCCCATCTTGCGTATCGATGAGCCTGCGCTGT 312
QY 525 GCCTGCTCCCGCTTGTGAGGGAAGACATTAGAAATGAATATGTGTCTCTTAAGGA 584
DB 313 GCCTGCTCCCGCTTGTGAGGGAAGACATTAGAAATGAATATGTGTCTCTTAAGGA 372
QY 585 TGG 587
DB 373 TGG 375
```

```
RESULT 10
US-09-352-616A-313
Sequence 313, Application US/09352616A
Patent No. 6395278
GENERAL INFORMATION:
APPLICANT: Dillon, Davin C.
APPLICANT: Harlocker, Susan Louise
APPLICANT: Jiang, Yugu
APPLICANT: Xu, Jiangchun
APPLICANT: Mitcham, Jennifer Lynn
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
TITLE OF INVENTION: OF PROSTATE CANCER AND METHODS FOR THEIR USE
FILE REFERENCE: 210121.427C8
CURRENT APPLICATION NUMBER: US/09/352,616A
CURRENT FILING DATE: 1999-07-13
NUMBER OF SEQ ID NOS: 472
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 313
LENGTH: 718
```

```
TYPE: DNA
ORGANISM: Homo sapien
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(718)
OTHER INFORMATION: n = A,T,C or G
US-09-352-616A-313
```

```
Query Match
Best Local Similarity 99.38; Score 201; DB 4; Length 718;
Matches 301; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY 285 GGTGAGAAATTAAGAAAGGCTGCTGACTTACATCTGAGGCCACACATCTGCTGAATGG 344
DB 73 GGTGAGAAATTAAGAAAGGCTGCTGACTTACATCTGAGGCCACACATCTGCTGAATGG 132
QY 345 AGATTAATTAACATCACTAGAAACAGCAAGATGACATATATATCTTAAGTAGACATGT 404
DB 133 AGATTAATTAACATCACTAGAAACAGCAAGATGACATATATATCTTAAGTAGACATGT 192
QY 405 TTTTGACATTTCCAGCCCTTTAAATATCCACACACAGAGACAAAAGAGACAC 464
DB 193 TTTTGACATTTCCAGCCCTTTAAATATCCACACACAGAGACAAAAGAGACAC 252
QY 465 AGAGATCCCTGGGAGAAATGCCCGGCCCATCTTGCGTATCGATGAGCCTGCGCTGT 524
DB 253 AGAGATCCCTGGGAGAAATGCCCGGCCCATCTTGCGTATCGATGAGCCTGCGCTGT 312
QY 525 GCCTGCTCCCGCTTGTGAGGGAAGACATTAGAAATGAATATGTGTCTCTTAAGGA 584
DB 313 GCCTGCTCCCGCTTGTGAGGGAAGACATTAGAAATGAATATGTGTCTCTTAAGGA 372
QY 585 TGG 587
DB 373 TGG 375
```

```
RESULT 11
US-09-232-149A-313
Sequence 313, Application US/09232149A
Patent No. 6465611
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer Lynn
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE
TITLE OF INVENTION: CANCER AND METHODS FOR THEIR USE
FILE REFERENCE: 210121.427C6
CURRENT APPLICATION NUMBER: US/09/232,149A
CURRENT FILING DATE: 1999-01-15
NUMBER OF SEQ ID NOS: 338
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 313
LENGTH: 718
TYPE: DNA
ORGANISM: Homo sapien
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(718)
OTHER INFORMATION: n = A,T,C or G
US-09-232-149A-313
```

```
Query Match
Best Local Similarity 99.38; Score 201; DB 4; Length 718;
Matches 301; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY 285 GGTGAGAAATTAAGAAAGGCTGCTGACTTACATCTGAGGCCACACATCTGCTGAATGG 344
DB 73 GGTGAGAAATTAAGAAAGGCTGCTGACTTACATCTGAGGCCACACATCTGCTGAATGG 132
QY 345 AGATTAATTAACATCACTAGAAACAGCAAGATGACATATATATCTTAAGTAGACATGT 404
DB 133 AGATTAATTAACATCACTAGAAACAGCAAGATGACATATATATCTTAAGTAGACATGT 192
```

QY	405	TTTTGCACATTTCCAGCCCCCTTAATATATCCACACACACAGGAGACCAAAAGGAGCAC	464
Db	193	TTTTGCACATTTCCAGCCCCCTTTAATATATCCACACACACAGGAGACCAAAAGGAGCAC	252
QY	465	AGAGATCCCTGGGAGAAATGCCCGGCGGCATCTTGGGTCATCGATGAGCGTGGCCCTGT	524
Db	253	AGAGATCCCTGGGAGAAATGCCCGGCGGCATCTTGGGTCATCGATGAGCGTGGCCCTGT	312
QY	525	GCCTGGTCCGCTCTGTGAGGGAAGACATTAGAAAAATGATGTGTTCTCTTAAAGCA	584
Db	313	GCCTGGTCCGCTCTGTGAGGGAAGACATTAGAAAAATGATGTGTTCTCTTAAAGCA	372
QY	585	TGG 587	
Db	373	TGG 375	

```

RESULT 12
US-09-439-313-287/c
; Sequence 287, Application US/09439313
; Patent No. 6329505
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan Louise
; APPLICANT: Jiang Yugu
; APPLICANT: Reed, Steven G.
; APPLICANT: Kalos, Michael
; APPLICANT: Fanger, Gary
; APPLICANT: Retter, Mark
; APPLICANT: Solk, John
; APPLICANT: Day, Craig
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C9
; CURRENT APPLICATION NUMBER: US/09/439,313
; CURRENT FILING DATE: 1999-11-12
; NUMBER OF SEQ ID NOS: 575
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 287
; LENGTH: 301
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-439-313-287

```

```

? APPLICANT: Dillon, Davin C.
? APPLICANT: Harlocker, Susan Louise
? APPLICANT: Jiang, Yuguai
? APPLICANT: Xu, Jlangchun
? APPLICANT: Mitcham, Jennifer Lynn
? TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
? TITLE OF INVENTION: OF PROSTATE CANCER AND METHODS FOR THEIR USE
? FILE REFERENCE: 210121.427C8
? CURRENT APPLICATION NUMBER: US/09/352,616A
? CURRENT FILING DATE: 1999-07-13
? NUMBER OF SEQ ID NOS: 472
? SOFTWARE: FASTSEQ FOR WINDOWS VERSION 3.0
? SEQ ID NO 287
? LENGTH: 301
? TYPE: DNA
? ORGANISM: Homo sapien
US-09-352-616A-287

Query Match          5.0%;      Score 179;  DB 4;      Length 301;
Best Local Similarity 99.6%;      Pred. No. 2.3e-74;
Matches 229; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

RESULT 13
US-09-352-616A-287/c
; Sequence 287, Application US/09352616A
; Patent No. 6395278
; GENERAL INFORMATION:

```

; APPLICANT: Mitcham, Jennifer Lynn
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE
; TITLE OF INVENTION: CANCER AND METHODS FOR THEIR USE
; FILE REFERENCE: 210121.427C6
; CURRENT APPLICATION NUMBER: US/09/232,149A
; CURRENT FILING DATE: 1999-01-15
; NUMBER OF SEQ ID NOS: 338
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 287
; LENGTH: 301
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-232-149A-287

Query Match          5.0%; Score 179; DB 4; Length 301;
Best Local Similarity 99.6%; Pred. No. 2,3e-74;
Matches 229; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy      659 AGCATTTACCATGTAGAGAGAAAACGAGACAGAGAAAATCTTTGATGCGCTTACCAAGACATGCAA 718
        |||||||
Db      301 AGCATTTACCAATGAGAGAAAACGAGACAGAGAAAATCTTTGATGCGCTTACCAAGACATGCAA 242

Oy      719 CAAACAAAAATGCATACGTCGATGATACATGAGCGACGCCAACGCTGGGGAGAGGATTAACCAAG 778
        |||||||
Db      241 CAAACAAAAATGCATACGTCGATGATACATGAGCGACGCCAACGCTGGGGAGAGGATTAACCAAG 182

Oy      779 GGGCAGAGAGGTCAGGATTTGGCCCTCGTGCCTTAACGTGTCGCTTAAACCAATCATTT 838

```

```

Db      181  GGGCAGAGGGTCAGATCTGCGCCCTGACCTAACTGCGCTCATACCAATCATT 122
QY      839  TCATATTTCTAACCCCAAAACAAAGCTGTGTAATATCTGATCTACG 888
Db      121  TCATATTTCTAACCCCAAAACAAAGCTGTGTAATATCTGATCTACG 72

```

RESULT 15

```

US-09-439-313-235
; Sequence 235, Application US/09439313
; Patent No. 6329505
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan Louise
; APPLICANT: Jiang Yuqi
; APPLICANT: Reed, Steven G.
; APPLICANT: Kalos, Michael
; APPLICANT: Fanger, Gary
; APPLICANT: Retter, Mark
; APPLICANT: Solk, John
; APPLICANT: Day, Craig
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C9
; CURRENT APPLICATION NUMBER: US/09/439,313
; CURRENT FILING DATE: 1999-11-12
; NUMBER OF SEQ ID NOS: 575
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 235
; LENGTH: 283
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-439-313-235

```

Query Match 3.5%; Score 127; DB 4; Length 283;

Best Local Similarity 100.0%; Pred.No. 6.5e-50; Matches 127; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY      2581  TGTTCATGATAGTCCAAATAATATGTATCTTGAAGTATGCTCATAGAGAGATA 2640
Db      157  TGTTCATGATAGTCCAAATAATATGTATCTTGAAGTATGCTCATAGAGAGATA 216
QY      2641  TAAGAACTCTGAGTATATCAACATTAGGATTCAAAGAAATATTAGATTAAAGCTCACA 2700
Db      217  TAAGAACTCTGAGTATATCAACATTAGGATTCAAAGAAATATTAGATTAAAGCTCACA 276
QY      2701  CTGGTCA 2707
Db      277  CTGGTCA 283

```

Search completed: September 27, 2003, 11:43:59
Job time : 208.585 secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 26, 2003, 21:44:18 : Search time 830.096 Seconds
(without alignments)
10742.554 Million cell updates/sec

Title: US-09-402-713a-6
Perfect score: 3582
Sequence: 1 acagaagaataatgcaatgctgc.....tgattcttgttacaacttt 3582

Scoring table: OLIGO_NWC
Gapop 60.0 , Gapext 60.0

Searched: 1678620 seqs, 1244745471 residues

Word size : 0

Total number of hits satisfying chosen parameters: 3357240

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

Published Applications_NA:*

- 1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
- 2: /cgn2_6/ptodata/2/pubpna/PCF_NEM_PUB.seq:*
- 3: /cgn2_6/ptodata/2/pubpna/US06_NEM_PUB.seq:*
- 4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
- 5: /cgn2_6/ptodata/2/pubpna/US07_NEM_PUB.seq:*
- 6: /cgn2_6/ptodata/2/pubpna/PCFUS_PUBCOMB.seq:*
- 7: /cgn2_6/ptodata/2/pubpna/US08_NEM_PUB.seq:*
- 8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
- 9: /cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:*
- 10: /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
- 11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
- 12: /cgn2_6/ptodata/2/pubpna/US09_NEM_PUB.seq:*
- 13: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
- 14: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
- 15: /cgn2_6/ptodata/2/pubpna/US10_NEM_PUB.seq:*
- 16: /cgn2_6/ptodata/2/pubpna/US60_NEM_PUB.seq:*
- 17: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3036	84.8	3923	9	US-09-759-143-690
2	3036	84.8	3923	9	US-09-780-669-690
3	3036	84.8	3923	9	US-09-822-827-690
4	3036	84.8	3923	10	US-09-895-793-690
5	3036	84.8	3923	12	US-09-895-814-690
6	3036	84.8	3923	10	US-10-144-678A-690
7	3036	84.8	3923	13	US-10-012-896-690
8	3036	84.8	3923	14	US-10-205-823-316
9	1364	38.1	3112	9	US-09-759-143-468
10	1364	38.1	3112	9	US-09-780-669-468
11	1364	38.1	3112	9	US-09-822-827-468
12	1364	38.1	3112	10	US-09-895-793-468
13	1364	38.1	3112	10	US-09-895-814-468
14	1364	38.1	3112	12	US-10-144-678A-468
15	1364	38.1	3112	13	US-10-012-896-468
16	1364	38.1	3112	14	US-10-010-940-468

C 17	1357	37.9	2426	9	US-09-759-143-470	Sequence 470, App
C 18	1357	37.9	2426	9	US-09-780-669-470	Sequence 470, App
C 19	1357	37.9	2426	9	US-09-822-827-470	Sequence 470, App
C 20	1357	37.9	2426	10	US-09-895-793-470	Sequence 470, App
C 21	1357	37.9	2426	10	US-09-895-814-470	Sequence 470, App
C 22	1357	37.9	2426	12	US-10-144-678A-470	Sequence 470, App
C 23	1357	37.9	2426	13	US-10-012-896-470	Sequence 470, App
C 24	1357	37.9	2426	14	US-10-010-940-470	Sequence 470, App
C 25	1357	37.9	2426	14	US-10-205-823-448	Sequence 448, App
C 26	1123	31.4	2229	9	US-09-759-143-469	Sequence 469, App
C 27	1123	31.4	2229	9	US-09-780-669-469	Sequence 469, App
C 28	1123	31.4	2229	9	US-09-822-827-469	Sequence 469, App
C 29	1123	31.4	2229	10	US-09-895-793-469	Sequence 469, App
C 30	1123	31.4	2229	10	US-09-895-814-469	Sequence 469, App
C 31	1123	31.4	2229	12	US-10-144-678A-469	Sequence 469, App
C 32	1123	31.4	2229	13	US-10-012-896-469	Sequence 469, App
C 33	1123	31.4	2229	14	US-10-010-940-469	Sequence 469, App
C 34	738	20.6	876	11	US-09-957-708-3	Sequence 3, Appl1
C 35	720	20.1	812	9	US-09-759-143-471	Sequence 471, App
C 36	720	20.1	812	9	US-09-780-669-471	Sequence 471, App
C 37	720	20.1	812	9	US-09-822-827-471	Sequence 471, App
C 38	720	20.1	812	10	US-09-895-793-471	Sequence 471, App
C 39	720	20.1	812	10	US-09-895-814-471	Sequence 471, App
C 40	720	20.1	812	12	US-10-144-678A-471	Sequence 471, App
C 41	720	20.1	812	13	US-10-012-896-471	Sequence 471, App
C 42	720	20.1	812	14	US-10-010-940-471	Sequence 471, App
C 43	524	14.6	684	8	US-08-926-626-7	Sequence 7, Appl1
C 44	524	14.6	684	12	US-10-191-252-7	Sequence 7, Appl1
C 45	473	13.2	597	12	US-10-195-730-46	Sequence 46, Appl1

ALIGNMENTS

RESULT 1
US-09-759-143-690
Sequence 690, Application US/09759143
Patent No. US200202248A1
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Jiang, Yuqui
APPLICANT: Henderson, Robert A.
APPLICANT: Kalos, Michael D.
APPLICANT: Fanger, Gary R.
APPLICANT: Retter, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Day, Craig H.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Darrick
APPLICANT: Wang, Aljun
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Hepler, William
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
FILE REFERENCE: 210121.427C23
CURRENT APPLICATION NUMBER: US/09/759,143
CURRENT FILING DATE: 2001-01-12
NUMBER OF SEQ ID NOS: 934
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 690
LENGTH: 3923
TYPE: DNA
ORGANISM: Homo saplen
US-09-759-143-690
Query Match 84.8%; Score 3036; DB 9; Length 3923;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3036; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	I	ACAGAGAATATGCAATGTGCCGAGAACTGGCATCAGAAAAACAGAGGGAGATTGTGT	60
Db	1	ACAGAGAATAATAGCAAGTGCAGGAAGCTGGCATCAGAAAAACAGAGGGAGATTGTGT	60
QY	61	GGCTCACCCCGGGGAGACAGAGAAATCTGCATGTGGGAAGACCCTGATGATTCAGAG	120
Db	61	GGCTCAGCCGAGGGAGACAGAGAAATCTGCATGTGGGAAGACCCTGATGATTCAGAG	120
QY	121	GAAATTACAACACATTTACTTAGTGTTTTAATGACACACAGATTAATTAAGTAAAGCTA	180
Db	121	GAAATTACAACACATTTACTTAGTGTTTTAATGACACACAGATTAATTAAGTAAAGCTA	180
QY	181	GTCGCGCTGTAGTCTCTCTCAGTACACAGGGCTGATCACCATCGAGGGCACTTCTGAG	240
Db	181	GTCGCGCTGTAGTCTCTCTCAGTACACAGGGCTGATCACCATCGAGGGCACTTCTGAG	240
QY	241	TACTAGTGCAGCAAGAAGACTCTCAGACATCTGAATGGCGGGGTAGAAATTAAGAAA	300
Db	241	TACTAGTGCAGCAAGAAGACTCTCAGACATCTGAATGGCGGGGTAGAAATTAAGAAA	300
QY	301	GGCTGCTGACTTTTACCATCTGAGGCGACACATCTGCTGAAATGAGATTAATTAACATCAC	360
Db	301	GGCTGCTGACTTTTACCATCTGAGGCGACACATCTGCTGAAATGAGATTAATTAACATCAC	360
QY	361	TAGAAACAGCAGAATGACATTAATGTGTCTAAGTGTACATGTTTTGTCACATTTCCAG	420
Db	361	TAGAAACAGCAGAATGACATTAATGTGTCTAAGTGTACATGTTTTGTCACATTTCCAG	420
QY	421	CCCCCTTTAAATPCTCCACACACACAGAAAGCACAAAAGAGACAGACATCCCTGGGAGA	480
Db	421	CCCCCTTTAAATPCTCCACACACAGAAAGCACAAAAGAGACAGACATCCCTGGGAGA	480
QY	481	AATGCGCGCGCCCATCTTGGGTCAATGATGAGCCTCGCCCTGTGCTCCGCTTGT	540
Db	481	AATGCGCGCGCCCATCTTGGGTCAATGATGAGCCTCGCCCTGTGCTCCGCTTGT	540
QY	541	GAGGAGAGACATTTGAAAAATGATTAATGTGTCTTTAAAGATGGCGAGAAAAACAGA	600
Db	541	GAGGAGAGACATTTGAAAAATGATTAATGTGTCTTTAAAGATGGCGAGAAAAACAGA	600
QY	601	TCCGTGTGGATTTATTTTGAACGGGATTAACGATTTGAAATGAATCAATCCAAAGTAG	660
Db	601	TCCGTGTGGATTTATTTTGAACGGGATTTACGATTTGAAATGAATCAATCCAAAGTAG	660
QY	661	CATTACCATGAGAGAAACAGACGAAAAATCTGTATGCTTACACAAGCATGCAACA	720
Db	661	CATTACCATGAGAGAAACAGACGAAAAATCTGTATGCTTACACAAGCATGCAACA	720
QY	721	AACAAATGGAATTAAGTATGATGACATGAGCAGCCAGCTGGGGAGAGATTAACACGGG	780
Db	721	AACAAATGGAATTAAGTATGATGACATGAGCAGCCAGCTGGGGAGAGATTAACACGGG	780
QY	781	GCAGAGGGTCAGGANTCTGGCCGCTGCTGCTAAACTGTGCGTTCTAATACCAATCATTTTC	840
Db	781	GCAGAGGGTCAGGANTCTGGCCGCTGCTGCTAAACTGTGCGTTCTAATACCAATCATTTTC	840
QY	841	ATATTTCAACCCCTCAAAAACAAGCTGTTGTAATCTGATCTCAGCGTTCTCTGG	900
Db	841	ATATTTCAACCCCTCAAAAACAAGCTGTTGTAATCTGATCTCAGCGTTCTCTGG	900
QY	901	CCCAACATTTCTCATATATATCCAGCCACACTCATTTTAAATATTAGTTCCAGATCTGTA	960
Db	901	CCCAACATTTCTCATATATATCCAGCCACACTCATTTTAAATATTAGTTCCAGATCTGTA	960
QY	961	CTGTGACCTTTCTACCTGTAGAAATACATTAATCTATTTGTTCAAAACCCCTCGTGT	1020
Db	961	CTGTGACCTTTCTACCTGTAGAAATACATTAATCTATTTGTTCAAAACCCCTCGTGT	1020
QY	1021	GCTGCGCTAATATGTAGCTGACTGTTTTCTCAAAGAGTGTCTGGCCCGAGGGAAATCTGT	1080
Db	1021	GCTGCGCTAATATGTAGCTGACTGTTTTCTCAAAGAGTGTCTGGCCCGAGGGAAATCTGT	1080
QY	1081	AACAGGCTGGAGAGCATCTCAAGATCTTTCCAGGGTTTACTTACTAGCACACAGCATGA	1140

Db	1081	AAACAGCGTGGGAAGCATCTCAAGATCTTTCCAGGGTATACTTACATAGACACACAGTGA	1144
Qy	1141	TCATTACGGAGGAAATTAATCTATACAACTCATCTCCAGTGTCTTTGGCCATACAGAAAT	1200
Db	1141	TCATTACGGAGGAAATTAATCTATACAACTCATCTCCAGTGTCTTTGGCCATACAGAAAT	1200
Qy	1201	TCATTTCACACTTTGTGGCCATTCCTCAAGACCTCAAAATGTCATTCCATTATATCA	1266
Db	1201	TCATTTCACACTTTGTGGCCATTCCTCAAGACCTCAAAATGTCATTCCATTATATCA	1266
Qy	1261	GGATTAACTTTTTTTTTTAACCTGAGAAATTCATGTTACATGCACTGATGGAATTTA	1320
Db	1261	GGATTAACTTTTTTTTTTAACCTGAGAAATTCATGTTACATGCACTGATGGAATTTA	1320
Qy	1321	ATTACATATTTTGTGTTCCAGTGCAGAAAGTGCATAGTCCCTTATCCCTCCCTTGTT	1380
Db	1321	ATTACATATTTTGTGTTCCAGTGCAGAAAGTGCATAGTCCCTTATCCCTCCCTTGTT	1380
Qy	1381	GATTTTTTTTCCAGATAAAGTTAAATGCTTAGCTTAGCTGAGGCTGATATACAGAC	1440
Db	1381	GATTTTTTTTCCAGATAAAGTTAAATGCTTAGCTTAGCTGAGGCTGATATACAGAC	1440
Qy	1441	AACCTCTCCCATCCCTCCAGCCTTATCTGTATACATCAACCCCTCCCTTACACCT	1500
Db	1441	AACCTCTCCCATCCCTCCAGCCTTATCTGTATACATCAACCCCTCCCTTACACCT	1500
Qy	1501	AAACAAAATCTAAGTTGTAAATCTGTAACATGTGAGACATACATTTTCCCTTGCT	1560
Db	1501	AAACAAAATCTAAGTTGTAAATCTGTAACATGTGAGACATACATTTTCCCTTGCT	1560
Qy	1561	GAGAAAGCTCTCTCTCTCTTAAATCTAGAAATGATGTAAATGTTTGAATAAGTTGACTA	1620
Db	1561	GAGAAAGCTCTCTCTCTCTTAAATCTAGAAATGATGTAAATGTTTGAATAAGTTGACTA	1620
Qy	1621	TCCTTACTTCATCAAGAAAGGACACATGTGATTCATCATCATGTGACACAGCAATA	1680
Db	1621	TCCTTACTTCATCAAGAAAGGACACATGTGATTCATCATCATGTGACACAGCAATA	1680
Qy	1681	CTAAAGAGTAAATTTGATTATATAGAGTTAGATTAATATATGAAATATGCAAGGCCACAGA	1740
Db	1681	CTAAAGAGTAAATTTGATTATATAGAGTTAGATTAATATATGAAATATGCAAGGCCACAGA	1740
Qy	1741	GGGAATGTTTATGGGGCAGCTTTGTACACCTTGGATGTGAAGCAAGGACAGGAACTCA	1800
Db	1741	GGGAATGTTTATGGGGCAGCTTTGTACACCTTGGATGTGAAGCAAGGACAGGAACTCA	1800
Qy	1801	TAGTATCTTATATATATATCACTTCTCTCTCTATCAATATCAACAAACAGCTTTT	1860
Db	1801	TAGTATCTTATATATATATCACTTCTCTCTCTATCAATATCAACAAACAGCTTTT	1860
Qy	1861	CACACAATTCAGCAGCTGCAATTCGCCAAAGTAACTTATCCATTCATAGTGAAGTGC	1920
Db	1861	CACACAATTCAGCAGCTGCAATTCGCCAAAGTAACTTATCCATTCATAGTGAAGTGC	1920
Qy	1921	GCTTATAGATTTTGGCAATCATCTAGTGTCACTTATCTCAACTTTGAAATGTGTTGTCC	1980
Db	1921	GCTTATAGATTTTGGCAATCATCTAGTGTCACTTATCTCAACTTTGAAATGTGTTGTCC	1980
Qy	1981	TTGTAGTTAATGAAAGAAATAGGCGACTTTGTGAGCGCACTTAAAGGTTCACTCTGGC	2040
Db	1981	TTGTAGTTAATGAAAGAAATAGGCGACTTTGTGAGCGCACTTAAAGGTTCACTCTGGC	2040
Qy	2041	AATAAAGAAATTTACAAAGAGCTACACAGGACAGTGTGAAGAGCTGTGTGTGTGTGT	2100
Db	2041	AATAAAGAAATTTACAAAGAGCTACACAGGACAGTGTGAAGAGCTGTGTGTGTGTGT	2100
Qy	2101	GT	2160
Db	2101	GT	2160
Qy	2161	TTAAACACAGCATGTTTCAAAATGGCACATATGAGCTGCAATGATATCAACACATAT	2220
Db	2161	TTAAACACAGCATGTTTCAAAATGGCACATATGAGCTGCAATGATATCAACACATAT	2220

|||||
Db 661 CATTACCAATGAGAGGAAAACAGACGAGAAAATCTTGATGGCTTACAGACATGCACA 720
Qy 721 AACAAATGGAATACGTGTGATGACATGAGGACGACGCTGGGAGAGATTAACACGGG 780
Db 721 AACAAATGGAATACGTGTGATGACATGAGGACGACGCTGGGAGAGATTAACACGGG 780
Qy 781 GCAGAGGTCAGAGATTCGTGGCCCTGCTGCTTAACCTGTGCGTTCAATACCAATCATTT 840
Db 781 GCAGAGGTCAGAGATTCGTGGCCCTGCTGCTTAACCTGTGCGTTCAATACCAATCATTT 840
Qy 841 AATATTTCAACCCCAAAACAAGAGCTGTTGTAATCTGATCTCAGAGGTTCTCTGGG 900
Db 841 AATATTTCAACCCCAAAACAAGAGCTGTTGTAATCTGATCTCAGAGGTTCTCTGGG 900
Qy 901 CCCAATCTCCATATATATCCAGCCACACATCTTTTAATATTAATTTAGTTCCAGATCTGTA 960
Db 901 CCCAATCTCCATATATATCCAGCCACACATCTTTTAATATTAATTTAGTTCCAGATCTGTA 960
Qy 961 CTGTGACCTTTCTACACCTGTGAGATTAACATTAATCTTTGTTCAAGACCTTCGTGT 1020
Db 961 CTGTGACCTTTCTACACCTGTGAGATTAACATTAATCTTTGTTCAAGACCTTCGTGT 1020
Qy 1021 GCTGCTTAATATATAGTGTGAGTGTCTTTCTTAAGAGAGTGTCTGGCCAGGAGATCTGTG 1080
Db 1021 GCTGCTTAATATATAGTGTGAGTGTCTTTCTTAAGAGAGTGTCTGGCCAGGAGATCTGTG 1080
Qy 1081 AACAGGCTGGAGACATCTCAAGATCTTTCCAGGGTTATTAATTAATTAACACACAGCATGA 1140
Db 1081 AACAGGCTGGAGACATCTCAAGATCTTTCCAGGGTTATTAATTAATTAACACACAGCATGA 1140
Qy 1141 TCATTAGGAGTGAATTAATTAATCAACATCATCTCTGCTCTTGGCCATCTGAAT 1200
Db 1141 TCATTAGGAGTGAATTAATTAATCAACATCATCTCTGCTCTTGGCCATCTGAAT 1200
Qy 1201 TCATTTCCACTTTTGTGCCCATCTCTCAAGACCTCAAAATGCAATTCATTAATATCA 1260
Db 1201 TCATTTCCACTTTTGTGCCCATCTCTCAAGACCTCAAAATGCAATTCATTAATATCA 1260
Qy 1261 GGATTAACCTTTTAACTGGAAGATTTCAATGTTTACATGAGAGCTATGGGAATTTA 1320
Db 1261 GGATTAACCTTTTAACTGGAAGATTTCAATGTTTACATGAGAGCTATGGGAATTTA 1320
Qy 1321 ATTAACATTTTGTTTTCCAGTSCAAGATGACTTAAGTCTTTTACCTCCCTTTGTT 1380
Db 1321 ATTAACATTTTGTTTTCCAGTSCAAGATGACTTAAGTCTTTTACCTCCCTTTGTT 1380
Qy 1381 GATTTTTCAGATTAATTAATGCTTAGGCTGTACTGAGGCTGTATACAGAC 1440
Db 1381 GATTTTTCAGATTAATTAATGCTTAGGCTGTACTGAGGCTGTATACAGAC 1440
Qy 1441 AGCCTCTCCCATCCCTCCAGCCTTAATCTGTCAATCACCATCAACCCCTCCCATACACCT 1500
Db 1441 AGCCTCTCCCATCCCTCCAGCCTTAATCTGTCAATCACCATCAACCCCTCCCATACACCT 1500
Qy 1501 AAAAATAATCTAATCTGTAATCTTCTGAACATGTCAGAGCATATATTTCTCTCTGCT 1560
Db 1501 AAAAATAATCTAATCTGTAATCTTCTGAACATGTCAGAGCATATATTTCTCTCTGCT 1560
Qy 1561 GAGAGCTCTCTCTGCTCTTAATCTAGATGATGTAAGTTTGAATTAAGTTGACTA 1620
Db 1561 GAGAGCTCTCTCTGCTCTTAATCTAGATGATGTAAGTTTGAATTAAGTTGACTA 1620
Qy 1621 TCTTACTTCATGCAAGAGGACACATATGAGATTCATCATCATGAGACACAAATA 1680
Db 1621 TCTTACTTCATGCAAGAGGACACATATGAGATTCATCATCATGAGACACAAATA 1680
Qy 1681 CTAAATGTAATTTGATTAAGAGTTTATAGATTAATTAATTAATTAAGAGCCACAGA 1740
Db 1681 CTAAATGTAATTTGATTAAGAGTTTATAGATTAATTAATTAATTAAGAGCCACAGA 1740
Qy 1741 GGGAAATGTTATGGGACGTTTGTAAAGCTGGAGTGAAGCAAGGACAGGAACCTCA 1800
Db 1741 GGGAAATGTTATGGGACGTTTGTAAAGCTGGAGTGAAGCAAGGACAGGAACCTCA 1800

Db 1741 GGGAAATGTTATGGGACGTTTGTAAAGCTGGAGTGAAGCAAGGACAGGAACCTCA 1800
Qy 1801 TAGATCTTAATATAATATACTCATTTCTATCTATCTATCAATATATCAACAAAGCTTTT 1860
Db 1801 TAGATCTTAATATAATATACTCATTTCTATCTATCTATCAATATATCAACAAAGCTTTT 1860
Qy 1861 CACAGATTCATGCAGTGCAAATCCCAAAGTAACCTTTATCCATTTTCATGTGAGTGC 1920
Db 1861 CACAGATTCATGCAGTGCAAATCCCAAAGTAACCTTTATCCATTTTCATGTGAGTGC 1920
Qy 1921 GCTTTAGATTTTGGCAATCATATCTGCTGCTATCTATCAACTTTGAGATGTTTGGC 1980
Db 1921 GCTTTAGATTTTGGCAATCATATCTGCTGCTATCTATCAACTTTGAGATGTTTGGC 1980
Qy 1981 TTGATTAATTTGAAGAAATAGGCACTCTGTGAGCCACTTAAGGTTCACTCTGGC 2040
Db 1981 TTGATTAATTTGAAGAAATAGGCACTCTGTGAGCCACTTAAGGTTCACTCTGGC 2040
Qy 2041 AATAAGAAATTTACAAAGAGTACTCAGGACCACTTTGTAAGAGCTCTGTGTGTGT 2100
Db 2041 AATAAGAAATTTACAAAGAGTACTCAGGACCACTTTGTAAGAGCTCTGTGTGTGT 2100
Qy 2101 GT 2160
Db 2101 GT 2160
Qy 2161 TTAAACAAGCATGTTTCAAAATGACATATGACATGACATGATATCAACACCATAT 2220
Db 2161 TTAAACAAGCATGTTTCAAAATGACATATGACATGACATGATATCAACACCATAT 2220
Qy 2221 CTGATTAATCTCCAGTAATGTGATTAATGATCTGTGTGTGTGTGTGTGTGTGTGT 2280
Db 2221 CTGATTAATCTCCAGTAATGTGATTAATGATCTGTGTGTGTGTGTGTGTGTGTGT 2280
Qy 2281 TTCAAAAGAGAGCTGGAAATGAGCAACCAATATGATTAATCTAACTTACCTCAATCA 2340
Db 2281 TTCAAAAGAGAGCTGGAAATGAGCAACCAATATGATTAATCTAACTTACCTCAATCA 2340
Qy 2341 GCTACACAGCTCTTGACATATATTTGTAAGAACCTGCGCATTTGTGGGTTCTCTTAAGC 2400
Db 2341 GCTACACAGCTCTTGACATATATTTGTAAGAACCTGCGCATTTGTGGGTTCTCTTAAGC 2400
Qy 2401 AAAATACCTTGATTAAGTCTAGCTGGGCTGTGCTATCAGGCGTTTGAAGAAATTTCAA 2460
Db 2401 AAAATACCTTGATTAAGTCTAGCTGGGCTGTGCTATCAGGCGTTTGAAGAAATTTCAA 2460
Qy 2461 TTCTCAGAGAGGACAGATTTGAATTCCTCACTTTTGAAGATCAATTCACAGGTTTG 2520
Db 2461 TTCTCAGAGAGGACAGATTTGAATTCCTCACTTTTGAAGATCAATTCACAGGTTTG 2520
Qy 2521 GAGAGATTCAGACAGCTCAGGTCCTTCACTAATGTCCTGAACCTTCCTGCTCTTGG 2580
Db 2521 GAGAGATTCAGACAGCTCAGGTCCTTCACTAATGTCCTGAACCTTCCTGCTCTTGG 2580
Qy 2581 TGTTCATGAGATGATGATTAATTAATGTTTATCTTTGAACGTATGCTATAGAGAAATA 2640
Db 2581 TGTTCATGAGATGATGATTAATTAATGTTTATCTTTGAACGTATGCTATAGAGAAATA 2640
Qy 2641 TAAAGATCTGAGGATATCAACATTAAGGATTTCAAGAAATTTAGATTTAAAGCTCA 2700
Db 2641 TAAAGATCTGAGGATATCAACATTAAGGATTTCAAGAAATTTAGATTTAAAGCTCA 2700
Qy 2701 CTGTCAAAAGAAAGAAAGATTAAGAAAGTCTGAGCTGTCTGCCATCTCTGTGA 2760
Db 2701 CTGTCAAAAGAAAGAAAGATTAAGAAAGTCTGAGCTGTCTGCCATCTCTGTGA 2760
Qy 2761 GCCACAAACCAACAGAGAGCCCAACGATGTCTAGATCTCTTAATTAAGAAACCAAGT 2820
Db 2761 GCCACAAACCAACAGAGAGCCCAACGATGTCTAGATCTCTTAATTAAGAAACCAAGT 2820
Qy 2821 TCATGAGTGAATCTCTATTTATGAGTGAAGCTTCTGGGCATCTCTGGCTCTCTCT 2880
Db 2821 TCATGAGTGAATCTCTATTTATGAGTGAAGCTTCTGGGCATCTCTGGCTCTCTCT 2880

OY	2881	GACACATATAGCTTTCAGCCTTTGCTCCACGACTTTATCTTTCTCCAACACATCGC	2940
Db	2881	GACCAATATTAGCTTTCAGCCTTTGCTCCACGACTTTATCTTTCTCCAACACATCGC	2940
OY	2941	TTACCATTCCCTCTCTGCTCTGTGGCTTTGGAATTTGCCCAAGAATTTTAACGACTCT	3000
Db	2941	TTACCATTCCCTCTCTGCTCTGTGGCTTTGGAATTTGCCCAAGAATTTTAACGACTCT	3000
OY	3001	CAAGCTTTTCTTCATCCCACACATACTGTAAT	3036
Db	3001	CAAGCTTTTCTTCATCCCACACATACTGTAAT	3036

RESULT 3

```

US-09-822-827-690
: Sequence 690, Application US/09822827
: Patent No. US20020081680A1
:
: GENERAL INFORMATION:
:
: APPLICANT: Xu, Jiangchun
:
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
: TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
:
: FILE REFERENCE: 210121.534C1
:
: CURRENT APPLICATION NUMBER: US/09/822.827
:
: CURRENT FILING DATE: 2001-03-28
:
: NUMBER OF SEQ ID NOS: 982
:
: SOFTWARE: FastSeq for Windows Version 3.0
:
: SEQ ID NO 690
:
: LENGTH: 3923
:
: TYPE: DNA
:
: ORGANISM: Homo sapien
:
US-09-822-827-690

```

Query Match	84.8%;	Score 3036;	DB 9;	Length 3923;
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches 3036;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

OY	1	ACACAAGAAATAGCAAGTCCGACAAAGCTGGCATACAGAAAACAGAGGGAGATTGTG	60
Db	1	ACACAAGAAATAGCAAGTCCGACAAAGCTGGCATACAGAAAACAGAGGGAGATTGTG	60
OY	61	GGCTGCAGCCGAGGAGGACACAGGAAGATCTCATGTGTGGAAAGGACCTGATATACAGAG	120
Db	61	GGCTGCAGCCGAGGAGGACACAGGAAGATCTCATGTGTGGAAAGGACCTGATATACAGAG	120
OY	121	GAATTACACACATATCTTACTTATGTGTTTCAATGAACACCAAAATTAATTAAGTGAAGAGCTA	180
Db	121	GAATTACACACATATCTTACTTATGTGTTTCAATGAACACCAAAATTAATTAAGTGAAGAGCTA	180
OY	181	GTCCGCTGTGATGTTCTCTCACTGACACACAGGGCTGGATCACCATGACGGCACTTCTGAG	240
Db	181	GTCCGCTGTGATGTTCTCTCACTGACACACAGGGCTGGATCACCATGACGGCACTTCTGAG	240
OY	241	TACTCAGTGCACGCAAGAAAGACTACAGACATCTTCATGGCAGGGGTGAGAAATPAGAAA	300
Db	241	TACTCAGTGCACGCAAGAAAGACTACAGACATCTTCATGGCAGGGGTGAGAAATPAGAAA	300
OY	301	GGCTGCTGACTTACCATCTGAGGCCACACATCTGCTGAATGAGATTAATTAATCATAC	360
Db	301	GGCTGCTGACTTACCATCTGAGGCCACACATCTGCTGAATGAGATTAATTAATCATAC	360
OY	361	TAGAAACAGCAAGATGACAAATATATATGTCTAAGTAGTGACATGTTTTGCACATTTCCAG	420
Db	361	TAGAAACAGCAAGATGACAAATATATATGTCTAAGTAGTGACATGTTTTGCACATTTCCAG	420
OY	421	CCCCCTTAAATATCACAACACACAGGAAGCAAAAGGAACACAGAGATCCCGGGGAGA	480
Db	421	CCCCCTTAAATATCACAACACACAGGAAGCAAAAGGAACACAGAGATCCCGGGGAGA	480
OY	481	AATGCCCGCGCCGACATCTTGGGTATCATGATGAGCTCGCCCTGTGCTGGTCCGCTGTG	540
Db	481	AATGCCCGCGCCGACATCTTGGGTATCATGATGAGCTCGCCCTGTGCTGGTCCGCTGTG	540

QY	541	GAGGGAAGGACATTAAGAAATGATTTGATGCTGCTTAAAGGATGGGGGAGGAAACAGA	600
Db	541	GAGGGAAGGACATTAAGAAATGATTTGATGCTGCTTAAAGGATGGGGGAGGAAACAGA	600
QY	601	TCCGTGGTGATATTTATTTGAAACGGGATTCAGATTTTGAAATGAAGTCCAAAGTGAG	660
Db	601	TCCGTGGTGATATTTATTTTGAACGGGATTCAGATTTTGAAATGAAGTCCAAAGTGAG	660
QY	661	CATTACCAATGAGAGGAAACAGACGAGAAAATCTTGATGGCTTCACAGAATGCACA	720
Db	661	CATTACCAATGAGAGGAAACAGACGAGAAAATCTTGATGGCTTCACAGAATGCACA	720
QY	721	AACCAATGGAATCTGTGATGAATGAGGAGCCAAAGCTGGGGAGAGATTAACACAGGG	780
Db	721	AACCAAAATGGAATCTGTGATGAATGAGGAGCCAAAGCTGGGGAGAGATTAACACAGGG	780
QY	781	GCAAGGGTCAGAAATTCGGCCCTGCTGCCAAACCTGGCTGTATACCAAAATCATTTTC	840
Db	781	GCAAGGGTCAGAAATTCGGCCCTGCTGCCAAACCTGGCTGTATATACCAAAATCATTTTC	840
QY	841	ATATTTTCACCCCTCAAAACAAAGCTGTGTAATCTGATCTCAGGGTTCCTTCGGG	900
Db	841	ATATTTTCACCCCTCAAAACAAAGCTGTGTAATCTGATCTCAGGGTTCCTTCGGG	900
QY	901	CCCAACATCTCCATATATCCAGCCACACATATTTTAATATTTAGTTCCAGATCTGTA	960
Db	901	CCCAACATCTCCATATATCCAGCCACACATATTTTAATATTTAGTTCCAGATCTGTA	960
QY	961	CTGAGACCTTCTACACGTAGATTAACATTAATCTGTTGTGAAAGACCCCTCGGTT	1020
Db	961	CTGAGACCTTCTACACGTAGATTAACATTAATCTGTTGTGAAAGACCCCTCGGTT	1020
QY	1021	GCTGCCTAATATGATGACTGACTGTTTTCTTAAGAGAGTCTGCGCCAGGGATCTGTG	1080
Db	1021	GCTGCCTAATATGATGACTGACTGTTTTCTTAAGAGAGTCTGCGCCAGGGATCTGTG	1080
QY	1081	AACAGGCTGGGAAGCATCTCAAGATCTTTCCAGGGTATTAATCTAGTACACACAGCATGA	1140
Db	1081	AACAGGCTGGGAAGCATCTCAAGATCTTTCCAGGGTATTAATCTAGTACACACAGCATGA	1140
QY	1141	TCATTAGGAGTGAATTAATTAATCAACATATCTCAGTCTGTCGCTTGGCCCTACTGGAAT	1200
Db	1141	TCATTAGGAGTGAATTAATTAATCAACATATCTCAGTCTGTCGCTTGGCCCTACTGGAAT	1200
QY	1201	TCATTTGCCATTTTGTGCCCCATCTCAGACCTCAAAATGTCATTCATTAATATACAA	1260
Db	1201	TCATTTGCCATTTTGTGCCCCATCTCAGACCTCAAAATGTCATTCATTAATATACAA	1260
QY	1261	GGATTTACTTTTTTTTTAACCTGGAAGAAATTCATGTTACATGACACTATGGAAATTTA	1320
Db	1261	GGATTTACTTTTTTTTTAACCTGGAAGAAATTCATGTTACATGACACTATGGAAATTTA	1320
QY	1321	ATTACATATTTTGTTCCTCACTGCAAAAGATGACATTAAGCTTTATGCCCTTCCTTGT	1380
Db	1321	ATTACATATTTTGTTCCTCACTGCAAAAGATGACATTAAGCTTTATGCCCTTCCTTGT	1380
QY	1381	GATTTTTTTTCCAGATTAAGTAAAAATGCTTAGCCTGTACTGAGGCTGATACAGAC	1440
Db	1381	GATTTTTTTTCCAGATTAAGTAAAAATGCTTAGCCTGTACTGAGGCTGATACAGAC	1440
QY	1441	AGCCTCTCCCATCCCTCCAGCCTTATCTGTGATCACCATCAACCCCTCCCATACCACT	1500
Db	1441	AGCCTCTCCCATCCCTCCAGCCTTATCTGTGATCACCATCAACCCCTCCCATACCACT	1500
QY	1501	AAACAAAATCTAATCTGTAATTCCTTGCAACATGTCAGAGACATTAATTCCTTCGCT	1560
Db	1501	AAACAAAATCTAATCTGTAATTCCTTGCAACATGTCAGAGACATTAATTCCTTCGCT	1560
QY	1561	GAGAGGCTCTCTGCTGCTTAAATCTAGAAATGAAAGTTTGAAATTAAGTTGACTA	1620
Db	1561	GAGAGGCTCTCTGCTGCTTAAATCTAGAAATGAAAGTTTGAAATTAAGTTGACTA	1620
QY	1621	TCTTACTTCATGACAAAGAGGACATATAGATTATCATCATGACATGAGACACAATA	1680

|||||
Db 1621 TCTTACCTTCATGCAAGAGGACACATATGAGATTCTCATCATGACATGACAGCAATA 1680
OY 1681 CTAAGAAGTATTTGATTTATAGAGTTTATGATAATATATGAATGCAAGACCAAGA 1740
Db 1681 CTAAGAAGTATTTGATTTATAGAGTTTATGATAATATATGAATGCAAGACCAAGA 1740
OY 1741 GGGAAATGTTATGSGGACGTTTGTAAAGCTGGATGTGAAGCAAAAGGAGGAACTCA 1800
Db 1741 GGGAAATGTTATGSGGACGTTTGTAAAGCTGGATGTGAAGCAAAAGGAGGAACTCA 1800
OY 1801 TAGTATCTTAT 1860
Db 1801 TAGTATCTTAT 1860
OY 1861 CACAGAATTCATGACAGTGCATATCCCAAGTAACCTTTATCCATTTTCATGAGTATGC 1920
Db 1861 CACAGAATTCATGACAGTGCATATCCCAAGTAACCTTTATCCATTTTCATGAGTATGC 1920
OY 1921 GCTTTAGAAATTTGGCAAAATCATACTGCTCATATGCTCAACTTTGAGATGTGTGTC 1980
Db 1921 GCTTTAGAAATTTGGCAAAATCATACTGCTCATATGCTCAACTTTGAGATGTGTGTC 1980
OY 1981 TTGTAGTAAATTTGAAGAAATAGGGCACTCTGTGAGCACTTTAGGGTTCACTCTGCGC 2040
Db 1981 TTGTAGTAAATTTGAAGAAATAGGGCACTCTGTGAGCACTTTAGGGTTCACTCTGCGC 2040
OY 2041 AATAAGAAATTTACAAAGAGCTTACAGAGCAGTTGTAAGAGCTGTGTGTGTGTGTGT 2100
Db 2041 AATAAGAAATTTACAAAGAGCTTACAGAGCAGTTGTAAGAGCTGTGTGTGTGTGTGT 2100
OY 2101 GT 2160
Db 2101 GT 2160
OY 2161 TTTAAACAAAGCATGTTTCAATGAGCTATGAGTGGCAATGATGTCACCCACCATAT 2220
Db 2161 TTTAAACAAAGCATGTTTCAATGAGCTATGAGTGGCAATGATGTCACCCACCATAT 2220
OY 2221 CTCATTTATCTCCAGTAATGTGATTAATGTGATCTGTGTGTGTGTGTGTGTGTGTGT 2280
Db 2221 CTCATTTATCTCCAGTAATGTGATTAATGTGATCTGTGTGTGTGTGTGTGTGTGTGT 2280
OY 2281 TTTCACAAAGAGCTGGAAGGAAAGCAACCAATATGATTAATCTTAATCTTAATCTTA 2340
Db 2281 TTTCACAAAGAGCTGGAAGGAAAGCAACCAATATGATTAATCTTAATCTTAATCTTA 2340
OY 2341 GCTACACAGCTGCTGACATATATGTTGTGAAGACAGCTGCAATTTGTGGTCTCTTAAGC 2400
Db 2341 GCTACACAGCTGCTGACATATATGTTGTGAAGACAGCTGCAATTTGTGGTCTCTTAAGC 2400
OY 2401 AAAATTTCTTGCAATTAAGTCTGAGCTGGGGCTGTGCATCAGGCGTTTGAGAAATTTTCA 2460
Db 2401 AAAATTTCTTGCAATTAAGTCTGAGCTGGGGCTGTGCATCAGGCGTTTGAGAAATTTTCA 2460
OY 2461 TTTCCACAGAGAGGCAAGATTTGGAATCCCTCATCTTTTGAAGAAATTTTCAAGGTTTG 2520
Db 2461 TTTCCACAGAGAGGCAAGATTTGGAATCCCTCATCTTTTGAAGAAATTTTCAAGGTTTG 2520
OY 2521 GAGAGATTCAGACAGCTGAGCTGCTTCACTAATGCTGGAAGCTGCTGCTGCTGCTGCT 2580
Db 2521 GAGAGATTCAGACAGCTGAGCTGCTTCACTAATGCTGGAAGCTGCTGCTGCTGCTGCT 2580
OY 2581 TGTTCATGATAGTCCATTAATATGTTATCTTTGAAGCTGATCTCATAGAGAGATA 2640
Db 2581 TGTTCATGATAGTCCATTAATATGTTATCTTTGAAGCTGATCTCATAGAGAGATA 2640
OY 2641 TAAGAACTGAGAGATATCAACATTTAGGGAATTTCAAGAAATTTTGAAGCTGATCA 2700
Db 2641 TAAGAACTGAGAGATATCAACATTTAGGGAATTTCAAGAAATTTTGAAGCTGATCA 2700
OY 2701 CTGCTCAAAAGAAACCAAGATACAAAGAACTGAGCTGCTGCTGCTGCTGCTGCTGCTGCT 2760
|||||

Db 2701 CTGCTCAAAAGAAACCAAGATACAAAGAACTGTGAGCTGTATCTGCCATCTGTGA 2760
OY 2761 GCCACACCAACAGAGAGGAGCCACAGCATGTGTGAGATCTTAATTCAGAAAGACAGTG 2820
Db 2761 GCCACACCAACAGAGAGGAGCCACAGCATGTGTGAGATCTTAATTCAGAAAGACAGTG 2820
OY 2821 TCATGAGTTGAATTCCTCTATTTATGATGCAAGCTTGTGGCCATCTGTGCTCTCTT 2880
Db 2821 TCATGAGTTGAATTCCTCTATTTATGATGCAAGCTTGTGGCCATCTGTGCTCTCTT 2880
OY 2881 GACACATATATAGCTTCTAGCTTGTGCTTGTGAGCTTTTATCTTTTTCACAAATATGC 2940
Db 2881 GACACATATATAGCTTCTAGCTTGTGCTTGTGAGCTTTTATCTTTTTCACAAATATGC 2940
OY 2941 TTACCAATCT 3000
Db 2941 TTACCAATCT 3000
OY 3001 CAAGCTTTTCTTCATCCCAACCACTAACCTGAAT 3036
Db 3001 CAAGCTTTTCTTCATCCCAACCACTAACCTGAAT 3036

RESULT 4
US-09-895-793-690
; Sequence 690, Application US/09895793
; Publication No. US20020192763A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yugu
; APPLICANT: Kalos, Michael D.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedrick, Thomas S.
; APPLICANT: Carter, Darlick
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skelky, Yasir A.W.
; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Vinals de Bassols, Carlota
; APPLICANT: Foy, Teresa
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.534C2
; CURRENT APPLICATION NUMBER: US/09/895,793
; NUMBER OF SEQ ID NOS: 982
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 690
; LENGTH: 3923
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-895-793-690

Query Match 84.8%; Score 3036; DB 10; Length 3923;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3036; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ACAGAGAAATATGCAAGTCCCGAGAGCTGGCATCAGAAAAACAGAGGGAGATTGTGT 60
Db 1 ACAGAGAAATATGCAAGTCCCGAGAGCTGGCATCAGAAAAACAGAGGGAGATTGTGT 60
OY 61 GCGTCGACGCGAGGAGACAGAGAAATGCAATGATGGGGAAGGAGCTGATATACAGAG 120
|||||

[illegible]

2281 TTCACAAAAGCAGCTGGAATAGACACACAAATATGCAATTAATCTAACCTCTACCAATCA 2340
2281 TTCACAAAAGCAGCTGGAATAGACACACAAATATGCAATTAATCTAACCTCTACCAATCA 2340
2341 GCTACACAGCTGCTGACATATATGTTGTAAGACACCTGCACTTGTGGTCTCTTAAGC 2400
2341 GCTACACAGCTGCTGACATATATGTTGTAAGACACCTGCACTTGTGGTCTCTTAAGC 2400
2401 AAAATACCTTGCATTAAGTCTCAGCTGGGCTGTGCATCAGGCGGTTTGAAGAAATATCA 2460
2401 AAAATACCTTGCATTAAGTCTCAGCTGGGCTGTGCATCAGGCGGTTTGAAGAAATATCA 2460
2461 TTTCACAGCAAGACCAAGAAATTTGAATTCCTTCATCTTTTGAAGATCATTTACCGGTTTG 2520
2461 TTTCACAGCAAGACCAAGAAATTTGAATTCCTTCATCTTTTGAAGATCATTTACCGGTTTG 2520
2521 GAGAGGATTCAGACAGCTCAGGCTGCTTCACTAATGTCTGCACTTGTGACCTGCTTGG 2580
2521 GAGAGGATTCAGACAGCTCAGGCTGCTTCACTAATGTCTGCACTTGTGACCTGCTTGG 2580
2581 TGTTCATGAGATAGTCCAAATTAATATGTTATCTTTGAACGATGCTCATAGAGAGATA 2640
2581 TGTTCATGAGATAGTCCAAATTAATATGTTATCTTTGAACGATGCTCATAGAGAGATA 2640
2641 TAAAGACTCTGAGTATATCAACATTTAGGATTCAGAGAAATTTAGATTTAAGCTACA 2700
2641 TAAAGACTCTGAGTATATCAACATTTAGGATTCAGAGAAATTTAGATTTAAGCTACA 2700
2701 CTGGCAAAAGAACCAAGATACAAAGAACTGTGAGCTGTGATGCTGCCATCTCTGTGA 2760
2701 CTGGCAAAAGAACCAAGATACAAAGAACTGTGAGCTGTGATGCTGCCATCTCTGTGA 2760
2761 GCCACAAACCAAGAGAGACCAACGATGTCTGAGATCTTAAATCAAGAAACCAAGT 2820
2761 GCCACAAACCAAGAGAGACCAACGATGTCTGAGATCTTAAATCAAGAAACCAAGT 2820
2821 TCATGAGTTGAATCTCTATATTAAGATGAGTGTGAGCTGTGAGCTGTGAGCTGTGAG 2880
2821 TCATGAGTTGAATCTCTATATTAAGATGAGTGTGAGCTGTGAGCTGTGAGCTGTGAG 2880
2881 GACACATATTAAGCTTACGCTTGTGCTTCCAGCATTTTATCTTTTCCAAACATGCG 2940
2881 GACACATATTAAGCTTACGCTTGTGCTTCCAGCATTTTATCTTTTCCAAACATGCG 2940
2941 TTACCAATCCCTCTCTGCTGTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTG 3000
2941 TTACCAATCCCTCTCTGCTGTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTG 3000
3001 CAAGCTTTTCTTCATCCCAACCACTAACCTGAAT 3036
3001 CAAGCTTTTCTTCATCCCAACCACTAACCTGAAT 3036
3001 CAAGCTTTTCTTCATCCCAACCACTAACCTGAAT 3036
3001 CAAGCTTTTCTTCATCCCAACCACTAACCTGAAT 3036
RESULT 5
US-09-895-814-690
Publication No. US20020193296A1
GENERAL INFORMATION:
APPLICANT: Xu, Jianshun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Jiang, Yugu
APPLICANT: Kalos, Michael D.
APPLICANT: Retter, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Day, Craig H.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Derrick
APPLICANT: Li, Samuel X.
APPLICANT: Wang, Aijun
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Hepler, William T.

APPLICANT: Henderson, Robert A.
APPLICANT: Hural, John
APPLICANT: McNeill, Patricia D.
APPLICANT: Houghton, Raymond L.
APPLICANT: Vinals de Bassols, Carlota
APPLICANT: Foy, Teresa
APPLICANT: Fanger, Gary R.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
FILE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427C26
CURRENT APPLICATION NUMBER: US/09/895,814
CURRENT FILING DATE: 2001-06-29
NUMBER OF SEQ ID NOS: 990
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 690
LENGTH: 3923
TYPE: DNA
ORGANISM: Homo sapien
US-09-895-814-690
Query Match 84.8%; Score 3036; DB 10; Length 3923;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3036; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1 ACAGAGAAATAGCAAGTCCGAGAGCTGCAATCAGAAAAACAGAGGAGATTTGTGT 60
1 ACAGAGAAATAGCAAGTCCGAGAGCTGCAATCAGAAAAACAGAGGAGATTTGTGT 60
61 GCGTCAGCCGAGGAGAGCCAGAAATCTGATGTTGGGAGAGCCTGATGATACAGAG 120
61 GCGTCAGCCGAGGAGAGCCAGAAATCTGATGTTGGGAGAGCCTGATGATACAGAG 120
121 GAATTAACACATATATCTTATGTTTCAATGAACACCAAGATTAATGAAGAGCTA 180
121 GAATTAACACATATATCTTATGTTTCAATGAACACCAAGATTAATGAAGAGCTA 180
121 GAATTAACACATATATCTTATGTTTCAATGAACACCAAGATTAATGAAGAGCTA 180
121 GAATTAACACATATATCTTATGTTTCAATGAACACCAAGATTAATGAAGAGCTA 180
181 GTCCGCTGTGAGTCTCTCAATGACACAGAGCTGATCAGCATGAGGAGCTTCTGAG 240
181 GTCCGCTGTGAGTCTCTCAATGACACAGAGCTGATCAGCATGAGGAGCTTCTGAG 240
181 GTCCGCTGTGAGTCTCTCAATGACACAGAGCTGATCAGCATGAGGAGCTTCTGAG 240
241 TATCAGTGTGAGTCTCTCAATGACACAGAGCTGATCAGCATGAGGAGCTTCTGAG 300
241 TATCAGTGTGAGTCTCTCAATGACACAGAGCTGATCAGCATGAGGAGCTTCTGAG 300
241 TATCAGTGTGAGTCTCTCAATGACACAGAGCTGATCAGCATGAGGAGCTTCTGAG 300
241 TATCAGTGTGAGTCTCTCAATGACACAGAGCTGATCAGCATGAGGAGCTTCTGAG 300
301 GCGTCGATCTTACATCTGAGGCGCACATCTGCTGAATGAGATTAATTAATCAATCAC 360
301 GCGTCGATCTTACATCTGAGGCGCACATCTGCTGAATGAGATTAATTAATCAATCAC 360
301 GCGTCGATCTTACATCTGAGGCGCACATCTGCTGAATGAGATTAATTAATCAATCAC 360
301 GCGTCGATCTTACATCTGAGGCGCACATCTGCTGAATGAGATTAATTAATCAATCAC 360
361 TAGAAGACAGCAAGATGACAAATATATGTTAAGTACATGTTTGGACATTTTCAG 420
361 TAGAAGACAGCAAGATGACAAATATATGTTAAGTACATGTTTGGACATTTTCAG 420
421 CCCCTTAATATATCACACACACAGAGCAACAAAGAGACAGAGATCCCTGGGAGA 480
421 CCCCTTAATATATCACACACACAGAGCAACAAAGAGAGACAGAGATCCCTGGGAGA 480
481 AATGCCGCGCGCCATCTTGGGTCATGATGAGGCTGCGCTGTGCTGCTGCTGCTGCT 540
481 AATGCCGCGCGCCATCTTGGGTCATGATGAGGCTGCGCTGTGCTGCTGCTGCTGCTG 540
481 AATGCCGCGCGCCATCTTGGGTCATGATGAGGCTGCGCTGTGCTGCTGCTGCTGCTG 540
481 AATGCCGCGCGCCATCTTGGGTCATGATGAGGCTGCGCTGTGCTGCTGCTGCTGCTG 540
541 GAGGAGAGGACATTAAGAAATGAATGATGTGCTTAAAGATGAGGAGGAGAAACAGA 600
541 GAGGAGAGGACATTAAGAAATGAATGATGTGCTTAAAGATGAGGAGGAGAAACAGA 600
541 GAGGAGAGGACATTAAGAAATGAATGATGTGCTTAAAGATGAGGAGGAGAAACAGA 600
541 GAGGAGAGGACATTAAGAAATGAATGATGTGCTTAAAGATGAGGAGGAGAAACAGA 600
601 TCCGTTGTGATATTTATTTGAAGGAGATTTAGATTTGAATGAAGTACAAAGTGA 660
601 TCCGTTGTGATATTTATTTGAAGGAGATTTAGATTTGAATGAAGTACAAAGTGA 660
601 TCCGTTGTGATATTTATTTGAAGGAGATTTAGATTTGAATGAAGTACAAAGTGA 660
601 TCCGTTGTGATATTTATTTGAAGGAGATTTAGATTTGAATGAAGTACAAAGTGA 660
661 CATTAACATGAGAGGAGAAACAGAGCAAGAAATTTGATGCTTACAAAGATGACACA 720
661 CATTAACATGAGAGGAGAAACAGAGCAAGAAATTTGATGCTTACAAAGATGACACA 720
661 CATTAACATGAGAGGAGAAACAGAGCAAGAAATTTGATGCTTACAAAGATGACACA 720
661 CATTAACATGAGAGGAGAAACAGAGCAAGAAATTTGATGCTTACAAAGATGACACA 720
721 AACAAATGGAATATCTGATGACATGAGGAGCAAGCTGGGAGAGATTAACACGCG 780

|||||
Db 721 AACAAATGGAATGATGTGATGACATGAGGCAAGCCAGCTGGGAGGAGATACCAACGCG 780
OY 781 GGAGAGGGGACAGATTCGCGCCCTGCTGCTAAACGTGCGCTTCATACCAATCATCTTC 840
Db 781 GGAGAGGGGACAGATTCGCGCCCTGCTGCTAAACGTGCGCTTCATACCAATCATCTTC 840
OY 841 ATATTTCTAACCCCTCAAAACAAAGCTGTGTATATCTGATCTCAAGGCTTCCTGCG 900
Db 841 ATATTTCTAACCCCTCAAAACAAAGCTGTGTATATCTGATCTCAAGGCTTCCTGCG 900
OY 901 CCCAATCTCCATATATTCACAGCCACACTATTTTAAATATTTAGTCCAGATCTGTA 960
Db 901 CCCAATCTCCATATATTCACAGCCACACTATTTTAAATATTTAGTCCAGATCTGTA 960
OY 961 CTGTACCCCTTCTACACCTGATAGATTAATTAATCTACTCTCTTTGTCAAAGACCCCTGCTGT 1020
Db 961 CTGTACCCCTTCTACACCTGATAGATTAATTAATCTACTCTCTTTGTCAAAGACCCCTGCTGT 1020
OY 1021 GCTGCCATATATGTAGCTGACTGTTTTTCTTAAGAGAGTGTCTGCGCCAGGGGATCTGT 1080
Db 1021 GCTGCCATATATGTAGCTGACTGTTTTTCTTAAGAGAGTGTCTGCGCCAGGGGATCTGT 1080
OY 1081 AACAGGCTGGAGACATCTCAAGATCTTCCAGGGTTATACTAGACACAGCATGA 1140
Db 1081 AACAGGCTGGAGACATCTCAAGATCTTCCAGGGTTATACTAGACACAGCATGA 1140
OY 1141 TCATTAACGAGATGATTAATTAATCAACATCATCTCAGTGTCTTGCCCATATCTAAT 1200
Db 1141 TCATTAACGAGATGATTAATTAATCAACATCATCTCAGTGTCTTGCCCATATCTAAT 1200
OY 1201 TCATTTCCACATTTTGTGCGCATTCCTCAAGACCTCAAAATGTCAATCCATTAATATCA 1260
Db 1201 TCATTTCCACATTTTGTGCGCATTCCTCAAGACCTCAAAATGTCAATCCATTAATATCA 1260
OY 1261 GGATTAACCTTTTTTTTAACTGGAAGAAATCAATGTTACATGACGATAGGGAATTA 1320
Db 1261 GGATTAACCTTTTTTTTAACTGGAAGAAATCAATGTTACATGACGATAGGGAATTA 1320
OY 1321 ATTACATATTTTGTTCAGAGTCAAGAGATGACTAAGTCTTATTCCTCCCTTTGTT 1380
Db 1321 ATTACATATTTTGTTCAGAGTCAAGAGATGACTAAGTCTTATTCCTCCCTTTGTT 1380
OY 1381 GATTTTTTTCAGATATAAGTTAAATGCTTAGCTGTAGAGGCTGTATACGAC 1440
Db 1381 GATTTTTTTCAGATATAAGTTAAATGCTTAGCTGTAGAGGCTGTATACGAC 1440
OY 1441 AGCTTCGCCCATTCCTCCAGGCTTATCTGTCATCAACATCAACCCCTCCATACGCT 1500
Db 1441 AGCTTCGCCCATTCCTCCAGGCTTATCTGTCATCAACATCAACCCCTCCATACGCT 1500
OY 1501 AAACAAAATCTAACCTTGTAAATCTTGAACATGTGACATACATATATTCCTGCGCT 1560
Db 1501 AAACAAAATCTAACCTTGTAAATCTTGAACATGTGACATACATATATTCCTGCGCT 1560
OY 1561 GAGAGCTCTCTCTCTCTTAAATCTAGAAATGATTAAGTTTGAATAGTTGACTA 1620
Db 1561 GAGAGCTCTCTCTCTCTTAAATCTAGAAATGATTAAGTTTGAATAGTTGACTA 1620
OY 1621 TCTTACTTCATCAAGAGGAGACATATGAGATTCATCATCAGACAGCAATA 1680
Db 1621 TCTTACTTCATCAAGAGGAGACATATGAGATTCATCATCAGACAGCAATA 1680
OY 1681 CTAAAGTGTATTTGATTAATAGAGTTAGATTAATATATGAATAGCAAGGCCACATA 1740
Db 1681 CTAAAGTGTATTTGATTAATAGAGTTAGATTAATATATGAATAGCAAGGCCACATA 1740
OY 1741 GGGAAATGTTTATGGGACAGTTTGTAAAGCTGGAGTGTAGCAAGGACAGGAACTCA 1800
Db 1741 GGGAAATGTTTATGGGACAGTTTGTAAAGCTGGAGTGTAGCAAGGACAGGAACTCA 1800
OY 1801 TAGATCTTATTAATATACCTTCTATCTCTATCAATATCCAAAGCTTTT 1860
Db 1801 TAGATCTTATTAATATACCTTCTATCTCTATCAATATCCAAAGCTTTT 1860

Db 1801 TAGATCTTATTAATATACCTTCTATCTCTATCAATATCCAAAGCTTTT 1860
OY 1861 CACAGATTCATGACAGTGCAGAAATCCCAAGGTAACCTTATCATTTGATGGTAGTC 1920
Db 1861 CACAGATTCATGACAGTGCAGAAATCCCAAGGTAACCTTATCATTTGATGGTAGTC 1920
OY 1921 GCTTTTGAATTTTGGCAATCATACGTGCTACTTATCTCAACTTGAATGTGTTGTC 1980
Db 1921 GCTTTTGAATTTTGGCAATCATACGTGCTACTTATCTCAACTTGAATGTGTTGTC 1980
OY 1981 TTGTACTTATTTGAAGAAATAGGAGCACTTGTAGGCCACTTTAGGTTCACTCTGCG 2040
Db 1981 TTGTACTTATTTGAAGAAATAGGAGCACTTGTGTAGGCCACTTTAGGTTCACTCTGCG 2040
OY 2041 AATTAAGATTTTACAAAGAGCTATGAGGACAGTGTAAAGAGCTGTGTGTGTGT 2100
Db 2041 AATTAAGATTTTACAAAGAGCTATGAGGACAGTGTGTAAAGAGCTGTGTGTGTGT 2100
OY 2101 GTGTGTGTGTGTGTATGATGCCAAAGTGTGCTCTCTCTGACCCATTAATTTAGAC 2160
Db 2101 GTGTGTGTGTGTGTATGATGCCAAAGTGTGCTCTCTCTGACCCATTAATTTAGAC 2160
OY 2161 TTTAAACAAAGCATGTTTCAATGGCATAATGCTGCTGCCAATGATATACCAATAT 2220
Db 2161 TTTAAACAAAGCATGTTTCAATGGCATAATGCTGCTGCCAATGATATACCAATAT 2220
OY 2221 CTGATTAATCTCCAGTAATGTGATTAATGATCATCTGTTAATCAATAAAAAGTTGAC 2280
Db 2221 CTGATTAATCTCCAGTAATGTGATTAATGATCATCTGTTAATCAATAAAAAGTTGAC 2280
OY 2281 TTCACAAAGAGCTGGAATGGACAAACACATATGCAATTAATCTCACTACCATCA 2340
Db 2281 TTCACAAAGAGCTGGAATGGACAAACACATATGCAATTAATCTCACTACCATCA 2340
OY 2341 GCTACACACTGCTTGACATATATGTTAGAGACCTCGCATTTGGGTTCTTTAAGC 2400
Db 2341 GCTACACACTGCTTGACATATATGTTAGAGACCTCGCATTTGGGTTCTTTAAGC 2400
OY 2401 AAAATCTGTGANTAGTGTGAGGCTGTGAGTCAAGGGGTTGGAATATTTCA 2460
Db 2401 AAAATCTGTGANTAGTGTGAGGCTGTGAGTCAAGGGGTTGGAATATTTCA 2460
OY 2461 TTCTCAGCAGAGCCAGAAATTTGAATTTCCCTCATCTTTTGAATCATTTACAGTTTG 2520
Db 2461 TTCTCAGCAGAGCCAGAAATTTGAATTTCCCTCATCTTTTGAATCATTTACAGTTTG 2520
OY 2521 GAGAGATTCAGACAGCTAGGTTGCTTCAATATGCTCTGACCTTGTCTCTTTG 2580
Db 2521 GAGAGATTCAGACAGCTAGGTTGCTTCAATATGCTCTGACCTTGTCTCTTTG 2580
OY 2581 TGTTCATGGATGTCCAAATTAATTAATGTTATCTTTGAAGTGAATGCTCATAGAGAAATA 2640
Db 2581 TGTTCATGGATGTCCAAATTAATTAATGTTATCTTTGAAGTGAATGCTCATAGAGAAATA 2640
OY 2641 TAAGACTGTGAGTATATCAACATTTAGGATTCAAAGAAATTAATGATTTAAGCTCACA 2700
Db 2641 TAAGACTGTGAGTATATCAACATTTAGGATTCAAAGAAATTAATGATTTAAGCTCACA 2700
OY 2701 CTGTGTAAAGAGAACCAATACAAAGAACTGTGAGCTGTCACTGCTCCCATCTGTGTA 2760
Db 2701 CTGTGTAAAGAGAACCAATACAAAGAACTGTGAGCTGTCACTGCTCCCATCTGTGTA 2760
OY 2761 GGCACAAACAGCAGCAGGAGCCCAAGGCAATGTGAGATCTTAATTAATCAAGAAACAGTA 2820
Db 2761 GGCACAAACAGCAGCAGGAGCCCAAGGCAATGTGAGATCTTAATTAATCAAGAAACAGTA 2820
OY 2821 TCATGAGTTGAATTCCTATTAATGATGCTAGCTTGTGGCATCTCTGCTCTCTT 2880
Db 2821 TCATGAGTTGAATTCCTATTAATGATGCTAGCTTGTGGCATCTCTGCTCTCTT 2880
OY 2881 GACACATATTAGCTTGTAGCTTGTCTTCAAGACATTTATCTTTCTCCACACATGCG 2940
Db 2881 GACACATATTAGCTTGTAGCTTGTCTTCAAGACATTTATCTTTCTCCACACATGCG 2940

QY	2941	TTACCAATCCGCTCCTCCTCCTGTGTCCTTGGACTTCCCCACAAGAAATTTAAAGACTCT	3000
Db	2941	TTTACCAATCCGCTCCTCCTCCTGTGTCCTTGGACTTCCCCACAAGAAATTTAAAGACTCT	3000
QY	3001	CAAGTCCTTTCTTCATCCCCACCACTAACCTGTAAT	3036
Db	3001	CAAGTCCTTTCTTCATCCCCACCACTAACCTGTAAT	3036

RESULT 6

US-10-144-678A-690
; Sequence 690, Application US/10144678A
; Publication No. US20030157089A1

APPLICANT: Xu, Jiangchun
 APPLICANT: Dillon, Davin C.
 APPLICANT: Mitcham, Jennifer L.
 APPLICANT: Harlocker, Susan L.
 APPLICANT: Jiang, Yugu
 APPLICANT: Henderson, Robert A.
 APPLICANT: Kalos, Michael D.
 APPLICANT: Fanger, Gary R.
 APPLICANT: Retter, Marc W.
 APPLICANT: Stolk, John A.
 APPLICANT: Day, Craig H.
 APPLICANT: Vedvick, Thomas S.
 APPLICANT: Carter, Darlick
 APPLICANT: Li, Samuel X.
 APPLICANT: Wang, Aijun
 APPLICANT: Skelky, Yasir A. W.
 APPLICANT: Hepler, William T.
 APPLICANT: Hural, John
 APPLICANT: McNeill, Patricia D.
 APPLICANT: Houghton, Raymond L.
 APPLICANT: Vinals y de Bassols, Carlota
 APPLICANT: Foy, Teresa M.
 APPLICANT: Matanabe, Yoshihiro
 APPLICANT: Deng, Ta
 TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
 TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
 FILE REFERENCE: 210121.42/C28
 CURRENT APPLICATION NUMBER: US/10/144,678A
 NUMBER OF FILING DATE: 2002-08-12
 NUMBER OF SEQ ID NOS: 1033
 SOFTWARE: FastSeq for Windows Version 3.0
 SEQ ID NO 690
 LENGTH: 3923
 TYPE: DNA
 ORGANISM: Homo sapiens
 US-10-144-678A-690

Query Match	84.8%	Score 3036;	DB 12;	Length 3923;
Best Local Similarity	100.0%	Pred. No. 0;		
Matches 3036; Conservative	0;	Mismatches	0;	Indels 0;
		Gaps	0;	Gaps 0;

QY	1	ACAGAAAGAAATAGCAAGTCCGCGAAGCTGGCATCAGAAAAACAGAGGGGAGATTTGTGT	60
Db	1	ACAGAAAGAAATAGCAAGTCCGCGAAGCTGGCATCAGAAAAACAGAGGGGAGATTTGTGT	60
QY	61	GGTGGACGCGGAGGGGAGACAGAGAATCTGATGTGTGGGAAGGACCTGATGATACAGAG	120
Db	61	GGTGGACGCGGAGGGGAGACAGAGAATCTGATGTGTGGGAAGGACCTGATGATACAGAG	120
QY	61	GGCTGACGCCGAGGGGAGACAGAGAATCTGATGTGTGGGAAGGACCTGATGATACAGAG	120
Db	61	GGCTGACGCCGAGGGGAGACAGAGAATCTGATGTGTGGGAAGGACCTGATGATACAGAG	120
QY	121	GAATTACAAACACATATACTTACTGTGTTCAATGAACACCACAGATAAATAGTGAAGACTA	180
Db	121	GAATTACAAACACATATACTTACTGTGTTCAATGAACACCACAGATAAATAGTGAAGACTA	180
QY	121	GAATTACAAACACATATACTTACTGTGTTCAATGAACACCACAGATAAATAGTGAAGACTA	180
Db	121	GAATTACAAACACATATACTTACTGTGTTCAATGAACACCACAGATAAATAGTGAAGACTA	180
QY	181	GTCCGGGTGAGATCTCCCTAGTGAACAGAGGCTGGATCACCATGAGAGGCACTTTCGAG	240
Db	181	GTCCGGGTGAGATCTCCCTAGTGAACAGAGGCTGGATCACCATGAGAGGCACTTTCGAG	240
QY	181	GTCCGGGTGAGATCTCCCTAGTGAACAGAGGCTGGATCACCATGAGAGGCACTTTCGAG	240
Db	181	GTCCGGGTGAGATCTCCCTAGTGAACAGAGGCTGGATCACCATGAGAGGCACTTTCGAG	240
QY	241	TACTCAGTGCAGCAAGAAAGACTCAACACATCTCAATGAGCGGGGTGAGAAATAGAAA	300
Db	241	TACTCAGTGCAGCAAGAAAGACTCAACACATCTCAATGAGCGGGGTGAGAAATAGAAA	300

Db	241	TACTAGTGCACGAAAGAAAGACTACAGCATCTCATGCGAGGGGTGGAATATAGAA	300
QY	301	GGCTGCTGACATTYTAACATCTGAAGGCACACATCTGCTGAATGAGATAAATACATCAC	360
Db	301	GCCTGCTGACTTGTACCATCTGAGGCGACACATCTGCTGAATGAGATAAATACATCAC	360
QY	361	TGGAAMACACAGATGACATATATATATGCTAGTGTAGTGACATGTTTTGCCAATTTCCAG	420
Db	361	TGGAAMACACAGATGACATATATATGCTAGTGTAGTGACATGTTTTGCCAATTTCCAG	420
QY	421	CCCCCTTAAATATCCACACACACAGAGACACAAAAGAACACACAGATCCCTGGAGAA	480
Db	421	CCCCCTTAAATATCCACACACACAGAGACACAAAAGAACACACAGATCCCTGGAGAA	480
QY	481	AATGCCCGGGCCCATCTTGGGTCAATCGATGAGCCTCGCCCTGTGCTGTGCTCCGCTTGT	540
Db	481	AATGCCCGGGCCCATCTTGGGTCAATCGATGAGCCTCGCCCTGTGCTGTGCTCCGCTTGT	540
QY	541	GAGGAGAGACATTAAGAAATGAATTTGATGTCTTCCTTAAAGATGAGGAGAGAAACAGA	600
Db	541	GAGGAGAGACATTAAGAAATGAATTTGATGTCTTCCTTAAAGATGAGGAGAGAAACAGA	600
QY	601	TCCTGTGTGATATTTATTTTGAACGGGATTAACAGATTTGAATGAAGTACACAAAGTAG	660
Db	601	TCCTGTGTGATATTTATTTTGAACGGGATTAACAGATTTGAATGAAGTACACAAAGTAG	660
QY	661	CATTACCAATGAGAGAAAACAGACAGAAATCTGTGATGGCTGCACAAACATGACACA	720
Db	661	CATTACCAATGAGAGAAAACAGACAGAAATCTGTGATGGCTGCACAAACATGACACA	720
QY	721	AACAAATATGAAATCTGTGATGACATGAGGCGACCAAGCTGGGGAGAGATTAACACAGGG	780
Db	721	AACAAATATGAAATCTGTGATGACATGAGGCGACCAAGCTGGGGAGAGATTAACACAGGG	780
QY	781	GCAGAGGGGTACAGGATTTCTGGCCCTCTGCTTAACATGTGCGTTCAACCAATATATTC	840
Db	781	GCAGAGGGGTACAGGATTTCTGGCCCTCTGCTTAACATGTGCGTTCAACCAATATATTC	840
QY	841	ATATTTCTAACCCTCAAAAACAAGCTGTGTGAATATCTGANTCTACGAGTTCTCTGGG	900
Db	841	ATATTTCTAACCCTCAAAAACAAGCTGTGTGAATATCTGANTCTACGAGTTCTCTGGG	900
QY	901	CCCAACATTTCTCATAATATCCAGCACACTCTATTAATATTTAGTTCCACAGATCTGTA	960
Db	901	CCCAACATTTCTCATAATATCCAGCACACTCTATTAATATTTAGTTCCACAGATCTGTA	960
QY	961	CTGTACCCCTTCTACAGTGTGAATATACATTAATCTCATTTGTTGTCAAAACCCCTTGTGTT	1020
Db	961	CTGTACCCCTTCTACAGTGTGAATATACATTAATCTCATTTGTTGTCAAAACCCCTTGTGTT	1020
QY	1021	GCTGCTATATATGTAGTGAAGTCTGTTTTCTTAAGAGAGTCTTGCGCCAGGGGATCTGTG	1080
Db	1021	GCTGCTATATATGTAGTGAAGTCTGTTTTCTTAAGAGAGTCTTGCGCCAGGGGATCTGTG	1080
QY	1081	AACAGGCTGGGAAGCATCTCAAGATCTTTCCAGGGTTATACTTACTAGCACACAGCATGA	1140
Db	1081	AACAGGCTGGGAAGCATCTCAAGATCTTTCCAGGGTTATACTTACTAGCACACAGCATGA	1140
QY	1141	TCATTACGAGAGATTAATCTAATACATCACTCTAGTGTCTTGGCCCATCTGAAAT	1200
Db	1141	TCATTACGAGAGATTAATCTAATACATCACTCTAGTGTCTTGGCCCATCTGAAAT	1200
QY	1201	TCATTTCGCACCTTTGTGCCCATCTCTCAAGACCTCAAAATGTCAATTCATTATATACAA	1260
Db	1201	TCATTTCGCACCTTTGTGCCCATCTCTCAAGACCTCAAAATGTCAATTCATTATATACAA	1260
QY	1261	GGATTAACCTTTTTTTTAAACCTGGAAATATTCATGTATACATGACGTATAGGGGAATTTA	1320
Db	1261	GGATTAACCTTTTTTTTAAACCTGGAAATATTCATGTATACATGACGTATAGGGGAATTTA	1320
QY	1321	ATTACATATTTTGTGTTTCCAGTGCAAAATACATTAAGTCAAGCTTAAATCCCTCCCTTGTGTT	1380

FILE REFERENCE: 210121.427C27
CURRENT APPLICATION NUMBER: US/10/012.896
CURRENT FILING DATE: 2001-12-10
NUMBER OF SEQ ID NOS: 1011
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO: 690
LENGTH: 3923
TYPE: DNA
ORGANISM: Homo sapiens
US-10-012-896-690

Query Match 84.8%; Score 3036; DB 13; Length 3923;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3036; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY 1 ACAGAGAATATAGCAAGTGCAGAGAGCTGGCATCAGAAAAACAGAGGGAGATTGTGT 60
DB 1 ACAGAGAATATAGCAAGTGCAGAGAGCTGGCATCAGAAAAACAGAGGGAGATTGTGT 60
QY 61 GCGTCGACCCGAGGAGACCCAGGAAGATCTGCATGTTGGGAAGGACCTGATGATACAGAG 120
DB 61 GCGTCGACCCGAGGAGACCCAGGAAGATCTGCATGTTGGGAAGGACCTGATGATACAGAG 120
QY 61 GCGTCGACCCGAGGAGACCCAGGAAGATCTGCATGTTGGGAAGGACCTGATGATACAGAG 120
DB 61 GCGTCGACCCGAGGAGACCCAGGAAGATCTGCATGTTGGGAAGGACCTGATGATACAGAG 120
QY 121 GAATTACACACATATCTAGTGTTCATGTAACACCAATATAATAGTGAAGAGCTA 180
DB 121 GAATTACACACATATCTAGTGTTCATGTAACACCAATATAATAGTGAAGAGCTA 180
QY 181 GTCCGTGTGAGTCTCTCACTGACACAGGGCTGGATCCATGACGACGCACTTTCTGAG 240
DB 181 GTCCGTGTGAGTCTCTCACTGACACAGGGCTGGATCCATGACGACGCACTTTCTGAG 240
QY 241 TACTCAGTCGACGACAAAGAAAGACTACAGACATCTCAATGGCAGGGGTGAGAAATPAGAAA 300
DB 241 TACTCAGTCGACGACAAAGAAAGACTACAGACATCTCAATGGCAGGGGTGAGAAATPAGAAA 300
QY 301 GCGCTGTGACTTTCACATCTGAGGCCACACATCTGTAATGAGATTAATTAACATCAC 360
DB 301 GCGCTGTGACTTTCACATCTGAGGCCACACATCTGTAATGAGATTAATTAACATCAC 360
QY 361 TAGAAGACGACAGATGACAAATATATGTCTAAGTATGATGATGTTTTCACATTTCCAG 420
DB 361 TAGAAGACGACAGATGACAAATATATGTCTAAGTATGATGATGTTTTCACATTTCCAG 420
QY 421 CCCCTTAAATATCCACACACACAGAAAGCAAAAGAGACACAGAGATCCCTGGGAGA 480
DB 421 CCCCTTAAATATCCACACACAGAAAGCAAAAGAGACACAGAGATCCCTGGGAGA 480
QY 481 AATGCCCGGCCCATCTTGGGTATGATGATGAGCTGCGCTGCTGCTGCTGCTGCTGCT 540
DB 481 AATGCCCGGCCCATCTTGGGTATGATGATGAGCTGCGCTGCTGCTGCTGCTGCTGCT 540
QY 541 GAGGGAAGACATAGAAAATGAATGATGATGATGATGATGATGATGATGATGATGATGAT 600
DB 541 GAGGGAAGACATAGAAAATGAATGATGATGATGATGATGATGATGATGATGATGATGAT 600
QY 601 TCCGTGTGAGTATTTATTTGAAACGGGATTAACGATTGTAATGAAGTCAACAAAGTAC 660
DB 601 TCCGTGTGAGTATTTATTTGAAACGGGATTAACGATTGTAATGAAGTCAACAAAGTAC 660
QY 661 CATTTACCATGAGAGGAAAACAGACGAGAAATCTTGTGCTTCAACAGCATGCAACA 720
DB 661 CATTTACCATGAGAGGAAAACAGACGAGAAATCTTGTGCTTCAACAGCATGCAACA 720
QY 721 AACAAAATGGAATATCTGTATGACATGAGCAGCAAGCTGGGAGAGATTAACACAGGG 780
DB 721 AACAAAATGGAATATCTGTATGACATGAGCAGCAAGCTGGGAGAGATTAACACAGGG 780
QY 781 GCGAGGAGTACAGATTTGCGCTGCTTAAACTGTGCTTCAATACCAAAATCATTTT 840
DB 781 GCGAGGAGTACAGATTTGCGCTGCTTAAACTGTGCTTCAATACCAAAATCATTTT 840
QY 841 ATATTCTAACCTCAAAACAAAGCTGTGTAATATGATGATCTCTAGGTTCTCTTGGG 900
DB 841 ATATTCTAACCTCAAAACAAAGCTGTGTAATATGATGATCTCTAGGTTCTCTTGGG 900
```

```
DB 841 ATATTCTAACCTCAAAACAAAGCTGTGTAATATGATGATCTCTAGGTTCTCTTGGG 900
QY 901 CCCAACATTTCTCCATATATACGACACATCTATTTATATATATAGTTCCAGATCTGTA 960
DB 901 CCCAACATTTCTCCATATATACGACACATCTATTTATATATATAGTTCCAGATCTGTA 960
QY 961 CTGTGACCTTTCTACACTGTAGAAATATACATTAATCTATTTGTGTAAGACCCCTTGCTT 1020
DB 961 CTGTGACCTTTCTACACTGTAGAAATATACATTAATCTATTTGTGTAAGACCCCTTGCTT 1020
QY 1021 GCTGCTTAATATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1080
DB 1021 GCTGCTTAATATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1080
QY 1081 AACAGCTGGGAGACATCTCAAGATCTTTCCAGGGTTTACTTACTTACACACAGCATGA 1140
DB 1081 AACAGCTGGGAGACATCTCAAGATCTTTCCAGGGTTTACTTACTTACACACAGCATGA 1140
QY 1141 TCATTACGAGTGAATATATCTAATCAACATCATCTCAGTGTCTTGGCCATTAAGTAAT 1200
DB 1141 TCATTACGAGTGAATATATCTAATCAACATCATCTCAGTGTCTTGGCCATTAAGTAAT 1200
QY 1201 TCATTTCGACCTTTTGTGCTCCATCTCAAGACCTCAAAATGTCAATTCATTAATACCA 1260
DB 1201 TCATTTCGACCTTTTGTGCTCCATCTCAAGACCTCAAAATGTCAATTCATTAATACCA 1260
QY 1261 GATTTAACTTTTCTTAACTGGAAGAAATTCATATGATGATGATGATGATGATGATGATGAT 1320
DB 1261 GATTTAACTTTTCTTAACTGGAAGAAATTCATATGATGATGATGATGATGATGATGATGAT 1320
QY 1321 ATTTACATATTTTGTGTTTCCAGTGAAGAAATGATGATGATGATGATGATGATGATGATGAT 1380
DB 1321 ATTTACATATTTTGTGTTTCCAGTGAAGAAATGATGATGATGATGATGATGATGATGATGAT 1380
QY 1381 GATTTTCTTCCAGTGAAGAAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1440
DB 1381 GATTTTCTTCCAGTGAAGAAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1440
QY 1441 AGCCTTCGCCCATCTTCCAGTGAAGAAATGATGATGATGATGATGATGATGATGATGATGAT 1500
DB 1441 AGCCTTCGCCCATCTTCCAGTGAAGAAATGATGATGATGATGATGATGATGATGATGATGAT 1500
QY 1501 AACAAAATCTAATCTGTAATCTTGAACATGTCAGACATTAATTTCTTCTGCT 1560
DB 1501 AACAAAATCTAATCTGTAATCTTGAACATGTCAGACATTAATTTCTTCTGCT 1560
QY 1561 GAGAAAGCTCTTCTGCTTCTTAAATCTAGATGATGATGATGATGATGATGATGATGATGAT 1620
DB 1561 GAGAAAGCTCTTCTGCTTCTTAAATCTAGATGATGATGATGATGATGATGATGATGATGAT 1620
QY 1621 TCTTACTTCAATGCAAAAGGAGACATATGATGATGATGATGATGATGATGATGATGATGAT 1680
DB 1621 TCTTACTTCAATGCAAAAGGAGACATATGATGATGATGATGATGATGATGATGATGATGAT 1680
QY 1681 CTAAAAGTGAATTTGATTTAAGAGTTTGAATTAATGAATCAAGAGCCACAGA 1740
DB 1681 CTAAAAGTGAATTTGATTTAAGAGTTTGAATTAATGAATCAAGAGCCACAGA 1740
QY 1741 GGGAGATTTATGGGAGAGCTTTGTAAGCCGAGGATGTAAGGCAAGGAGGAGAGCTCA 1800
DB 1741 GGGAGATTTATGGGAGAGCTTTGTAAGCCGAGGATGTAAGGCAAGGAGGAGAGCTCA 1800
QY 1801 TAGTATCTTATATATATATATATATATATATATATATATATATATATATATATATATAT 1860
DB 1801 TAGTATCTTATATATATATATATATATATATATATATATATATATATATATATATATAT 1860
QY 1861 CACAGAAATTCATGACGTGCAAAATCCCAAGGTAACCTTTATCCATTTCAATGAGTGC 1920
DB 1861 CACAGAAATTCATGACGTGCAAAATCCCAAGGTAACCTTTATCCATTTCAATGAGTGC 1920
QY 1921 GCTTTAGAAATTTGGCAAAATCATACGTCGATCTCAACTTCAACTTGAATGATGATGATGAT 1980
DB 1921 GCTTTAGAAATTTGGCAAAATCATACGTCGATCTCAACTTCAACTTGAATGATGATGATGAT 1980
```



```
QY 1981 TTGAGTAAATGAAAGAAATAGGGCACTTGTGAGCCACTTTAGGGTTCACTCCTGGC 2040
    |||||||
Db 1981 TTGTAGTTAATGAAAAGAAATAGGGCACTTGTGAGCCACTTTAGGGTTCACTCCTGGC 2040
QY 2041 AATTAAGAAATTTACAAAGAGCTACTGAGCAGCAGTTGTTAAGAGCTCTGTGTGTGTGT 2100
    |||||||
Db 2041 AATTAAGAAATTTACAAAGAGCTACTGAGCAGCAGTTGTTAAGAGCTCTGTGTGTGTGT 2100
QY 2101 GTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2160
    |||||||
Db 2101 GTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2160
QY 2161 TTTAAACAAGCAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2220
    |||||||
Db 2161 TTTAAACAAGCAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2220
QY 2221 CTCATTATTTCTCCAGTAAATGTGATTAATGTATGTATGTATGTATGTATGTATGTATGT 2280
    |||||||
Db 2221 CTCATTATTTCTCCAGTAAATGTGATTAATGTATGTATGTATGTATGTATGTATGTATGT 2280
QY 2281 TTTCACAAAAGCAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2340
    |||||||
Db 2281 TTTCACAAAAGCAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2340
QY 2341 GCTACACACTGCTGTGACATATATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2400
    |||||||
Db 2341 GCTACACACTGCTGTGACATATATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2400
QY 2401 AAAATATCTTGATTAAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2460
    |||||||
Db 2401 AAAATATCTTGATTAAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2460
QY 2461 TTCTCAGCAGAAAGCAGAAATTTGAATTTCCCTCATCTTTAGGAAATATTATACAGGTTTG 2520
    |||||||
Db 2461 TTCTCAGCAGAAAGCAGAAATTTGAATTTCCCTCATCTTTAGGAAATATTATACAGGTTTG 2520
QY 2521 GAGAGATTCAGACAGCTGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2580
    |||||||
Db 2521 GAGAGATTCAGACAGCTGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2580
QY 2581 TGTTCATGAGTATGTCATTAATTAATGTATGTATGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2640
    |||||||
Db 2581 TGTTCATGAGTATGTCATTAATTAATGTATGTATGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2640
QY 2641 TTAAGAACTGTGAGTGTATCAACATTAGGATTCAAAAGAAATTTAGATTAAAGTCACAA 2700
    |||||||
Db 2641 TTAAGAACTGTGAGTGTATCAACATTAGGATTCAAAAGAAATTTAGATTAAAGTCACAA 2700
QY 2701 CTGATCAAAAGAAACCAAGATATCAAAAGACTGTGAGCTGTGATCGTCCCATCTCTGTGA 2760
    |||||||
Db 2701 CTGATCAAAAGAAACCAAGATATCAAAAGACTGTGAGCTGTGATCGTCCCATCTCTGTGA 2760
QY 2761 GCCACAAACAGCAGAGAGCAAGCATGTCTGAGATCTTAAATCAAGAAACCAAGTGT 2820
    |||||||
Db 2761 GCCACAAACAGCAGAGAGCAAGCATGTCTGAGATCTTAAATCAAGAAACCAAGTGT 2820
QY 2821 TATATAGTTGAATTTCTCTATATATGATGTAGCTTCTGGCATCTCTGGCTCTCTCTT 2880
    |||||||
Db 2821 TATATAGTTGAATTTCTCTATATATGATGTAGCTTCTGGCATCTCTGGCTCTCTCTT 2880
QY 2881 GACACATATTAGCTTCTAGCTTTGCTGTGACAGCTTATCTTTTCTGCAACACATGTGC 2940
    |||||||
Db 2881 GACACATATTAGCTTCTAGCTTTGCTGTGACAGCTTATCTTTTCTGCAACACATGTGC 2940
QY 2941 TTACCAATCTCTCTCTCTCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 3000
    |||||||
Db 2941 TTACCAATCTCTCTCTCTCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 3000
QY 3001 CAAAGCTTTTCTTCCATCCCAACCACTTAACCTGAAT 3036
    |||||||
Db 3001 CAAAGCTTTTCTTCCATCCCAACCACTTAACCTGAAT 3036
```

```
RESULT 8
US-10-205-823-316
; Sequence 316, Application US/10205823
; Publication No. US20030108963A1
; GENERAL INFORMATION:
; APPLICANT: Schlegel, Robert
; APPLICANT: Monahan, John E.
; APPLICANT: Endege, Wilson O.
; APPLICANT: Gannavarapu, Manjula
; APPLICANT: Gorbacheva, Bella
; APPLICANT: Hoersch, Sebastian
; APPLICANT: Kamatkar, Shubhangt
; APPLICANT: Monsey, Angela M.
; APPLICANT: Glatz, Karen
; APPLICANT: Zhao, Xumei
; APPLICANT: Anderson, Dustin
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
; METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITILE OF INVENTION: THERAPY OF PROSTATE CANCER
; FILE REFERENCE: MRI-044
; CURRENT APPLICATION NUMBER: US/10/205,823
; CURRENT FILING DATE: 2002-07-25
; PRIOR APPLICATION NUMBER: 60/307,982
; PRIOR FILING DATE: 2001-07-25
; PRIOR APPLICATION NUMBER: 60/314,356
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/325,020
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: 60/341,746
; PRIOR FILING DATE: 2001-12-12
; PRIOR APPLICATION NUMBER: 60/362,158
; PRIOR FILING DATE: 2002-03-05
; NUMBER OF SEQ ID NOS: 455
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 316
; LENGTH: 3923
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-205-823-316

Query Match      84.8%; Score 3036; DB 14; Length 3923;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3036; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACAGAAAGAAATAGCAAGTCCGAGAGCTGTGATTCAGAAAACAGAGGGAGATTGTGT 60
    |||||||
Db 1 ACAGAAAGAAATAGCAAGTCCGAGAGCTGTGATTCAGAAAACAGAGGGAGATTGTGTGT 60
QY 61 GCGTCAGCGAGGAGGAGACAGAGATGTCATGTGGGAGAGACCTGATTAACAGAG 120
    |||||||
Db 61 GCGTCAGCGAGGAGGAGACAGAGATGTCATGTGGGAGAGACCTGATTAACAGAG 120
QY 121 GAATTCAACACATATATAGTGTTCATGTGAACACCAAGATTAATAGTGAAGCTA 180
    |||||||
Db 121 GAATTCAACACATATATAGTGTTCATGTGAACACCAAGATTAATAGTGAAGCTA 180
QY 181 GTCCGCTGTGAGTCTCTCTAATGATGACACAGGCTGTGATCACCATGACAGGACTTTTGTGAG 240
    |||||||
Db 181 GTCCGCTGTGAGTCTCTCTAATGATGATGACACAGGCTGTGATCACCATGACAGGACTTTTGTGAG 240
QY 241 TACTGATGAGTGAAGAAAGAAAGCTACAGACATCTCAATGAGGAGGAGGAGAAATTAAGAAA 300
    |||||||
Db 241 TACTGATGAGTGAAGAAAGAAAGCTACAGACATCTCAATGAGGAGGAGGAGAAATTAAGAAA 300
QY 301 GCGTCGTGACTTTACCATCTGAGGCGCACACATCTGCTGAATGAGATTAATTAACATCAC 360
    |||||||
Db 301 GCGTCGTGACTTTACCATCTGAGGCGCACACATCTGCTGAATGAGATTAATTAACATCAC 360
QY 361 TAGAAACAGCAAGATGACAAATATATGTCTTAAGTATGACATGTTTTCACATTTTCAG 420
    |||||||
Db 361 TAGAAACAGCAAGATGACAAATATATGTCTTAAGTATGACATGTTTTCACATTTTCAG 420
```


Db 2581 TGTTCATGATAGTCCCAATTAATATTATCTTTGAACTGATGCTCATAGAGAGATA 2640
QY 2641 TAGAAGCTGAGTGTATCAACATTAGGATTCAGAAATATTGATTATAGCTCACA 2700
Db 2641 TAGAAGCTGAGTGTATCAACATTAGGATTCAGAAATATTGATTATAGCTCACA 2700
QY 2701 CTGTGCAAAAGGAAAGCAAGATACAAAGAACTGTGACGTGCATGCTCCCATCTGTGA 2760
Db 2701 CTGTGCAAAAGGAAAGCAAGATACAAAGAACTGTGACGTGCATGCTCCCATCTGTGA 2760
QY 2761 GCCACACCAACAGCAGGAGCCCAACCATGTGTGAATCTTAAATCAAGAAACCAAGT 2820
Db 2761 GCCACACCAACAGCAGGAGCCCAACCATGTGTGAATCTTAAATCAAGAAACCAAGT 2820
QY 2821 TCATGAGTTGAATTCCTATTTATGATGCTAGCTCTGGCCATCTGCTGCTCTCT 2880
Db 2821 TCATGAGTTGAATTCCTATTTATGATGCTAGCTCTGGCCATCTGCTGCTCTCTCT 2880
QY 2881 GACACATATTAGCTTCTAGCTTCTGCTCCACGACTTTATCTTTCTCCACACATCGC 2940
Db 2881 GACACATATTAGCTTCTAGCTTCTGCTCCACGACTTTATCTTTCTCCACACATCGC 2940
QY 2941 TTACCAATCTCTCTCTGCTGTGCTTTGGACTTCCACAGAAATTTCAACGACTCT 3000
Db 2941 TTACCAATCTCTCTCTGCTGTGCTTTGGACTTCCACAGAAATTTCAACGACTCT 3000
QY 3001 CAAGCTTTTCTTCATCCCAACCACTAACCTGAAT 3036
Db 3001 CAAGCTTTTCTTCATCCCAACCACTAACCTGAAT 3036

RESULT 9
US-09-759-143-468
Sequence 468 Application US/09759143
Patent No. US2002022481
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, David C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Jiang, Yuqun
APPLICANT: Henderson, Robert A.
APPLICANT: Kalos, Michael D.
APPLICANT: Fanger, Gary R.
APPLICANT: Retter, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Wang, Aljun
APPLICANT: Skelky, Yasir A.W.
APPLICANT: Hepler, William
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
FILE REFERENCE: 210121.427C23
CURRENT APPLICATION NUMBER: US/09/759,143
CURRENT FILING DATE: 2001-01-12
NUMBER OF SEQ ID NOS: 934
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 468
LENGTH: 3112
TYPE: DNA
ORGANISM: Homo sapiens
US-09-759-143-468

Query Match 38.1%; Score 1364; DB 9; Length 3112;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1774; Conservative 0; Mismatches 1; Indels 3; Gaps 3;

QY 285 GGTGAGAAATTAAGAAAGCTGCTGACTTACCATCTGAGGCCACACATCTGTGAATGG 344
Db 1313 GGTGAGAAATTAAGAAAGCTGCTGACTTACCATCTGAGGCCACACATCTGTGAATGG 1372

QY 345 AGATAATTAACATCACTAGAAACAGCAAGATGCAATATATGCTTAAGTAGACATGT 404
Db 1373 AGATAATTAACATCACTAGAAACAGCAAGATGCAATATATGCTTAAGTAGACATGT 1432
QY 405 TTTTGCACATTTTCACGCCCTTTAAATATCCACACACAGAGAACACAAAGAAAGCAC 464
Db 1433 TTTTGCACATTTTCACGCCCTTTAAATATCCACACACAGAGAACACAAAGAAAGCAC 1492
QY 465 AGAGATCCCTGGGAGAAATGCCCCGCCCATCTTGGGTCATGATGAGCTCGCCCTGT 524
Db 1493 AGAGATCCCTGGGAGAAATGCCCCGCCCATCTTGGGTCATGATGAGCTCGCCCTGT 1552
QY 525 GCCTGGCCCGCTTGGAGGAAAGGACATTAGAAATGAAATGATGTTGCTTAAAGG 584
Db 1553 GCCTGGCCCGCTTGGAGGAAAGGACATTAGAAATGAAATGATGTTGCTTAAAGG 1612
QY 585 TGGGACAGAAACAGATCCCTGTGTGATATTTATTTGAAAGGATTCAGATTTGAAAT 644
Db 1613 TGGGACAGAAACAGATCCCTGTGTGATATTTATTTGAAAGGATTCAGATTTGAAAT 1672
QY 645 GAAGTCAAAAGTACGACTTACCAATGACAGGAAACAGACGAAATCTTGATGGCTT 704
Db 1673 GAAGTCAAAAGTACGACTTACCAATGACAGGAAACAGACGAAATCTTGATGGCTT 1732
QY 705 CACAGACATGCAAAACAAATGGAATCTGTGATGACATGAGGACGCAAGCTGGGG 764
Db 1733 CACAGACATGCAAAACAAATGGAATCTGTGATGACATGAGGACGCAAGCTGGGG 1792
QY 765 AGGAGATTAACACAGGGGACAGAGGTGAGATTCCTGACCTGCTTAAACCTGGCGTTC 824
Db 1793 AGGAGATTAACACAGGGGACAGAGGTGAGATTCCTGACCTGCTTAAACCTGGCGTTC 1852
QY 825 ATTAACAATCATTTCAATATTTTAAACCTGCAAAACAAAGCTTTGATATGTGATCTC 884
Db 1853 ATTAACAATCATTTCAATATTTTAAACCTGCAAAACAAAGCTTTGATATGTGATCTC 1912
QY 885 TACGGTTCCTTGGGGCCCAACATTCCTCATATATCCAGACACATCTTTTAAATTT 944
Db 1913 TACGGTTCCTTGGGGCCCAACATTCCTCATATATCCAGACACATCTTTTAAATTT 1972
QY 945 AGTTCCAGATCTGTACTGTGACTGACCTTCTACACTGTAGATTAACATTTACTTTGTC 1004
Db 1973 AGTTCCAGATCTGTACTGTGACTGACCTTCTACACTGTAGATTAACATTTACTTTGTC 2032
QY 1005 AAAGACCTTGTGTTGCTGCTGCTTAATATGTAGCTGACTGTTTCTTAAGAGCTGTTCTG 1064
Db 2033 AAAGACCTTGTGTTGCTGCTGCTTAATATGTAGCTGACTGTTTCTTAAGAGCTGTTCTG 2092
QY 1065 GCCCAGGGATCTGTGAACAGGCTGGGAAACATCTGAAGATCTTTCAGAGGTATACTTA 1124
Db 2093 GCCCAGGGATCTGTGAACAGGCTGGGAAACATCTGAAGATCTTTCAGAGGTATACTTA 2152
QY 1125 CTAGCACACAGCATGATCATTTAGAGGTGAATATGTAATCAACATCATCTCAGAGTCT 1184
Db 2153 CTAGCACACAGCATGATCATTTAGAGGTGAATATGTAATCAACATCATCTCAGAGTCT 2212
QY 1185 TTGCCATACATGAATTCATTTCCACCTTTTGCCCATTCGACACTGCAAAATGTCA 1244
Db 2213 TTGCCATACATGAATTCATTTCCACCTTTTGCCCATTCGACACTGCAAAATGTCA 2272
QY 1245 TTGCCATTAATACAGGATTAATCTTTTAAACCTGGAAGATTCGAATGATGATGATG 1304
Db 2273 TTGCCATTAATACAGGATTAATCTTTTAAACCTGGAAGATTCGAATGATGATGATG 2332
QY 1305 CAGCTATGGGAATTTAATACATATTTGTTTCCAGTGAAGATGACTAAGTCCCTTA 1364
Db 2333 CAGCTATGGGAATTTAATACATATTTGTTTCCAGTGAAGATGACTAAGTCCCTTA 2392
QY 1365 TCCCTGCCCTTGTGATTTTTCACAGTATTAAGTTAAATGCTTAGCCTGTGACTG 1424
Db 2393 TCCCTGCCCTTGTGATTTTTCACAGTATTAAGTTAAATGCTTAGCCTGTGACTG 2452

QY 1425 AGGCTGTATACG-CACAGCCTCTCCCATCCCTCCAGCCCTTATCTGTCATCACAATCAA 1483
 Db 2453 AGGCTGTATACG-CACAGCCTCTCCCATCCCTCCAGCCCTTATCTGTCATCACAATCAA 2512
 QY 1484 CCCCTCCATACCACTTAACAAATCTAATCTGTAATCTTGAACATGTCAGACATA 1543
 Db 2513 CCCCTCCAT-CCACTTAACAAATCTAATCTGTAATCTTGAACATGTCAG-CAATA 2570
 QY 1544 CATTTATCTCTGCTGCTGAGAAAGCTCTTCTGCTCTTAATCTAGATGATGTAAGT 1603
 Db 2571 CATTTATCTCTGCTGCTGAGAAAGCTCTTCTGCTCTTAATCTAGATGATGTAAGT 2630
 QY 1604 TTTGATAGTGTAGTACTTACTTACTTACATGCAAGAAGGACATATGATGATCTATC 1663
 Db 2631 TTTGATAGTGTAGTACTTACTTACTTACATGCAAGAAGGACATATGATGATCTATC 2690
 QY 1664 ACATGAGACAGCAATTAATAAAGTATTTGATTTAGAGTTAGATTAATATATGA 1723
 Db 2691 ACATGAGACAGCAATTAATAAAGTATTTGATTTAGAGTTAGATTAATATATGA 2750
 QY 1724 AATGCAAGACCCACAGAGGAAATGTTATGAGGACGTTTGTAGCCTGGAGTGAAGC 1783
 Db 2751 AATGCAAGACCCACAGAGGAAATGTTATGAGGACGTTTGTAGCCTGGAGTGAAGC 2810
 QY 1784 AAAGCAGGAGACCTCATAGTATCTTATATATATACTTCTCTATCTCTATCA 1843
 Db 2811 AAAGCAGGAGACCTCATAGTATCTTATATATATACTTCTCTATCTCTATCA 2870
 QY 1844 ATATCCAAACAAGCTTTTCACAGAAATTCATGCAAGTGCACAAATCCCAAGTAACCTTTATC 1903
 Db 2871 ATATCCAAACAAGCTTTTCACAGAAATTCATGCAAGTGCACAAATCCCAAGTAACCTTTATC 2930
 QY 1904 CATTTATGTTGAGTGGCCTTTAGAAATTTGGCAATCATACTGCTACTTATCTCAACT 1963
 Db 2931 CATTTATGTTGAGTGGCCTTTAGAAATTTGGCAATCATACTGCTACTTATCTCAACT 2990
 QY 1964 TTTGATAGTGTGTTGCTTGTAGTAAATTTGAAAGAAATAGGCACTCTGAGGCACT 2023
 Db 2991 TTTGATAGTGTGTTGCTTGTAGTAAATTTGAAAGAAATAGGCACTCTGAGGCACT 3050
 QY 2024 TAGGTTCTACTCTGCGCAATTAAGAATTTACAAAGAGC 2061
 Db 3051 TAGGTTCTACTCTGCGCAATTAAGAATTTACAAAGAGC 3088
 RESULT 10
 US-09-780-669-468
 ; Sequence 468, Application US/09780669
 ; Patent No. US20020051977A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Xu, Jiangchun
 ; APPLICANT: Dillon, Davin C.
 ; APPLICANT: Mitcham, Jennifer L.
 ; APPLICANT: Harlocker, Susan L.
 ; APPLICANT: Jiang, Yuqi
 ; APPLICANT: Henderson, Robert A.
 ; APPLICANT: Kelos, Michael D.
 ; APPLICANT: Fangel, Gary R.
 ; APPLICANT: Retter, Marc W.
 ; APPLICANT: Stoik, John A.
 ; APPLICANT: Day, Craig H.
 ; APPLICANT: Vedvick, Thomas S.
 ; APPLICANT: Carter, Darick
 ; APPLICANT: Li, Samuel
 ; APPLICANT: Wang, Aijun
 ; APPLICANT: Skeiky, Yasir A.W.
 ; APPLICANT: Hepler, William
 ; APPLICANT: Hural, John
 ; APPLICANT: McNeill, Patricia D.
 ; APPLICANT: Houghton, Raymond L.
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
 ; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
 ; FILE REFERENCE: 210121.427C24

; CURRENT APPLICATION NUMBER: US/09/780,669
 ; CURRENT FILING DATE: 2001-02-09
 ; NUMBER OF SEQ ID NOS: 943
 ; SOFTWARE: PastSeq for Windows Version 3.0
 ; SEQ ID NO: 468
 ; LENGTH: 3112
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-09-780-669-468
 Query Match 38.1%; Score 1364; DB 9; Length 3112;
 Best Local Similarity 99.8%; Pred. No. 0;
 Matches 1774; Conservative 0; Mismatches 1; Indels 3; Gaps 3;
 QY 285 GGTGGAATTAAGAAAGCTGCTGCTTACATCTGAGGCACATCTGCTGAATAGG 344
 Db 1313 GGTGGAATTAAGAAAGCTGCTGCTTACATCTGAGGCACATCTGCTGAATAGG 1372
 QY 345 AGATATTAATACATCTAGAAAACAGCAAGATGACAAATATATGCTAAAGTATGATGT 404
 Db 1373 AGATATTAATACATCTAGAAAACAGCAAGATGACAAATATATGCTAAAGTATGATGT 1432
 QY 405 TTTTGACATTTCCAGCCCTTTAAATTCACACACACAGAGACCAAAAGGAGAC 464
 Db 1433 TTTTGACATTTCCAGCCCTTTAAATTCACACACACAGAGACCAAAAGGAGAC 1492
 QY 465 AGAGATCCCTGGGAAATATGCCCGCCCATCTTGAGTCAATGATGAGCCTCGCCGT 524
 Db 1493 AGAGATCCCTGGGAAATATGCCCGCCCATCTTGAGTCAATGATGAGCCTCGCCGT 1552
 QY 525 GCCTGCTCCGCTTGTGAGGAGACATTTGAAAATGATGATGCTTCTTAAAGGA 584
 Db 1553 GCCTGCTCCGCTTGTGAGGAGACATTTGAAAATGATGATGCTTCTTAAAGGA 1612
 QY 585 TGGCAGGAAACAGATCTGTTGATTTATTTGAACGGATTAACAGATTTGAAT 644
 Db 1613 TGGCAGGAAACAGATCTGTTGATTTATTTGAACGGATTTACAGATTTGAAT 1672
 QY 645 GAACTCAAAAGTACATTAACAAATGAGAGAAACAGACGAGAAATCTTGATGCTT 704
 Db 1673 GAACTCAAAAGTACATTAACAAATGAGAGAAACAGACGAGAAATCTTGATGCTT 1732
 QY 705 CACAAGACATGCAACAAACAAATGGAATCTGATGACATGAGGACGCAAGCTGGG 764
 Db 1733 CACAAGACATGCAACAAACAAATGGAATCTGATGACATGAGGACGCAAGCTGGG 1792
 QY 765 AGGATTAACACAGGCGCAGAGGCTCAGAGATTTGGCCCTGCTCTAAACTGAGCTTC 824
 Db 1793 AGGATTAACACAGGCGCAGAGGCTCAGAGATTTGGCCCTGCTCTAAACTGAGCTTC 1852
 QY 825 ATAAACAATCATTTCAATTTCTTACCCCTCAAAACAAAGCTGTTGTAATATGATCTC 884
 Db 1853 ATAAACAATCATTTCAATTTCTTACCCCTCAAAACAAAGCTGTTGTAATATGATCTC 1912
 QY 885 TACGTTCTCTTGGGCGCAACATCTCCATATCTCAGCAGACACTATTTTATATTT 944
 Db 1913 TACGTTCTCTTGGGCGCAACATCTCCATATCTCAGCAGACACTATTTTATATTT 1972
 QY 945 AGTTCCAGATCTTACTGTGACCTTCTACAGTGTGAATTAACATTAATCTTCTTTC 1004
 Db 1973 AGTTCCAGATCTTACTGTGACCTTCTACAGTGTGAATTAACATTAATCTTCTTTC 2032
 QY 1005 AAAGACCTTCTGTTGCTGCTTAATATGATGACTGTTTCTTAAGAGTGTCTG 1064
 Db 2033 AAAGACCTTCTGTTGCTGCTTAATATGATGACTGTTTCTTAAGAGTGTCTG 2092
 QY 1065 GCCCAGGAGTCTGTGACAGGCTGGGAGACATCTCAAGATCTTTCAGGGTTATCTTA 1124
 Db 2093 GCCCAGGAGTCTGTGACAGGCTGGGAGACATCTCAAGATCTTTCAGGGTTATCTTA 2152
 QY 1125 CTAGCAACAGCATGATTTAGGAGTGAATATCTAATCAACATCATCTCAGTGTCT 1184
 Db 2153 CTAGCAACAGCATGATTTAGGAGTGAATATCTAATCAACATCATCTCAGTGTCT 2212

1185 TTGCCATACGAAATTCATTTCCACCTTTTGCCCATTCACAGACCTCAAAATGTCA 1244
1223 TTGCCATACGAAATTCATTTCCACCTTTTGCCCATTCACAGACCTCAAAATGTCA 2272
1245 TTCCATTAATACAGAGATTAACCTTTTAACTGGAAGATCAATGTTACATG 1304
2273 TTCCATTAATACAGAGATTAACCTTTTAACTGGAAGATCAATGTTACATG 2332
1305 CAGCTATGGAATTTAATACATTTTGTTCACGTCGAAAGATGACTAGTCTTAA 1364
2333 CAGCTATGGAATTTAATACATTTTGTTCACGTCGAAAGATGACTAGTCTTAA 2392
1365 TCCCTCCCTTTGTTGATTTTTTCCAGTAAAGTTAAATGCTTGACCTGACTG 1424
2393 TCCCTCCCTTTGTTGATTTTTTCCAGTAAAGTTAAATGCTTGACCTGACTG 2452
1425 AGGCTGTATACAG-CACAGCCTCTCCCATCCCTCCAGCCTTATCTGTCATCACA 1483
2453 AGGCTGTATACAGCAGCCTCTCCCATCCCTCCAGCCTTATCTGTCATCACA 2512
1484 CCCCTCCCTTACACCTTAACAATCTAATCTGTAATCTTGAACATGTCAGACAT 1543
2513 CCCCTCCCTTACACCTTAACAATCTAATCTGTAATCTTGAACATGTCAGACAT 2570
1544 CATTAATCTCTGCTGAGAGCTCTGCTGCTGCTTAAATCTGAATGATGTAAGT 1603
2571 CATTAATCTCTGCTGAGAGCTCTGCTGCTGCTTAAATCTGAATGATGTAAGT 2630
1604 TTTGATAATGTTGACTATCTTACTTCTCATCAAGAAGACATATGATGATCATCATC 1663
2631 TTTGATAATGTTGACTATCTTACTTCTCATCAAGAAGACATATGATGATCATCATC 2690
1664 ACATGACACAGCAATCTAATAAGTAAATTTGATTAATAGAGTTAGATTAATATGA 1723
2691 ACATGACACAGCAATCTAATAAGTAAATTTGATTAATAGAGTTAGATTAATATGA 2750
1724 AATGACACAGCAAGAGGAATGTTATGAGGACAGTGTGTAAGCTGGATGTGAAG 1783
2751 AATGACACAGCAAGAGGAATGTTATGAGGACAGTGTGTAAGCTGGATGTGAAG 2810
1784 AAGGACGAGGAACCTCATAGTATCTTATATATATATATATATATATATATATAT 1843
2811 AAGGACGAGGAACCTCATAGTATCTTATATATATATATATATATATATATATAT 2870
1844 ATATCCAAAGCTTTTTCACAGATTCATGACGTGCAAAATCCCAAGATTAACCTTATC 1903
2871 ATATCCAAAGCTTTTTCACAGATTCATGACGTGCAAAATCCCAAGATTAACCTTATC 2930
1904 CATTCATGCTGAGTGCCTTTAAGATTTTGGCAATTCATGCTGACCTTATCTCAAGT 1963
2931 CATTCATGCTGAGTGCCTTTAAGATTTTGGCAATTCATGCTGACCTTATCTCAAGT 2990
1964 TTGAGATGTTGTTGCTTGTAGTTAATTAAGAAATAGGACACTTGTGAGCAGCTT 2023
2991 TTGAGATGTTGTTGCTTGTAGTTAATTAAGAAATAGGACACTTGTGAGCAGCTT 3050
2024 TAGGTTCACTCCTGCAATTAAGATTTTACAAAGAGC 2061
3051 TAGGTTCACTCCTGCAATTAAGATTTTACAAAGAGC 3088

RESULT 11
US-09-822-827-468

; Sequence 468, Application US/09822827
; Patent No. US20020081680A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.534C1
; CURRENT APPLICATION NUMBER: US/09/822,827
; CURRENT FILING DATE: 2001-03-28

; NUMBER OF SEQ ID NOS: 982
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 468
; LENGTH: 3112
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-822-827-468

Query Match 38.1%; Score 1364; DB 9; Length 3112;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1774; Conservative 0; Mismatches 1; Indels 3; Gaps 3;

285 GGTGAGAAATTAAGAAAGCGTGCATTTAATACATCTGAGCGCACACATCTGCGAATG 344
1313 GGTGAGAAATTAAGAAAGCGTGCATTTAATACATCTGAGCGCACACATCTGCGAATG 1372
1373 AGATAATTAACATCACTAGAAACAGCAAGATGACAAATATATGTTAAGTAGACATGT 1432
345 AGATAATTAACATCACTAGAAACAGCAAGATGACAAATATATGTTAAGTAGACATGT 404
405 TTTTGCACATTTCCAGCCCTTTAATATTCACACACAGACAGCAACAAAGAGCAC 464
1433 TTTTGCACATTTCCAGCCCTTTAATATTCACACACAGACAGCAACAAAGAGCAC 1492
465 AGATATCCCTGGGAGAAATGCCGGCCCATCTTGATGATGATGAGCCTGCGCTGT 524
1493 AGATATCCCTGGGAGAAATGCCGGCCCATCTTGATGATGATGAGCCTGCGCTGT 1552
525 GCGTGTCCCGCTTGTGAGGAGAGACATTAAGAAATGAATGATGTGTTCTTAAGGA 584
1553 GCGTGTCCCGCTTGTGAGGAGAGACATTAAGAAATGAATGATGTGTTCTTAAGGA 1612
585 TGGGACAGAAACAGATCCCTGTTGATATTTATTTGAACGGGATTAACGATTTGAAT 644
1613 TGGGACAGAAACAGATCCCTGTTGATATTTATTTGAACGGGATTAACGATTTGAAT 1672
645 GAAGTCACAAAGTACATTTACCAATGAGAGGAAACACAGAGAAATCTTGATGCTT 704
1673 GAAGTCACAAAGTACATTTACCAATGAGAGGAAACACAGAGAAATCTTGATGCTT 1732
705 CACAGACATGCAACAAACAAATGGAATCTGTATGATGATGATGATGATGATGATG 764
1733 CACAGACATGCAACAAACAAATGGAATCTGTATGATGATGATGATGATGATGATG 1792
765 AGGATATACCAAGGGGAGAGGATGATGATGATGATGATGATGATGATGATGATG 824
1793 AGGATATACCAAGGGGAGAGGATGATGATGATGATGATGATGATGATGATGATG 1852
825 ATACCAAAATCATTTATATTTTCTAACCCCAAAAGAGCTGTTAATATCTGATCTC 884
1853 ATACCAAAATCATTTATATTTTCTAACCCCAAAAGAGCTGTTAATATCTGATCTC 1912
885 TACGTTCTCTTGGGCCCAACATTTCTCATATATTCACAGCAGCTCATATTTTAATTT 944
1913 TACGTTCTCTTGGGCCCAACATTTCTCATATATTCACAGCAGCTCATATTTTAATTT 1972
945 AGTTCCAGATCTGTACTGTGACCTTTCTACACTGTGAGATTAACATTAATCTATTTG 1004
1973 AGTTCCAGATCTGTACTGTGACCTTTCTACACTGTGAGATTAACATTAATCTATTTG 2032
1005 AAGACCCCTGCTGTGCTGCTGCTAATATAGCTGACTGTTTCTAAGAGAGTGTCTG 1064
2033 AAGACCCCTGCTGTGCTGCTGCTAATATAGCTGACTGTTTCTAAGAGAGTGTCTG 2092
1065 GCCCAGGAGATCTGTCAACAGCTGGGAACATCTCAAGATCTTCCAGGTTATCTTA 1124
2093 GCCCAGGAGATCTGTCAACAGCTGGGAACATCTCAAGATCTTCCAGGTTATCTTA 2152
1125 CTAGCACACAGCATGATCAATTAAGAGTGAATATCTAATCAACATCAATCTAGTGT 1184
2153 CTAGCACACAGCATGATCAATTAAGAGTGAATATCTAATCAACATCAATCTAGTGT 2212
1185 TTGCCATACGAAATTCATTTCCACCTTTTGTGCCATTCACAGACCTCAAAATGTCA 1244

Db 2213 TTGCCATACGTAATTTATTTCCACTTTGTGGCCATCTCAAGACCTCAAAATGTCA 2272
Oy 1245 TTCCATTAATATACAGAGATTAACTTTTTTTTTTAACCTGGAAGATTCAATGTTACATG 1304
Db 2273 TTCCATTAATATACAGAGATTAACTTTTTTTTTTAACCTGGAAGATTCAATGTTACATG 2332
Oy 1305 CAGCATATGGGAATTTAATTACATATTTTGTTCAGTGCAAAAGATGACTAAGTCTTTA 1364
Db 2333 CAGCATATGGGAATTTAATTACATATTTTGTTCAGTGCAAAAGATGACTAAGTCTTTA 2392
Oy 1365 TCCCTCCCTTTGTTGATTTTTTTTCCAGTAAAGTTAAAGTCTTAAAGCTTGTACTG 1424
Db 2393 TCCCTCCCTTTGTTGATTTTTTTTCCAGTAAAGTTAAAGTCTTAAAGCTTGTACTG 2452
Oy 1425 AGCGTATATACG-CACAGCCTTCCCATCTCCCTCCAGCCTTATCTGTATCACCACAA 1483
Db 2453 AGCGTATATACG-CACAGCCTTCCCATCTCCCTCCAGCCTTATCTGTATCACCACAA 2512
Oy 1484 CCCCCCATACACCTTAAACAAATCTAACTTGAATTCCTGAAACATGTCAGACATA 1543
Db 2513 CCCCCCAT-GCACCTTAAACAAATCTAACTTGAATTCCTGAAACATGTCAGG-CATA 2570
Oy 1544 CATTTATCTCTCTGCTGAGAGCTCTCTCTGCTTAAATCTAGATGATGTAAGT 1603
Db 2571 CATTTATCTCTCTGCTGAGAGCTCTCTCTGCTTAAATCTAGATGATGTAAGT 2630
Oy 1604 TTTGAAATAGTTGACTATCTTACTCATGCAAAAGAGGACACATATGATGATCCTC 1663
Db 2631 TTTGAAATAGTTGACTATCTTACTCATGCAAAAGAGGACACATATGATGATCCTC 2690
Oy 1664 ACATGAGACACAAATTAATAAGTATTTGATTAATTAAGTATTAATATATATNGA 1723
Db 2691 ACATGAGACACAAATTAATAAGTATTTGATTAATTAAGTATTAATATATATNGA 2750
Oy 1724 AATGCAAGAGCCACAGAGAGGATTTATGAGGACGCTTTGAAAGCCTGGAGTGGAGC 1783
Db 2751 AATGCAAGAGCCACAGAGAGGATTTATGAGGACGCTTTGAAAGCCTGGAGTGGAGC 2810
Oy 1784 AAAGGACAGGAACTCATATGATCTTATATATATATCTTCAATTTCTCTATCTATCA 1843
Db 2811 AAAGGACAGGAACTCATATGATCTTATATATATATCTTCAATTTCTCTATCTATCA 2870
Oy 1844 ATATCCAAACAGCTTTTACAGAAATTCATGCAAGTGCATATCCCAAGGTAACCTTTATC 1903
Db 2871 ATATCCAAACAGCTTTTACAGAAATTCATGCAAGTGCATATCCCAAGGTAACCTTTATC 2930
Oy 1904 CATTTCAATGAGTGGCTTTAGAAATTTTGGCAAAATCATGCTGCTTATATCTCAACT 1963
Db 2931 CATTTCAATGAGTGGCTTTAGAAATTTTGGCAAAATCATGCTGCTTATATCTCAACT 2990
Oy 1964 TTGAGATGTTGTTCTCTTGTAGTTAATTTGAAGAAATAGGGCACTCTTGTAGCCACT 2023
Db 2991 TTGAGATGTTGTTCTCTTGTAGTTAATTTGAAGAAATAGGGCACTCTTGTAGCCACT 3050
Oy 2024 TAGGGTCACTCCTGCGAATTAAGAAATTTACAAAGAGC 2061
Db 3051 TAGGGTCACTCCTGCGAATTAAGAAATTTACAAAGAGC 3088

RESULT 12
US-09-895-793-468

Sequence 468, Application US/09895793

Publication No. US20020192763A1

GENERAL INFORMATION:

APPLICANT: Xu, Jianshun

APPLICANT: Dillon, Davin C.

APPLICANT: Mitcham, Jennifer L.

APPLICANT: Jhang, Yungu

APPLICANT: Kalos, Michael D.

APPLICANT: Retter, Marc W.

APPLICANT: Stolk, John A.

APPLICANT: Day, Craig H.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Darrik
APPLICANT: Li, Samuel X.
APPLICANT: Wang, Aijun
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Hepier, William T.
APPLICANT: Henderson, Robert A.
APPLICANT: Hural, John
APPLICANT: McNeill, Patricia D.
APPLICANT: Houghton, Raymond L.
APPLICANT: Vinals de Bassols, Carlota
APPLICANT: Foy, Teresa
APPLICANT: Fanger, Gary R.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
FILE REFERENCE: 210121.534C2
CURRENT APPLICATION NUMBER: US/09/895,793
NUMBER OF SEQ ID NOS: 982
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 468
LENGTH: 3112
TYPE: DNA
ORGANISM: Homo sapiens
US-09-895-793-468

Query Match 38.1%; Score 1364; DB 10; Length 3112;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1774; Conservative 0; Mismatches 1; Indels 3; Gaps 3;

Oy 285 GGTGGAATTAAGAAAGGCTGCTGACTTACATCTGAGGCGACACATCTGCTGAATG 344
Db 1313 GGTGGAATTAAGAAAGGCTGCTGACTTACATCTGAGGCGACACATCTGCTGAATG 1372
Oy 345 AGATAATTAACATCACTGAAACAGCAAGATGACAAATTAATGTAAGTGAACATGT 404
Db 1373 AGATAATTAACATCACTGAAACAGCAAGATGACAAATTAATGTAAGTGAACATGT 1432
Oy 405 TTTTGACATTTCCAGCCCTTTAAATATCCACACACAGAGAGCAACAAAGAGACAC 464
Db 1433 TTTTGACATTTCCAGCCCTTTAAATATCCACACACAGAGAGCAACAAAGAGACAC 1492
Oy 465 AGAATCCCTGGGAGAAATGCGCGCCCATCTTGGGTATGATGAGCTCGCCCTGT 524
Db 1493 AGAATCCCTGGGAGAAATGCGCGCCCATCTTGGGTATGATGAGCTCGCCCTGT 1552
Oy 525 GCTGTGCCCTGTGAGGAGGACATTTGAATGAATGAATGATGTTCTTAAAGGA 584
Db 1553 GCTGTGCCCTGTGAGGAGGACATTTGAATGAATGAATGATGTTCTTAAAGGA 1612
Oy 585 TGGGCAAGAAACAGATCTGTTGTGATATTTTGAACGGGATTAAGATTTGAAT 644
Db 1613 TGGGCAAGAAACAGATCTGTTGTGATATTTTGAACGGGATTAAGATTTGAAT 1672
Oy 645 GAACTCACAAAGTACATTTCCATATGAGAGAGAAACAGAGAGAAATCTTGATGCTT 704
Db 1673 GAACTCACAAAGTACATTTCCATATGAGAGAGAAACAGAGAGAAATCTTGATGCTT 1732
Oy 705 CACAAGACATGCAACAAACAAATGGAATCTGATGACATGAGGAGCAAGCTGGGG 764
Db 1733 CACAAGACATGCAACAAACAAATGGAATCTGATGACATGAGGAGCAAGCTGGGG 1792
Oy 765 AGGAGATTAACACAGGCGCAGAGGCTCAGATTTGCGCCCTGCTAACTGTGCGTTC 824
Db 1793 AGGAGATTAACACAGGCGCAGAGGCTCAGATTTGCGCCCTGCTAACTGTGCGTTC 1852
Oy 825 ATTAACAAATCATTTCAATTTCTAACCCCTCAAAACAAAGCTGTTGAATATCTGATCTC 884
Db 1853 ATTAACAAATCATTTCAATTTCTAACCCCTCAAAACAAAGCTGTTGAATATCTGATCTC 1912
Oy 885 TAGGCTTCCTTGGGCGCAACATTCACATATTCAGGCGACATCTTAAATTTT 944

Db	1913	TACGGTTCCTTCTGGGCCCAACATTCCTCCATATATCCAGCCACACTCATTTTAAATATT	1912
OY	945	AGTTCCAGAGATCTGTACTGTGTACCTTTCTACACTGTAGAAATTAACATTACTCATTTTGTCTC	1004
Db	1973	AGTTTCCAGAGATCTGTACTGTGTACCTTTCTACACTGTAGAAATTAACATTACTCATTTTGTCTC	2032
OY	1005	AAAACACCTTGCTGTGTGCTGCTTAATATGTAGCTGACTGTTTTTCTTAAGAGCTGTCTG	1064
Db	2033	AAAACACCTTGCTGTGTGCTGCTTAATATGTAGCTGACTGTTTTTCTTAAGAGAGTGTCTG	2092
OY	1065	GCCCAAGGGAGATCTGTGAACAGAGCGTGGGAGACATCTCAAGATCTTCCAGGGTTPATCTTA	1124
Db	2093	GCCCAAGGGAGATCTGTGAACAGAGCGTGGGAGACATCTCAAGATCTTCCAGGGTTPATCTTA	2152
OY	1125	CTAGCACACAGACATGATCATTTACGAGAGTAATATATCAATCAATCATCTCCAGTGTCT	1184
Db	2153	CTAGCACACAGACATGATCATTTACGAGAGTAATATATCAATCAATCATCTCCAGTGTCT	2212
OY	1185	TTGGCCCATCTAGAAATTCATTTCCCACTTTTGTGCCCATCTCTCAAGACCTCAAAATGTCA	1244
Db	2213	TTGGCCCATCTAGAAATTCATTTCCCACTTTTGTGCCCATCTCTCAAGACCTCAAAATGTCA	2272
OY	1245	TTCCATTAATATACAGAGATTAACCTTTTAACTGGTAAATTAATCAATGTATACATG	1304
Db	2273	TTCCATTAATATACAGAGATTAACCTTTTAACTGGTAAATTAATCAATGTATACATG	2332
OY	1305	CAGCTATGCGAATTTAATACATATATTTGTGTTTCCAGTGCAGAAAGATGACTAAGCTTTTA	1364
Db	2333	CAGCTATGCGAATTTAATACATATATTTGTGTTTCCAGTGCAGAAAGATGACTAAGCTTTTA	2392
OY	1365	TTCCCTCCCTTTGTTGATTTTTTTTCCAGTATTAAGTTAAATGCTTGAAGCTTGTACTGTG	1424
Db	2393	TTCCCTCCCTTTGTTGATTTTTTTTCCAGTATTAAGTTAAATGCTTGAAGCTTGTACTGTG	2452
OY	1425	AGGCTGTATATACAG-CAGAGCCTCCGCCATCCCTCCAGCCTTAATCTGTGCATCACACATCAA	1483
Db	2453	AGGCTGTATATACAGCAGCCTCCGCCATCCCTCCAGCCTTAATCTGTGCATCACACATCAA	2512
OY	1484	CCCCCTCCCATTCACACCTAAACAAATATCACTGTATTAATCCCTTGAACATGTCCAGACATA	1543
Db	2513	CCCCCTCCCATTCACACCTAAACAAATATCACTGTATTAATCCCTTGAACATGTCCAGACATA	2570
OY	1544	CATTATTCCTTCTGCTGAGAGAGCTCTTCTGTCTCTTAATCTAGAAATGATGTAAAGT	1603
Db	2571	CATTATTCCTTCTGCTGAGAGAGCTCTTCTGTCTCTTAATCTAGAAATGATGTAAAGT	2630
OY	1604	TTTGAATATATGTGACTATCTTACTTCATGCAAAAGGAGACATATGAGATTTATCATC	1663
Db	2631	TTTGAATATATGTGACTATCTTACTTCATGCAAAAGGAGACATATGAGATTTATCATC	2690
OY	1664	ACATGAGACAGACAATACTAAAGCTGTAAATTTGAATTAAGATTTAGATTAATATATGA	1723
Db	2691	ACATGAGACAGACAATACTAAAGCTGTAAATTTGAATTAAGATTTAGATTAATATATGA	2750
OY	1724	AATGCAAGAGACACAGAGAGGAATGTTATGCGGACAGTTTGAAGCCTGGGATGTGAAGC	1783
Db	2751	AATGCAAGAGACACAGAGAGGAATGTTATGCGGACAGTTTGAAGCCTGGGATGTGAAGC	2810
OY	1784	AAAAGCGAGGAACTCTAGATATCTTATATATATATCTTCAATCTCTATCTCATATACA	1843
Db	2811	AAAAGCGAGGAACTCTAGATATCTTATATATATATATCTTCAATCTCTATCTCATATACA	2870
OY	1844	ATATTCACAAAGCTTTTTCACAGATTCATGACAGATCCCAAAAGTAACTTTATATC	1903
Db	2871	ATATTCACAAAGCTTTTTCACAGATTCATGACAGATCCCAAAAGTAACTTTATATC	2930
OY	1904	CATTTCATGTGATGCGCTTTAGAAATTTTGGCAAAATCATCTACTGCTACTATCTCAACT	1963
Db	2931	CATTTCATGTGATGCGCTTTAGAAATTTTGGCAAAATCATCTACTGCTACTATCTCAACT	2990
OY	1964	TTTGAGATGTCTTGTCTCTGTAGATTAATTTGAAGAAATAGGGCACTCTGTGAGCCACTT	2023
Db	2991	TTTGAGATGTCTTGTCTCTGTAGATTAATTTGAAGAAATAGGGCACTCTGTGAGCCACTT	3050

OY	2024	TAGGTTACCTCCCTGGCAATTAAGAATTACTAAAGAC	2061
Dd	3051	TAGGTTACCTCCCTGGCAATTAAGAATTACTAAAGAC	3088
 RESULT 13 US-09-895-814-468			
		; Sequence 468, Application US/09895814	
		; Publication No. US20020193296A1	
		GENERAL INFORMATION:	
		APPLICANT: Xu, Jiangchun	
		APPLICANT: Dillon, Davin C.	
		APPLICANT: Mitcham, Jennifer L.	
		APPLICANT: Harlocker, Susan L.	
		APPLICANT: Jiang, Yugu	
		APPLICANT: Kalos, Michael D.	
		APPLICANT: Retter, Marc W.	
		APPLICANT: Stolk, John A.	
		APPLICANT: Day, Craig H.	
		APPLICANT: Vedvick, Thomas S.	
		APPLICANT: Carter, Darlick	
		APPLICANT: Li, Samuel X.	
		APPLICANT: Wang, Aljun	
		APPLICANT: Skeiky, Yasir A.W.	
		APPLICANT: Hepler, William T.	
		APPLICANT: Henderson, Robert A.	
		APPLICANT: Hural, John	
		APPLICANT: McNeill, Patricia D.	
		APPLICANT: Houghton, Raymond L.	
		APPLICANT: Vinals de Bassols, Carlota	
		APPLICANT: Foy, Teresa	
		APPLICANT: Fanger, Gary R.	
		TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND	
		TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER	
		FILE REFERENCE: 210121.427C26	
		CURRENT APPLICATION NUMBER: US/09/895,814	
		CURRENT FILING DATE: 2001-06-29	
		NUMBER OF SEQ ID NOS: 990	
		SOFTWARE: FastSeq for windows Version 3.0	
		SEQ ID NO 468	
		LENGTH: 3112	
		TYPE: DNA	
		ORGANISM: Homo sapiens	
		US-09-895-814-468	
		Query Match	38.1%, Score 1364; DB 10; Length 3112;
		Best Local Similarity	99.8%; Pred. No. 0;
		Matches 1774; Conservative 0; Mismatches 1; Indels 3; Gaps 3;	
OY	285	GGTAGGAATAAGAAAGCGTCCTACTTACCATCTGAGGCCACACATCTGCCTAANTNG	344
Dd	1313	GGTAGGAATAAGAAAGCGTCCTACTTACCATCTGAGGCCACACATCTGCCTAANTNG	1372
OY	345	AGATAATTAACATCTAGTAAGAACAGCAAGATGACAATATAATGTCTAAGTAGACATGT	404
Dd	1373	AGATAATTAACATCTAGTAAGAACAGCAAGATGACAATATAATGTCTAAGTAGACATGT	1432
OY	405	TTTTTGACATTTCCAGCCCCCTTTAATATTCACACACACAGACAGCAACAAAAGAGACAC	464
Dd	1433	TTTTTGACATTTCCAGCCCCCTTTAATATTCACACACACAGAGAGCAACAAAAGAGACAC	1492
OY	465	AGATATCCCTGGGGAATAAGCCGGCCCATCTTGGGTATGATGATAGCCTGGCCCTGT	524
Dd	1493	AGATATCCCTGGGGAATAAGCCGGCCCATCTTGGGTATGATGATGATAGCCTGGCCCTGT	1552
OY	525	GCCGTGTCCTCCCTGTGTGAGGAGAGACATTGAAAAATGAATGTATGTCTCTTAAAGA	584
Dd	1553	GCCGTGTCCTCCCTGTGTGAGGAGAGACATTGAAAAATGAATGTATGTCTCTTAAAGA	1612
OY	585	TGGCAGAGAAAACAGATCTCTGTGTGATATTTATTTGAACGGGATTCAGATTTGAAT	644
Dd	1613	TGGCAGAGAAAACAGATCTCTGTGTGATATTTATTTGAACGGGATTCAGATTTGAAT	1672

QY	645	GAAGTGACAAAGTGGACATTACCAATTGAGAGGAAACAGACAGAAAACTTTGATGCGTT	704
Db	1673	GAAGTCACAAAGTGGACATTACCAATTGAGAGGAAACAGAGAAAACTTTGATGCGTT	1732
QY	705	CACAAGACATGCAACAAACAAATGGATACTGTATGACATGAGGCGCCAGCTGGGG	764
Db	1733	CACAAGACATGCAACAAACAAATGGATACTGTATGACATGAGGCGCCAGCTGGGG	1792
QY	765	AGGAGATAACCAAGGGGAGAGGGTCAGGATTTGGCCCTGCTGCTAACTGTCGTTG	824
Db	1793	AGGAGATAACCAAGGGGAGAGGGTCAGGATTTGGCCCTGCTGCTAACTGTCGTTG	1852
QY	825	ATAACCAATCATTTTCATATTTCTAACCTCAAAAACAAAGCTGTGTAAATGTCATCTC	884
Db	1853	ATAACCAATCATTTTCATATTTCTAACCTCAAAAACAAAGCTGTGTAAATGTCATCTC	1912
QY	885	TACGGTTCCTTCTGGGCCCAACATCTCCATATATACAGCCACACTCATTTTATATTT	944
Db	1913	TACGGTTCCTTCTGGGCCCAACATCTCCATATATACAGCCACACTCATTTTATATTT	1972
QY	945	AGTTCCCAAGATCTGACTGTGACCTTTCTAACCTGTAGAATPACTTACTATTTGTTG	1004
Db	1973	AGTTCCCAAGATCTGACTGTGACCTTTCTAACCTGTAGAATPACTTACTATTTGTTG	2032
QY	1005	AAAGACCTTGCTGTGGTCTGCTAATATGTAGCTACAGCTTTTCTTAAGAGGTCTG	1064
Db	2033	AAAGACCTTGCTGTGGTCTGCTAATATGTAGCTACAGCTTTTCTTAAGAGGTCTG	2092
QY	1065	GCCACGGGATCTGTAAACAGCTGGGAGACATCTCAAGATCTTTCACAGGTTATCTTA	1124
Db	2093	GCCACGGGATCTGTAAACAGCTGGGAGACATCTCAAGATCTTTCACAGGTTATCTTA	2152
QY	1125	CTAGACACAGCATATCATTAACGAGAGAAATTAATCAATCAATCTCTCGAGTCT	1184
Db	2153	CTAGACACAGCATATCATTAACGAGAGAAATTAATCAATCAATCTCTCGAGTCT	2212
QY	1185	TTGGCCATACGTAATTCATTTCCACATTTTGTGCCATTCCTCAAGACCTCAAAATGTCA	1244
Db	2213	TTGGCCATACGTAATTCATTTCCACATTTTGTGCCATTCCTCAAGACCTCAAAATGTCA	2272
QY	1245	TTCCATTAAATACACAGATTAACCTTTTCTTAACCTGGAGAAATTCATTTGTAATG	1304
Db	2273	TTCCATTAAATACACAGATTAACCTTTTCTTAACCTGGAGAAATTCATTTGTAATG	2332
QY	1305	CAGCATGAGATTAATTAACATATTTGTTCACAGCAAGATGCTAAGTCCTTA	1364
Db	2333	CAGCATGAGATTAATTAACATATTTGTTCACAGCAAGATGCTAAGTCCTTA	2392
QY	1365	TCCTTCCTCTTTGTTGATTTTTTCCAGTATAAAGTTAAATGCTTAAGCTTGTACTG	1424
Db	2393	TCCTTCCTCTTTGTTGATTTTTTCCAGTATAAAGTTAAATGCTTAAGCTTGTACTG	2452
QY	1425	AGGCTGTATACAG-CACAGCCCTCCCATCCCTCACCTTATCTGTCACACATCA	1483
Db	2453	AGGCTGTATACAGCCCTCCCATCCCTCACCTTATCTGTCACACATCA	2512
QY	1484	CCCTCCCATACCACTTAACAAATCTAATCTTAATCTCTTGACATGTCAGACATA	1543
Db	2513	CCCTCCCAT-CCACCTTAAACAAATCTAATCTTAATCTCTTGACATGTCAGACATA	2570
QY	1544	CATTATTCCTTCTGCTGAGAAAGCTCTTCTGCTCTTAATCTTAAGATCATGTAAAGT	1603
Db	2571	CATTATTCCTTCTGCTGAGAAAGCTCTTCTGCTCTTAATCTTAAGATCATGTAAAGT	2630
QY	1604	TTTGAATTAAGTGAATCTACTTACTTCATGCAAAAGAGGACACATATGATGATCATC	1663
Db	2631	TTTGAATTAAGTGAATCTACTTACTTCATGCAAAAGAGGACACATATGATGATCATC	2690
QY	1664	ACATGAGACAGCAATACTATAAAGTGTATTTGATATAGAAGTTAGATTAATATATGA	1723
Db	2691	ACATGAGACAGCAATACTATAAAGTGTATTTGATATAGAAGTTAGATTAATATATGA	2750

QY	1724	AAATGCAAGACGACAGAGGAGAAATGTTTATGGGGCACCTTTGTAAGCCTGGGATGTGAAGC	17683
Db	2751	AAATGCAAGACGACAGAGGAGAAATGTTTATGGGGCACCTTTGTAAGCCTGGGATGTGAAGC	2810
QY	1784	AAAGCAGAGGAACCCATAGTATCTTATATATATACTTCAATTTCTATCTATACACA	1843
Db	2811	AAAGCAGAGGAACCCATAGTATCTTATATATATACTTCAATTTCTATCTATACACA	2870
QY	1844	ATATCAACAAGCTTTTACAGAAATTCATGCAATGCCAAATCCCAAGGTAACTTTATC	1903
Db	2871	ATATCAACAAGCTTTTACAGAAATTCATGCAATGCCAAATCCCAAGGTAACTTTATC	2930
QY	1904	CATTTCATGTGAGTGGCCCTTTAGAAATTTGGCAAATATCTGGTCACTTATCTCAACT	1963
Db	2931	CATTTCATGTGAGTGGCCCTTTAGAAATTTGGCAAATATCTGGTCACTTATCTCAACT	2990
QY	1964	TTGACATGTGTTTGTCTCTGTAGTTAATTTGAAAGAAATAGGCGACTTTGTGAGCACCTT	2023
Db	2991	TTGACATGTGTTTGTCTCTGTAGTTAATTTGAAAGAAATAGGCGACTTTGTGAGCACCTT	3050
QY	2024	TAGGTTCACTCTCCGCAATATAAGAAATTTACAAAGAGC	2061
Db	3051	TAGGTTCACTCTCCGCAATATAAGAAATTTACAAAGAGC	3088
RESULT 14			
US-10-144-678A-468			
; Sequence 468, Application US/10144678A			
; Publication No. US20030157089A1			
; GENERAL INFORMATION:			
; APPLICANT: Xu, Jianshun			
; APPLICANT: Dillon, Davin C.			
; APPLICANT: Mitcham, Jennifer L.			
; APPLICANT: Harlocker, Susan L.			
; APPLICANT: Jiang, Yugu			
; APPLICANT: Henderson, Robert A.			
; APPLICANT: Kalos, Michael D.			
; APPLICANT: Fanger, Gary R.			
; APPLICANT: Retter, Marc W.			
; APPLICANT: Stolk, John A.			
; APPLICANT: Day, Craig H.			
; APPLICANT: Vedrick, Thomas S.			
; APPLICANT: Carter, Darriek			
; APPLICANT: Li, Samuel X.			
; APPLICANT: Wang, Aljun			
; APPLICANT: Skeiky, Yasir A. W.			
; APPLICANT: Hepler, William T.			
; APPLICANT: Hural, John			
; APPLICANT: McNeill, Patricia D.			
; APPLICANT: Houghton, Raymond L.			
; APPLICANT: Vinals y de Bassols, Carlota			
; APPLICANT: Foy, Teresa M.			
; APPLICANT: Watanabe, Yoshihiro			
; APPLICANT: Deng, Ta			
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND			
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER			
; FILE REFERENCE: 210121.427C28			
; CURRENT APPLICATION NUMBER: US/10/144.678A			
; NUMBER OF SEQ ID NOS: 1033			
; SOFTWARE: FastSeq for Windows Version 3.0			
; SEQ ID NO 468			
; LENGTH: 3112			
; TYPE: DNA			
; ORGANISM: Homo sapiens			
US-10-144-678A-468			
Query Match 38.1%; Score 1364; DB 12; Length 3112;			
Best Local Similarity 99.8%; Pred. No. 0;			
Matches 1774; Conservative 0; Mismatches 1; Indels 3; Gaps 3;			
QY	285	GGTGAAGAATTAAGAAAGCTTCGACTTACATCTGAGGCGACACATCTTGCTGAATGCG	344

Db 1313 GGATGAATAATGAAGAGCTGCTGACTTACCATCTGAGGCCACACATCTGCTGAATGG 1372
 QY 345 AGATATATTACATCTAGTAACAGCAATATGACATATATCTGATAGATATG 404
 Db 1373 AGATTAATTAACATCTAGTAACAGCAATATGACATATATCTGATAGATATG 1432
 QY 405 TTTTGCATTTTCACAGCCCTTTAAATATTCACACACAGAGAGCAAAAGAGACAC 464
 Db 1433 TTTTGCATTTTCACAGCCCTTTAAATATTCACACACAGAGAGCAAAAGAGACAC 1492
 QY 465 AGAGATCCCTGGAGAAATGCCCGCCCATCTTGGTCATCTGATAGCCTCGCCCTG 524
 Db 1493 AGAGATCCCTGGAGAAATGCCCGCCCATCTTGGTCATCTGATAGCCTCGCCCTG 1552
 QY 525 GCGTGGTCCCGCTTGGAGGAGAGCATTAGAAATGATGATGATGCTTCTTAAGGA 584
 Db 1553 GCGTGGTCCCGCTTGGAGGAGAGCATTAGAAATGATGATGATGCTTCTTAAGGA 1612
 QY 585 TGGGAGAGAAACAGATCCCTGTTGATATTTTATTTGAACGGGATTAAGATTTGAAT 644
 Db 1613 TGGGAGAGAAACAGATCCCTGTTGATATTTTATTTGAACGGGATTAAGATTTGAAT 1672
 QY 645 GAAGTCACAAAGTGAGCATTACCAATGAAGAGAAACAGAGAAATCTTGATGCTT 704
 Db 1673 GAAGTCACAAAGTGAGCATTACCAATGAAGAGAGAAACAGAGAAATCTTGATGCTT 1732
 QY 705 CACAGACATGCAACAAAGAAATGGAATGATGATGATGATGATGATGATGATGATG 764
 Db 1733 CACAGACATGCAACAAAGAAATGGAATGATGATGATGATGATGATGATGATGATG 1792
 QY 765 AGGAGATTAACAGAGGAGAGAGGATGATGATGATGATGATGATGATGATGATG 824
 Db 1793 AGGAGATTAACAGAGGAGAGAGGATGATGATGATGATGATGATGATGATGATG 1852
 QY 825 ATATACCAATCAATTTATTTTCTAACCTCAAAACAAAGCTGTTATATCTGATCTC 884
 Db 1853 ATATACCAATCAATTTATTTTCTAACCTCAAAACAAAGCTGTTATATCTGATCTC 1912
 QY 885 TACGGTTCCTTGGGCGCAACATCTCATATATCCAGCAACATTTTAAATATT 944
 Db 1913 TACGGTTCCTTGGGCGCAACATCTCATATATCCAGCAACATTTTAAATATT 1972
 QY 945 AGTTCACATCTGATCTGATCTGATCTTCTACACTGATGATGATGATGATGATG 1004
 Db 1973 AGTTCACATCTGATCTGATCTGATCTTCTACACTGATGATGATGATGATGATG 2032
 QY 1005 AAAGACCTTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1064
 Db 2033 AAAGACCTTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2092
 QY 1065 GCGCAGGGGATCTGTAACAGGCTGGAGAGCATCAAGATCTTCCAGGGTTATCTTA 1124
 Db 2093 GCGCAGGGGATCTGTAACAGGCTGGAGAGCATCAAGATCTTCCAGGGTTATCTTA 2152
 QY 1125 CTAGCACACAGCATGATCTAATGAGAGTAAATATCTAATCAACATCTTCAAGTCT 1184
 Db 2153 CTAGCACACAGCATGATCTAATGAGAGTAAATATCTAATCAACATCTTCAAGTCT 2212
 QY 1185 TTGCCCATCTGTAATTCATTTCCACTTTTGGCCCAATCTCAGACCTCAAAATGCA 1244
 Db 2213 TTGCCCATCTGTAATTCATTTCCACTTTTGGCCCAATCTCAGACCTCAAAATGCA 2272
 QY 1245 TTGCAATTAATCAACAGATTAATCTTTTAACTTTTAACTTTTAACTTTTAACTTT 1304
 Db 2273 TTGCAATTAATCAACAGATTAATCTTTTAACTTTTAACTTTTAACTTTTAACTTT 2332
 QY 1305 CAGCTATGGGAATTTAATTAATTAATTTTTCAGTCAAAAGATGATGATGATGATG 1364
 Db 2333 CAGCTATGGGAATTTAATTAATTAATTTTTCAGTCAAAAGATGATGATGATGATG 2392
 QY 1365 TCCCTCCCTTTGTTGATTTTTCAGATATAAAGTTAAAGTTAAAGTTAAAGTTAAAG 1424
 Db 2393 TCCCTCCCTTTGTTGATTTTTCAGATATAAAGTTAAAGTTAAAGTTAAAGTTAAAG 2452

QY 1425 AGGCTGATATACAG -CACAGGCTTCCCATCCCTCCAGGCTTATCTGATCAGATCA 1483
 Db 2453 AGGCTGATATACAG -CACAGGCTTCCCATCCCTCCAGGCTTATCTGATCAGATCA 2512
 QY 1484 CCCCTCCATACAG -CACAGGCTTCCCATCCCTCCAGGCTTATCTGATCAGATCA 1543
 Db 2513 CCCCTCCAT -GCACCTTAAACAAATCTAAGCTTATCTGATCAGATCA -CATA 2570
 QY 1544 CATTTATCTTCTGCTGAGAGCTTCTCTGCTTATCTGATCAGATCAAGT 1603
 Db 2571 CATTTATCTTCTGCTGAGAGCTTCTCTGCTTATCTGATCAGATCAAGT 2630
 QY 1604 TTTGATTAAGTTAGATATCTTCTGATCAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1663
 Db 2631 TTTGATTAAGTTAGATATCTTCTGATCAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2690
 QY 1664 ACATGAG 1723
 Db 2691 ACATGAG 2750
 QY 1724 AATGCAAG 1783
 Db 2751 AATGCAAG 2810
 QY 1784 AAAGGAG 1843
 Db 2811 AAAGGAG 2870
 QY 1844 ATATCCCAAG 1903
 Db 2871 ATATCCCAAG 2930
 QY 1904 CATTTATCTGAG 1963
 Db 2931 CATTTATCTGAG 2990
 QY 1964 TTAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2023
 Db 2991 TTAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3050
 QY 2024 TAGGTTCACTCTGCAATTAAGATTTTACAAAGAGC 2061
 Db 3051 TAGGTTCACTCTGCAATTAAGATTTTACAAAGAGC 3088

RESULT 15
 US-10 -012 -896 -468
 ; Sequence 468, Application US/10012896
 ; Publication No. US20020183251A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Xu, Jiangchun
 ; APPLICANT: Dillon, Devin C.
 ; APPLICANT: Mitcham, Jennifer L.
 ; APPLICANT: Harlocker, Susan L.
 ; APPLICANT: Jiang, Yuguang
 ; APPLICANT: Kalos, Michael D.
 ; APPLICANT: Reiter, Marc W.
 ; APPLICANT: Stolk, John A.
 ; APPLICANT: Day, Craig H.
 ; APPLICANT: Vedvick, Thomas S.
 ; APPLICANT: Carter, Darrick
 ; APPLICANT: Li, Samuel X.
 ; APPLICANT: Wang, Aijun
 ; APPLICANT: Skeiky, Yasir A.W.
 ; APPLICANT: Hepler, William T.
 ; APPLICANT: Henderson, Robert A.
 ; APPLICANT: Hural, John
 ; APPLICANT: McNeill, Patricia D.
 ; APPLICANT: Houghton, Raymond L.
 ; APPLICANT: Vinals de Bassols, Carlota
 ; APPLICANT: Foy, Teresa
 ; APPLICANT: Fanger, Gary R.

```
; APPLICANT: Watanabe, Yoshitiro
; APPLICANT: Weagher, Madeleine Joy
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C27
; CURRENT APPLICATION NUMBER: US/10/012,896
; NUMBER OF SEQ ID NOS: 1011
; SOFTWARE: FASTSEQ for Windows Version 3.0
; LENGTH: 3112
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-012-896-468

Query Match      38.1%; Score 1364; DB 13; Length 3112;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1774; Conservative 0; Mismatches 1; Indels 3; Gaps 3;

QY      285 GGTGAGAAATGAAGAAAGCTGCTGACTTTACCATGTGAGGCCACACATCTGCTGAATGG 344
DB      1313 GGTGAGAAATGAAGAAAGCTGCTGACTTTACCATGTGAGGCCACACATCTGCTGAATGG 1372

QY      345 AGATTAATTAACATCTAGAAACAGCAAGATGACAAATTAATGCTAGTAGTGCATGT 404
DB      1373 AGATTAATTAACATCTAGAAACAGCAAGATGACAAATTAATGCTAGTAGTGCATGT 1432

QY      405 TTTTGCACATTTCCAGCCCTTTAAATATCCACACACAGAGAAAGCAGAAAAGAGCAG 464
DB      1433 TTTTGCACATTTCCAGCCCTTTAAATATCCACACACAGAGAAAGCAGAAAAGAGCAG 1492

QY      465 AGAGATCCCTGGGAGAAATGCCGGCCGCATCTTGGGTGATCGATGAGCCTCGCCGTGT 524
DB      1493 AGAGATCCCTGGGAGAAATGCCGGCCGCATCTTGGGTGATCGATGAGCCTCGCCGTGT 1552

QY      525 GCTGTGTCCTGCTGTGAGGAGAGACATTTAGAAAATGAATTGATGCTTCTTAAGGA 584
DB      1553 GCTGTGTCCTGCTGTGAGGAGAGACATTTAGAAAATGAATTGATGCTTCTTAAGGA 1612

QY      585 TGGGAGAGAAACAGATCTGTGTGATATTATTGTAACGGGATTCAGATTTGAAAT 644
DB      1613 TGGGAGAGAAACAGATCTGTGTGATATTATTGTAACGGGATTCAGATTTGAAAT 1672

QY      645 GAAGTCACAAAGTGAGCATTTACCAATGAGAGAAAACAGAGAAAATCTTGATGCTT 704
DB      1673 GAAGTCACAAAGTGAGCATTTACCAATGAGAGAAAACAGAGAAAATCTTGATGCTT 1732

QY      705 CACAAGACATGCAACAACAATAATGAGATCTGTGATGACATGAGGAGCCAGCTGGGG 764
DB      1733 CACAAGACATGCAACAACAATAATGAGATCTGTGATGACATGAGGAGCCAGCTGGGG 1792

QY      765 AGAGATTAACAGGGGGCAGAGGGTCAAGATTTGGCCCTCTGCTAAACTGTGCGTT 824
DB      1793 AGAGATTAACAGGGGGCAGAGGGTCAAGATTTGGCCCTCTGCTAAACTGTGCGTT 1852

QY      825 ATAACCAATCATTTCAATTTCTAACCCCTCAAAAACAAGCTGTGTAATTCGATGTC 884
DB      1853 ATAACCAATCATTTCAATTTCTAACCCCTCAAAAACAAGCTGTGTAATTCGATGTC 1912

QY      885 TAGGGTTCCTTCTGGGGCCAAACATTTCCATATATCCAGCACACTCTTTTAAATAT 944
DB      1913 TAGGGTTCCTTCTGGGGCCAAACATTTCCATATATCCAGCACACTCTTTTAAATAT 1972

QY      945 AGTTCCAGATCTTACTGTGACCTTTCTACAGTGAATTAACATTAATCTATTTGTTTC 1004
DB      1973 AGTTCCAGATCTTACTGTGACCTTTCTACAGTGAATTAACATTAATCTATTTGTTTC 2032

QY      1005 AAAGACCTTGTGCTGTGCTGCTAAATATATGATGACGCTTTTCTTAAGAGGTCTTG 1064
DB      2033 AAAGACCTTGTGCTGTGCTGCTAAATATATGATGACGCTTTTCTTAAGAGGTCTTG 2092

QY      1065 GCCCAGGGATCTGTGAACAGGCTGGGAAGCATCTTAAGATCTTCCAGGGTTTACTTA 1124
DB      1124 GCCCAGGGATCTGTGAACAGGCTGGGAAGCATCTTAAGATCTTCCAGGGTTTACTTA 1124
```

```
DB      2093 GCCCAGGGATCTGTGAACAGGCTGGGAAGCATCTTAAGATCTTCCAGGGTTTACTTA 2152
QY      1125 CTAGCACACAGCATGATCATTTACGAGGAATTAATCTAATCAATCATCTCCAGTGTCT 1184
DB      2153 CTAGCACACAGCATGATCATTTACGAGGAATTAATCTAATCAATCATCTCCAGTGTCT 2212
QY      1185 TTGCCCATACCTGAATTTGATTTTCCACATTTTGTGCCCATCTTCAGAGACCTCAAAATGTCA 1244
DB      2213 TTGCCCATACCTGAATTTGATTTTCCACATTTTGTGCCCATCTTCAGAGACCTCAAAATGTCA 2272
QY      1245 TTCCATTAATATACAGAGATTAATCTTTTAACTGGAAGAAATCAATGTTACTATG 1304
DB      2273 TTCCATTAATATACAGAGATTAATCTTTTAACTGGAAGAAATCAATGTTACTATG 2332
QY      1305 CAGCTATGGAATTAATTAATCATATTTGTTTCCAGTGAAGAAATGATCAAGTCCCTTA 1364
DB      2333 CAGCTATGGAATTAATTAATCATATTTGTTTCCAGTGAAGAAATGATCAAGTCCCTTA 2392
QY      1365 TCCCTCCCTTTGTTGATTTTTCAGATATAAAGTTAAATGCTTAGCCTGTACTG 1424
DB      2393 TCCCTCCCTTTGTTGATTTTTCAGATATAAAGTTAAATGCTTAGCCTGTACTG 2452
QY      1425 AGGCTGTATAGAG-CACAGCCTCCGCCATCCCTCCACACCTTATCTGTCATCACCATCA 1483
DB      2453 AGGCTGTATAGAGCCACAGCCTCCGCCATCCCTCCACACCTTATCTGTCATCACCATCA 2512
QY      1484 CCCCTCCCATACCACTTAACAAATCTTAATCTTGAATCTCTGAACATGTCAGAGATA 1543
DB      2513 CCCCTCCCAT-CCACCTTAACAAATCTTAATCTTGAATCTCTGAACATGTCAGAG-CATA 2570
QY      1544 CATTAATCTCTTGTGCTGAGAGCTCTTCTGTCTTAAATCTAGAAATGATTAAGT 1603
DB      2571 CATTAATCTCTTGTGCTGAGAGCTCTTCTGTCTTAAATCTAGAAATGATTAAGT 2630
QY      1604 TTTGATTAAGTGTGATCTTACTTCAATGCAAAAGGAGACATATGAGATTCATATC 1663
DB      2631 TTTGATTAAGTGTGATCTTACTTCAATGCAAAAGGAGACATATGAGATTCATATC 2690
QY      1664 ACATGAGACAGCAATACTTAAGATGTAATTTAGATTTAGAGTTTGAATATATATGA 1723
DB      2691 ACATGAGACAGCAATACTTAAGATGTAATTTAGATTTAGAGTTTGAATATATATGA 2750
QY      1724 AATGCAAGAGCCACAGAGGGAATGTTATGCGGACGCTTTGTAAAGCTGGATGTGAAC 1783
DB      2751 AATGCAAGAGCCACAGAGGGAATGTTATGCGGACGCTTTGTAAAGCTGGATGTGAAC 2810
QY      1784 AAAGCAGAGGAACTCATAGTATCTTAATTAATTAATCTTCTATCTATATACA 1843
DB      2811 AAAGCAGAGGAACTCATAGTATCTTAATTAATTAATCTTCTATCTATATACA 2870
QY      1844 ATATCAACAAGCTTTTCACAGAAATTCATGAGTGAATCCCAAGGTAACCTTTATC 1903
DB      2871 ATATCAACAAGCTTTTCACAGAAATTCATGAGTGAATCCCAAGGTAACCTTTATC 2930
QY      1904 CATTTCAATGATGATGGCTTTTACAATTTTGGCAATCAATCTGTACTTATCTCACT 1963
DB      2931 CATTTCAATGATGATGGCTTTTACAATTTTGGCAATCAATCTGTACTTATCTCACT 2990
QY      1964 TTGAGATGTTGTTTCTCTGAGTTAATTTGAAGAAATTAAGGACCTCTGTGAGACCACT 2023
DB      2991 TTGAGATGTTGTTTCTCTGAGTTAATTTGAAGAAATTAAGGACCTCTGTGAGACCACT 3050
QY      2024 TAGGGTTCACCTCTGGCAATTAAGAAATTAACAAAGAGC 2061
DB      3051 TAGGGTTCACCTCTGGCAATTAAGAAATTAACAAAGAGC 3088
```

Search completed: September 27, 2003, 12:16:16
Job time : 836.096 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Comphen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 26, 2003, 21:39:38 ; Search time 7516.98 Seconds
(without alignments)
11581.589 Million cell updates/sec

Title: US-09-402-713a-6
Perfect score: 3582
Sequence: 1 acagaagaataagcaagtcg.....tgatcttctgttaacattt 3582

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 22781392 seqs, 12152238056 residues

Word size : 0
Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estnu:*
5: em_estrov:*
6: em_estrpl:*
7: em_estro:*
8: em_hic:*
9: gb_est1:*
10: gb_est2:*
11: gb_hic:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: em_gss_hum:*
18: em_gss_inu:*
19: em_gss_pin:*
20: em_gss_vrt:*
21: em_gss_fun:*
22: em_gss_mam:*
23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_rdg:*
26: em_gss_phg:*
27: em_gss_vrt1:*
28: gb_gss1:*
29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	533	14.9	542	28	AQ318297 RPC11-10
2	452	12.6	546	28	AQ318289 RPC11-10
3	367	10.2	402	9	AA578773 nb24a04.s
4	323	9.0	654	28	AQ319247 RPC11-10

Result No.	Score	Query Match	Length	DB ID	Description
5	319	8.9	346	10	AW948945 QV4-FT000
6	293	8.2	304	13	BQ372852 CM4-FT010
7	287	8.0	856	9	A1557225 PR2.1.15
8	280	7.8	700	13	BQ373258 MR0-FT017
9	247	6.9	319	13	BQ371438 RC6-FN011
10	238	6.6	290	10	BF373619 MR0-FT017
11	234	6.6	304	13	BQ338234 CM2-NN011
12	218	6.0	10	BF058371 RC5-FT019	
13	214	6.0	394	28	AQ206972 HS.3238.B
14	213	5.9	332	10	BF058286 RC5-FT019
15	198	5.5	282	10	BF373581 MR0-FT017
16	194	5.4	323	13	BQ338235 CM2-NN011
17	172	4.8	189	13	BQ372602 QV4-FT000
18	167	4.7	167	10	BF373406 IL2-FT015
19	152	4.2	197	13	BQ372624 QV4-FT000
20	146	4.1	332	13	BQ372858 CM4-FT010
21	142	4.0	441	10	BF058890 RC5-FT019
22	121	3.4	572	13	BQ292350 PM0-AN008
23	86	2.4	657	9	A1557495 PR2.1.7.H
24	83	2.3	245	13	BQ373093 RC2-FT012
25	62	1.7	451	28	AQ246715 HS.2059.B
26	61	1.7	376	28	AQ069980 HS.3027.B
27	51	1.4	111	13	BQ373237 RC2-FT012
28	44	1.2	863	28	B2190572 CH230-330
29	36	1.0	610	28	BH076212 RPC1-24-2
30	35	1.0	598	28	AZ323381 IM0044P06
31	35	1.0	602	28	AZ323366 IM0044P05
32	35	1.0	960	29	CNS02000 AL214785 Tetraodon
33	34	0.9	1166	14	CD498534 CDA34-B05
34	33	0.9	505	28	BH082184 RPC1-24-3
35	33	0.9	548	28	BH084129 RPC1-24-3
36	33	0.9	868	29	CNS015X0 AL165789 Tetraodon
37	33	0.9	909	29	CNS026P7 BE552517 UI-M-AR0-
38	32	0.9	189	10	BE552517 UI-M-AR0-
39	32	0.9	200	28	AZ758563 IM0550D10
40	32	0.9	266	28	AZ965467 2M0235N02
41	32	0.9	272	29	FR0047998 AL444783 Fugu rubr
42	32	0.9	429	10	BE953161 UI-M-CD1-
43	32	0.9	551	28	AZ037336 RPC1-23-2
44	32	0.9	577	28	AZ308663 IM001E22
45	32	0.9	581	10	BG086866 H3131E09-

ALIGNMENTS

RESULT 1
AQ318297/c
LOCUS
DEFINITION
RPC11-108A20.TV RPC1-11 Homo sapiens genomic clone RPC1-11-108A20,
genomic survey sequence.

ACCESSION
AQ318297
VERSION
AQ318297.1 GI:4050267
KEYWORDS
GSS.
SOURCE
Homo sapiens
ORGANISM
Homo sapiens (human)

REFERENCE
AUTHORS
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
Adams,M.D., Rounsley,S.D., Zhao,S., Bass,S., Linher,K., Golden,K.,
Berry,K., Granger,D., Suh,E., Wible,C., de Jong,P. and Venter,J.C.
TITLE
JOURNAL
COMMENT
Use of human BAC End Sequences for Sequence-Ready Map Building
Other_GSSs: RPC11-108A20.TV
Contact: Shaying Zhao, William Nierman, Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850
Tel: 301 838 0200
Fax: 301 838 0208
Email: nbeetlgr.org
Clones are derived from the human BAC library RPC1-11. For BAC
library availability, please contact Pieter de Jong

(pieteredejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (<http://bacpac.med.buffalo.edu/ordering>) or from Research Genetics (info@resgen.com). BAC end search page: http://www.tigr.org/tldb/hungen/bac_end_search/bac_end_search.html
Seq primer: T7
Class: BAC ends.

FEATURES
source

1. 542
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="GDB:7541107"
/db_xref="taxon:9606"
/clone="RPC1-11-108A20"
/sex="Male"
/cell_type="Lymphocytes"
/clone_11b="RPC1-11"
/note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
RPC111 Human Male BAC Library"
BASE COUNT 151 a 106 c 118 g 167 t
ORIGIN

Query Match 14.9%; Score 533; DB 28; Length 542;
Best Local Similarity 100.0%; Pred. No. 2.5e-224;

Matches 533; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2303 GACAAACCAATATGATATTAATCTTACTCTTACATCAGCTACACACTGCTTGACATATA 2362
|||||
DB 542 GACAAACCAATATGATATTAATCTTACTCTTACATCAGCTACACACTGCTTGACATATA 483
2363 TTGTTAGAGACCTCGCATTTGGGTTCTCTTAAGCAAAATCTTCATTAGGTCCTCA 2422
|||||
DB 482 TTGTTAGAGACCTCGCATTTGGGTTCTCTTAAGCAAAATCTTCATTAGGTCCTCA 423
OY 2423 GCTGGGGCTGTGCATCAGCGGTTTGAGAAATATTCATCTCAGCAGACAGAAATTT 2482
|||||
DB 422 GCTGGGGCTGTGCATCAGCGGTTTGAGAAATATTCATCTCAGCAGACAGAAATTT 363
OY 2483 GAATTCCTCATCTTTTGAATCATTTTACCAGGTTTGAGAGATTTAGACAGCTCAGG 2542
|||||
DB 362 GAATTCCTCATCTTTTGAATCATTTTACCAGGTTTGAGAGATTTAGACAGCTCAGG 303
2543 TGCTTTCACTATGCTCTGAACTTGTCCCTCTTTGTTCAATGATATCCAAATATA 2602
|||||
DB 302 TGCTTTCACTATGCTCTGAACTTGTCCCTCTTTGTTCAATGATATCCAAATATA 243
OY 2603 TAAATGTTCTTTGAACTGATGCTCATAGAGAGAAATTAAGAACTGAGTGAATCAA 2662
|||||
DB 242 TAAATGTTCTTTGAACTGATGCTCATAGAGAGAAATTAAGAACTGAGTGAATCAA 183
OY 2663 CATTAGGGAATCAAGAAATTTAGATTAGCTCACCTGCTCAAAAGGAACCAAGTAA 2722
|||||
DB 182 CATTAGGGAATCAAGAAATTTAGATTAGCTCACCTGCTCAAAAGGAACCAAGTAA 123
OY 2723 CAAGAAGCTGTGACCTGATCGTCCCATCTCTGTGAGCAGACAACCAAGCAGAGACC 2782
|||||
DB 122 CAAGAAGCTGTGACCTGATCGTCCCATCTCTGTGAGCAGACAACCAAGCAGAGACC 63
OY 2783 AACGATGTCTGAGATCTTAAATCAAGAAACCAAGTGTGAGTGAATTC 2835
|||||
DB 62 AACGATGTCTGAGATCTTAAATCAAGAAACCAAGTGTGAGTGAATTC 10

RESULT 2
AO318289/c 546 bp DNA linear GSS 04-MAY-1999
LOCUS RPC111-108A18.TV RPC1-11 Homo sapiens genomic clone RPC1-11-108A18.
DEFINITION genomic survey sequence.
ACCESSION AO318289
VERSION AO318289.1 GI:4050259
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE
1 (bases 1 to 546)
Adams M.D., Rounsley, S.D., Zhao, S., Bass, S., Linher, K., Golden, K.,
Berry, K., Granger, D., Suh, E., Wille, C., de Jong, P. and Venter, J.C.
Use of human BAC End Sequences for Sequence-Ready Map Building
Unpublished
Other-GSSs: RPC111-108A18.TV
Contact: Shaying Zhao, William Nierman, Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
712 Medical Center Dr., Rockville, MD 20850
Tel: 301 838 0200
Fax: 301 838 0208
Email: hbe@tigr.org
Clones are derived from the human BAC library RPC1-11. For BAC
library availability, please contact Pieter de Jong
(pieteredejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (<http://bacpac.med.buffalo.edu/ordering>) or from
Research Genetics (info@resgen.com). BAC end search page:
http://www.tigr.org/tldb/hungen/bac_end_search/bac_end_search.html
Seq primer: T7
Class: BAC ends.

FEATURES
source

1. 546
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="GDB:7541105"
/db_xref="taxon:9606"
/clone="RPC1-11-108A18"
/sex="Male"
/cell_type="Lymphocytes"
/clone_11b="RPC1-11"
/note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
RPC111 Human Male BAC Library"
BASE COUNT 150 a 106 c 116 g 172 t 2 others
ORIGIN

Query Match 12.6%; Score 452; DB 28; Length 546;
Best Local Similarity 99.8%; Pred. No. 1.7e-188;

Matches 502; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2330 TCCTACCACTGACGTACACACACTGTTGACATATATTTAGAGAACCTCGCATTTGGGG 2389
|||||
DB 503 TCCTACCACTGACGTACACACACTGTTGACATATATTTAGAGAACCTCGCATTTGGGG 444
2390 TTCTCTTAAGCAAAATCTTCATAGGTCACAGTGGGCTGTGCATCAGCGGTTTGA 2449
|||||
DB 443 TTCTCTTAAGCAAAATCTTCATAGGTCACAGTGGGCTGTGCATCAGCGGTTTGA 384
OY 2450 GAAATATTCATTTCTCAGCAGAACCCAGAAATTTAATTCCTCATCTTTTGAATCATTT 2509
|||||
DB 383 GAAATATTCATTTCTCAGCAGAACCCAGAAATTTAATTCCTCATCTTTTGAATCATTT 324
OY 2510 TACAGGTTTGAGAGAGATTGACAGACCTCGGTGCTTCACTAATGTCCTGAACTCT 2569
|||||
DB 323 TACAGGTTTGAGAGAGATTGACAGACCTCGGTGCTTCACTAATGTCCTGAACTCT 264
OY 2570 GTCCCTCTTTGTGTGATGATAGTATCAATTAATTAATGTTATCTTTGAACGATGCTCAT 2629
|||||
DB 263 GTCCCTCTTTGTGTGATGATAGTATCAATTAATTAATGTTATCTTTGAACGATGCTCAT 204
OY 2630 AGGAGAGATTAAGAACTGTGAGTATATCACATTAGGGATTCAAGAAATTTAGAT 2689
|||||
DB 203 AGGAGAGATTAAGAACTGTGAGTATATCAATTAAGGGATTCAAGAAATTTAGAT 144
OY 2690 TTAAGCTCACACCTGTGTAAGAAAGCAAGATTAAGAACTGTGACCTGTGATCGTCC 2749
|||||
DB 143 TTAAGCTCACACCTGTGTAAGAAAGCAAGATTAAGAACTGTGACCTGTGATCGTCC 84
OY 2750 CATCTGTGTGAGCCACACCAAGCAGAGCCCAAGCAGTGTGAGATCCTTAAATCAA 2809
|||||
DB 83 CATCTGTGTGAGCCACACCAAGCAGAGCCCAAGCAGTGTGAGATCCTTAAATCAA 24

QY 2810 GGAAACCATGTCATGAGTTGAA 2832
 |||||||
 Db 23 GGAAACCATGTCATGAGTTGAA 1

RESULT 3
 AA578773 402 bp mRNA linear EST 12-SEP-1997
 LOCUS nh24a04.s1 NCL_CGAP_Prl Homo sapiens CDNA clone IMAGE:953262, mRNA
 DEFINITION sequence.
 ACCESSION AA578773
 VERSION AA578773.1 GI:2356957
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 REFERENCE 1 (bases 1 to 402)
 AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
 TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 JOURNAL Unpublished
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-r@mail.nih.gov
 Tissue Procurement: W. Marston Linehan, M.D., Rodrigo Chuagui, M.D.,
 Michael Emmert-Buck, M.D., Ph.D.
 cDNA Library Preparation: David B. Krizman, Ph.D.
 cDNA Library Arrayed by: Genome Systems Inc., Greg Lennon, Ph.D.
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 www.bio.llnl.gov/bbrp/image/image.html
 Insert length: 565 Std Error: 0.00
 Seq primer: -40m13 fwd. ET from Amersham
 High quality sequence stop: 373.
 Location/Qualifiers
 1. 402
 /organism="Homo sapiens"
 /mol_type="mrna"
 /db_xref="taxon:9606"
 /clone="IMAGE:953262"
 /sex="Male"
 /dev_stage="45 years old"
 /lab_host="DH10B"
 /clone_lib="NCL_CGAP_Prl"
 /note="Vector: PAMP10; Site_1: NotI; Site_2: EcoRI; 1st
 strand cDNA was primed with oligo(dt)17 on 50 ng of
 DNase-treated, total cellular RNA obtained from 5,000-10
 ,000 microdissected, histologically normal prostate
 epithelial cells. Double-stranded cDNA was ligated to
 EcoRI adaptors, 5 cycles of PCR applied to the cDNA with
 an adaptor-specific primer, and the resulting PCR product
 subcloned into PAMP10 by the UDG-cloning method (Life
 Technologies). Average insert size is 600 bp. NOTE: Not
 directionally cloned. This library was constructed by
 David Krizman."

BASE COUNT 128 a 86 c 84 g 104 t
 ORIGIN
 Query Match 10.2%; Score 367; DB 9; Length 402;
 Best Local Similarity 100.0%; Pred. No. 9e-151;
 Matches 367; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 617 TATTTGAACGGGATTACAGATTGAAATGACACAAAGTGAGCATTTACCATGAGAG 676
 |||||||
 Db 36 TATTTGAACGGGATTACAGATTGAAATGAAATGAAAGTGAGCATTTACCATGAGAG 95

QY 677 AAACAGACGAGAAATCTTGATGCTTACACAGACATGCAACAAACAAATGGAATACT 736
 |||||||
 Db 96 AAACAGACGAGAAATCTTGATGCTTACACAGACATGCAACAAACAAATGGAATACT 155

QY 737 GTGATGACATGAGCAGCCAGCTGGGAGAGAGATACCAAGGGGAGAGAGGTTCAGATT 796
 |||||||

Db 156 GTGATGACATGAGCAGCCAGCCAGCTGGGAGAGAGATACCAAGGGGAGAGGTTCAGATT 215
 QY 797 CTGGCCCTGCTGCTTAACCTGTCCTTCAATACCAATATTTCAATTTCAACCTCA 856
 |||||||
 Db 216 CTGGCCCTGCTGCTTAACCTGTCCTTCAATACCAATATTTCAATTTCAACCTCA 275

QY 857 AAACAAAGCTGTTGTAATATGATCTACAGGTTCTTGGGCCCAACATTTCCATA 916
 |||||||
 Db 276 AAACAAAGCTGTTGTAATATGATCTACAGGTTCTTGGGCCCAACATTTCCATA 335

QY 917 TATCCAGCCACTCATTTTATATTTAGTTCCAGATCTGATGTAACCTTTTACA 976
 |||||||
 Db 336 TATCCAGCCACTCATTTTATATTTAGTTCCAGATCTGATGTAACCTTTTACA 395

QY 977 CTGTAGA 983
 |||||||
 Db 396 CTGTAGA 402

RESULT 4
 AQ319247/c 654 bp DNA linear GSS 06-MAY-1999
 LOCUS RPCI11-108L4.TV RPCI-11 Homo sapiens genomic clone RPCI-11-108L4,
 DEFINITION genomic survey sequence.
 ACCESSION AQ319247
 VERSION AQ319247.1 GI:4052212
 KEYWORDS GSS.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 REFERENCE 1 (bases 1 to 654)
 AUTHORS Adams, M.D., Rounsley, S.D., Zhao, S., Bass, S., Linher, K., Golden, K.,
 Berry, K., Granger, D., Suh, E., Wible, C., de Jong, P. and Venter, J.C.
 TITLE use of human BAC End Sequences for Sequence-Ready Map Building
 JOURNAL Unpublished
 COMMENT Contact: Shaying Zhao, William Nierman, Mark Adams
 Department of Eukaryotic Genomics
 The Institute for Genomic Research
 9712 Medical Center Dr., Rockville, MD 20850
 Tel: 301 838 0200
 Fax: 301 838 0208
 Email: hbe@ligr.org
 Clones are derived from the human BAC library RPCI-11. For BAC
 library availability, please contact Pieter de Jong
 (pieterdejong.med.bufileo.edu). Clones may be purchased from
 BACPAC Resources (http://bacpac.med.bufileo.edu/ordering) or from
 Research Genetics (info@resgen.com). BAC end search page:
 http://www.tigr.org/cdb/humgen/bac_end_search/bac_end_search.html
 Seq primer: r7
 Class: BAC ends.
 Location/Qualifiers
 1. 654
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"
 /db_xref="taxon:9606"
 /clone="RPCI-11-108L4"
 /sex="Male"
 /cell_type="Lymphocytes"
 /clone_lib="RPCI-11"
 /note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
 RPCI11 Human Male BAC Library"

BASE COUNT 213 a 100 c 139 g 202 t
 ORIGIN
 Query Match 9.0%; Score 323; DB 28; Length 654;
 Best Local Similarity 100.0%; Pred. No. 1.8e-131;
 Matches 323; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1540 CATACATTAATTCCTTCTGCTGAGAGCTCTTCTCTTAATCTAGAAATGATGTA 1599
 |||||||
 Db 332 CATACATTAATTCCTTCTGCTGAGAGCTCTTCTCTTAATCTAGAAATGATGTA 273

OY 1600 AAGTTTGAAATAGTTGACTATCTTACTTCATGCAAGAGGACACATATGAGATTTCAT 1659
|||||
DB 272 AAGTTTGAAATAGTTGACTATCTTACTTCATGCAAGAGGACACATATGAGATTTCAT 213
1660 CATACATGAGACAGCAAAATCTAAAGTGTATTTGTTATAGAGTTTGATTAATAT 1719
|||||
DB 212 CATACATGAGACAGCAAAATCTAAAGTGTATTTGTTATAGAGTTTGATTAATAT 153
1720 ATGAATGCAAGAGCCACAGAGGAGATGTTATGCGCAGCTTTGTATAGCCTGGAGTGTG 1779
|||||
DB 152 ATGAATGCAAGAGCCACAGAGGAGATGTTATGCGCAGCTTTGTATAGCCTGGAGTGTG 93
OY 1780 AAGCAAGCGAGGAGACTCTATGATATCTTATATATATCTTCAATTTCTCTATCTAT 1839
|||||
DB 92 AAGCAAGCGAGGAGACTCTATGATATCTTATATATATCTTCAATTTCTCTATCTAT 33
OY 1840 CACATATCCAAAGAGCTTTTCA 1862
|||||
DB 32 CACATATCCAAAGAGCTTTTCA 10

RESULT 5
AM948945 346 bp mRNA linear EST 31-MAY-2000
LOCUS AM948945
DEFINITION QV4-FT0004-130500-212-d11 FT0004 Homo sapiens cDNA, mRNA sequence.
ACCESSION AM948945
VERSION AM948945.1 GI:8126719
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 346)
AUTHORS Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H.,
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
Simpson,A.J.
Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
JOURNAL MEDLINE
PUBMED 20202663
10737800
CONTACT: Simpson A.J.G.
LABORATORY of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=CM4<2=QV4-FT0004-130
500-212-d11&t3=2000-05-13&t4=1)
Seq primer: puc 18 forward
High quality sequence stop: 344.
location/Qualifiers
1. 346
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="FT0004"

/note="Organ: prostate,tumor; Vector: puc18; Site_1: SmaI;
Site_2: SmaI; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."

BASE COUNT 104 a 81 c 63 g 98 t
ORIGIN
Query Match 8.9%; Score 319; DB 10; Length 346;
Best local similarity 100.0%; Pred. No. 1.2e-129;
Matches 319; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 2612 CTTGAACTGATGCTCATAGAGAGAAATATAGAACTCTGAGTATATCAATAGAGGA 2671
DB 28 CTTGAACTGATGCTCATAGAGAGAAATATAGAACTCTGAGTATATCAATAGAGGA 87
OY 2672 TTCAAAGAAATATAGATTTAGCTCACACGCGCAAAAGAACCAAGATCAAAAGACT 2731
DB 88 TTCAAAGAAATATAGATTTAGCTCACACGCGCTAAAGAACCAAGATCAAAAGACT 147
OY 2732 CTGAGCTGCATCGTCCCATCTCTGTGAGCCACAAACAGCAGAGACCCAGCATGT 2791
DB 148 CTGAGCTGCATCGTCCCATCTCTGTGAGCCACAAACAGCAGAGACCCAGCATGT 207
OY 2792 CTGAGATCTTAAATCAAGAAACCAAGTGTATGAGTTGAATTCCTATTATGAGATGT 2851
DB 208 CTGAGATCTTAAATCAAGAAACCAAGTGTATGAGTTGAATTCCTATTATGAGATGT 267
OY 2852 AGCTTCGGCATCTCGGCTCTCTCTGTGACATATATAGCTTCTAGCCCTTGTCCCA 2911
DB 268 AGCTTCGGCATCTCGGCTCTCTCTGTGACATATATAGCTTCTAGCCCTTGTCCCA 327
OY 2912 CGACTTTATCTTTTCTCC 2930
DB 328 CGACTTTATCTTTTCTCC 346

RESULT 6
BQ372852 304 bp mRNA linear EST 21-MAY-2002
LOCUS BQ372852
DEFINITION CM4-FT0103-230600-211-c09 FT0103 Homo sapiens cDNA, mRNA sequence.
ACCESSION BQ372852
VERSION BQ372852.1 GI:21048366
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 304)
AUTHORS Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H.,
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
Simpson,A.J.
Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
JOURNAL MEDLINE
PUBMED 20202663
10737800
CONTACT: Simpson A.J.G.
LABORATORY of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=CM4<2=CM4-FT0103-
230600-211-c09&t3=2000-06-23&t4=1)
Seq primer: puc 18 forward
High quality sequence stop: 304.
location/Qualifiers
1. 304
/organism="Homo sapiens"
/mol_type="mRNA"

FEATURES
source

	/db_xref="taxon:9606"	
	/dev_stage="Adult"	
	/clone_lib="PT0103"	
	/note="Organ: prostate_tumor; Vector: puc18; site_1: SmaI; site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."	
BASE COUNT	68 a 97 c 45 g 94 t	
ORIGIN		
Query Match	8.2%; Score 293;	DB 13; Length 304;
Best Local Similarity	100.0%;	Pred. No. 3.9e-118;
Matches 293:	Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
OY	2742 ATGCTCCCATCTGTGGAGCCACAAACAGCAGAGGCCCAAGCATGTCTGAGATCCT	2801
Dd	12 ATGCTCCCCATCTGTGGAGCCACAACAGCAGAGGCCCAAGCATGTCTGAGATCCT	71
OY	2802 TAAATCAAGAAACCAGTGCATGATTGAATTCCTATTATGAGATGCTAGCTTGCGC	2861
Dd	72 TAAATCAAGAAACCAGTGCATGATTGAATTCCTATTATGAGATGCTAGCTTGCGC	131
OY	2862 CATCTGTGGCTCTCTCTTGACACATATTTACTTTCTAGCTTTGCTTCCAGACTTTAT	2921
Dd	132 CATCTGTGGCTCTCTCTTGACACATATTTACTTTCTAGCTTTGCTTCCAGACTTTAT	191
OY	2922 CTTTTTCACACATCGCTTACCAATCCCTCTCTGCTGTGTTGCTTGACCTTCCC	2981
Dd	192 CTTTTTCACACATCGCTTACCAATCCCTCTCTGCTGTGTTGCTTGACCTTCCC	251
OY	2982 CAAGAATTTCAACGACTCTCAAGTCTTTTCTTCATCCCAACCACTAACCTGA	3034
Dd	252 CAAGAATTTCAACGACTCTCAAGTCTTTTCTTCATCCCAACCACTAACCTGA	304
RESULT 7		
LOCUS	A1557225	856 bp mRNA linear EST 09-AUG-1999
DEFINITION	PT2.1.15_B05.r tumor2 Homo sapiens CDNA 3', mRNA sequence.	
ACCESSION	A1557225	
VERSION	A1557225.1 GI:4489588	
KEYWORDS	EST.	
SOURCE	Homo sapiens (human)	
ORGANISM	Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. Huang,G.M., Ng,W.L., Parkas,J., He,L., Liang,H.A., Gordon,D., Yu,J.J. and Hood,L. Prostate cancer expression profiling by cDNA sequencing analysis Genomics 59 (2), 178-186 (1999) 10409429	
TITLE	Contact: Guyang Matthew Huang	
JOURNML MEDLINE PUBMED	Leroy Hood University of Washington Department of Molecular Biotechnology, Box 357730, University of Washington, Seattle, WA 98195 Tel: 5106280100 Fax: 5106280108 Email: huanggm@yahoo.com. Location/Qualifiers 1..856	
FEATURES	location/Qualifiers	
source	1..856	
	/organism="Homo sapiens"	
	/mol_type="mRNA"	
	/db_xref="taxon:9606"	
	/clone_lib="tumor2"	
	/note="Organ: Prostate; Vector: pBluescript; Directional cDNA library was constructed using lambda ZP II kit (Stratagene). mRNA was extracted from a frozen prostate	

BASE COUNT	237 a	191 c	180 g	214 t	34 others
ORIGIN	tumor tissue (Mayo Clinics) "				
Query Match	8.0%; Score 287; DB 9; Length 856;				
Best Local Similarity	100.0%; Pred. No. 1,5e-115;				
Matches 287;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;	
QY	1540 CATACATTATTCCTTCTGCTGAGAGAGCCTCTTCCTTCTTCTTAAATCTAGAAATGATGA 1599				
DB	205 CATACATTATTCCTTCTGCTGAGAGAGCCTCTTCCTTCTTCTTAAATCTAGAAATGATGA 264				
QY	1600 AAGTTTGAATTAAGTTGACTATCTTACTTCTATGCAAGAGAGGACACATATGACATTCAT 1659				
DB	265 AAGTTTGAATTAAGTTGACTATCTTACTTCTATGCAAGAGAGGACACATATGACATTCAT 324				
QY	1660 CATACATGAGACAGCAAAATCTTAAAGTGAATTTGATATAGAGTTTATAGATTAATAT 1719				
DB	325 CATACATGAGACAGCAAAATCTTAAAGTGAATTTGATATAGAGTTTATAGATTAATAT 384				
QY	1720 ATGAATGCAAGAGCCACAGAGGGAATGTTTATGGGACGCTTTGTAAGCCTGGGATG 1779				
DB	385 ATGAATGCAAGAGCCACAGAGGGAATGTTTATGGGACGCTTTGTAAGCCTGGGATG 444				
QY	1780 AAGCAAGGCGAGGAGACCTCATATCTTATCTTATTAATATCTTCAT 1826				
DB	445 AAGCAAGGCGAGGAGACCTCATATCTTATCTTATTAATATCTTCAT 491				
RESULT 8					
LOCUS	B0373258 700 bp mRNA linear EST 21-MAY-2002				
DEFINITION	MR0-FT016-040900-202-907 FT0176 Homo sapiens cDNA, mRNA sequence.				
ACCESSION	B0373258				
VERSION	B0373258.1 GI:21048772				
KEYWORDS	EST.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
AUTHORS	1 (bases 1 to 700)				
	Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M. R., Nagai, M. A., da Silva, W. Jr., Zago, M. A., Bordin, S., Costa, F. F., Goldman, G. H., Carvalho, A. F., Matsukuma, A., Bala, G. S., Simpson, D. H., Brunstein, A., de Oliveira, P. S., Bucher, P., Jongeneel, C. V., O'Hare, M. J., Soares, F., Brentani, R. R., Reis, L. F., de Souza, S. J. and Simpson, A. J.				
TITLE	Shotgun sequencing of the human transcriptome with ORF expressed sequence tags				
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)				
MEDLINE	20202663				
PUBMED	10737800				
COMMENT	Contact: Simpson A.J.G. Laboratory of Cancer Genetics Ludwig Institute for Cancer Research Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil Tel: +55-11-2704922 Fax: +55-11-2707001 Email: asimpson@ludwig.org.br This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?li=MR06t2-MR0-FT0176-040900-202-907&t3=2000-09-04&t4=1) Seq primer: puc 18 forward High quality sequence start: 19 High quality sequence stop: 625. Location/Qualifiers 1..700 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /dev_stage="Adult"				
FEATURES	Source				

/clone.lib="FT0176"
 /note="Organ: prostate,tumor; Vector: puc18; Site.1: Sma1;
 Site.2: Sma1; A mini-library was made by cloning products
 derived from ORESTES PCR (U.S. Letters Patent application
 No. 196,716 - Ludwig Institute for Cancer Research)
 profiles into the puc 18 vector. Reverse transcription of
 tissue mRNA and cDNA amplification were performed under
 low stringency conditions."
 BASE COUNT 201 a 122 c 156 g 221 t
 ORIGIN

Query Match 7.8%; Score 280; DB 13; Length 700;
 Best Local Similarity 99.3%; Pred. No. 1.9e-112;
 Matches 430; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 2405 TACTTCATTAGTCTCAGTCTGGGCTGTGCATCAGCGGTTTGAGAAATTCATCT 2464
 |||||||
 DB 450 TACTTCATTAGTCTCAGTCTGGGCTGTGCATCAGCGGTTTGAGAAATTCATCT 391
 |||||||
 OY 2465 CAGCAGAACCCAGAAATTTGAATTCCTTCATCTTTTAGAATCATTTACAGGTTTGAGA 2524
 |||||||
 DB 390 CAGCAGAACCCAGAAATTTGAATTCCTTCATCTTTTAGAATCATTTACAGGTTTGAGA 331
 |||||||
 OY 2525 GGATTTCAGACGCTCAGGCTGCTTCTACTAATGCTCTCAACTTCTGCTCTTTGTT 2584
 |||||||
 DB 330 GGATTTCAGACGCTCAGGCTGCTTCTACTAATGCTCTCAACTTCTGCTCTTTGTT 271
 |||||||
 OY 2585 CATGGATAGTCCATTAATTAATGTTATCTTGAACGTAGGCTCAGAGAGAAATTAAG 2644
 |||||||
 DB 270 CATGGATAGTCCATTAATTAATGTTATCTTGAACGTAGGCTCAGAGAGAAATTAAG 211
 |||||||
 OY 2645 AACTCTGAGTATTCACAACTTAGAGATTCAAGAAATATTAGATTAAAGTCACTGG 2704
 |||||||
 DB 210 AACTCTGAGTATTCACAACTTAGAGATTCAAGAAATATTAGATTAAAGTCACTGG 151
 |||||||
 OY 2705 TCAGAAAGAACCAAGATTCAGAAAGACTGTGAGTGTGCTCCCATCTCTGAGGCA 2764
 |||||||
 DB 150 TCAGAAAGAACCAAGATTCAGAAAGACTGTGAGTGTGCTCCCATCTCTGAGGCA 91
 |||||||
 OY 2765 CAACCAACAGCAGAGACCCCAACGATGTCTGAGATCCTTAATCAAGAAACAGTGTAT 2824
 |||||||
 DB 90 CAACCAACAGCAGAGACCCCAACGATGTCTGAGATCCTTAATCAAGAAACAGTGTAT 31
 |||||||
 OY 2825 GAGTTGAATTCCTC 2837
 |||||||
 DB 30 GAGTTGAATTCCTC 18
 |||||||

RESULT 9 319 bp mRNA linear EST 21-MAY-2002
 B0371438
 LOCUS R06-FN0116-200700-011-D08 FN0116 Homo sapiens cDNA, mRNA sequence.
 B0371438
 ACCESSION B0371438.1 GI:21046952
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Homo sapiens (human)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 319)
 REFERENCE
 AUTHORS
 Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
 Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
 Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
 Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
 'M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
 Simpson,A.J.
 Shotgun sequencing of the human transcriptome with ORF expressed
 sequence tags

TITLE
 JOURNAL
 MEDLINE
 PUBMED
 COMMENT
 Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
 2020263
 10737800
 Contact: Simpson A.J.G.
 Laboratory of Cancer Genetics

Ludwig Institute for Cancer Research
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
 Brazil
 Tel: +55-11-2704922
 Fax: +55-11-2707001
 Email: asimpson@ludwig.org.br
 This sequence was derived from the FAPESP/ICR Human Cancer Genome
 Project. This entry can be seen in the following URL
 (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=R06-FN0116-
 200700-011-D08&t3=2000-07-20&t4=1)
 Seq primer: puc 18 forward
 High quality sequence start: 17
 High quality sequence stop: 319.
 Location/Qualifiers
 1..319
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /dev_stage="Adult"
 /clone_lib="FN0116"
 /note="Organ: prostate,normal; Vector: puc18; Site.1: Sma1
 ; Site.2: Sma1; A mini-library was made by cloning
 products derived from ORESTES PCR (U.S. Letters Patent
 application No. 196,716 - Ludwig Institute for Cancer
 Research) profiles into the puc 18 vector. Reverse
 transcription of tissue mRNA and cDNA amplification were
 performed under low stringency conditions."

BASE COUNT 85 a 74 c 67 g 93 t
 ORIGIN

Query Match 6.9%; Score 247; DB 13; Length 319;
 Best Local Similarity 100.0%; Pred. No. 8.5e-98;
 Matches 247; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2293 GCTGGAATGGACACACCAATATGCAATATCAATCTACATAGCTACACACTGC 2352
 |||||||
 DB 27 GCTGGAATGGACACACCAATATGCAATATCAATCTACATAGCTACACACTGC 86
 |||||||
 OY 2353 TTGACATATATTTAGAAAGCAGCTGCATTGTGGGTTCTTTAGCAAAATATTGCA 2412
 |||||||
 DB 87 TTGACATATATTTAGAAAGCAGCTGCATTGTGGGTTCTTTAGCAAAATATTGCA 146
 |||||||
 OY 2413 TTAGCTCTCAGCTGGGCTGTGCATCAGGGGTTTGAGAAATATTCAATTCTAGCGAA 2472
 |||||||
 DB 147 TTAGCTCTCAGCTGGGCTGTGCATCAGGGGTTTGAGAAATATTCAATTCTAGCGAA 206
 |||||||
 OY 2473 GCCAGAAATTTGAATTCCTCATCTTTTAGAATCATTTACAGGTTGGAGAGATTACG 2532
 |||||||
 DB 207 GCCAGAAATTTGAATTCCTCATCTTTTAGAATCATTTACAGGTTGGAGAGATTACG 266
 |||||||
 OY 2533 ACAGCTC 2539
 |||||||
 DB 267 ACAGCTC 273
 |||||||

RESULT 10 290 bp mRNA linear EST 24-NOV-2000
 BF373619
 LOCUS M00-FN0175-310800-106-h09 FN0175 Homo sapiens cDNA, mRNA sequence.
 BF373619
 ACCESSION BF373619.1 GI:11335644
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Homo sapiens (human)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 290)
 REFERENCE
 AUTHORS
 Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
 Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
 Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
 Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
 'M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
 Simpson,A.J.

TITLE
 JOURNAL
 MEDLINE
 PUBMED
 COMMENT
 Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
 2020263
 10737800
 Contact: Simpson A.J.G.
 Laboratory of Cancer Genetics

TITLE Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE 20202663
PUBMED 10737800
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=MR0<2=MR0-FT0175-310800-106-h09<3=2000-08-31<4=1)
Seq primer: puc 18 forward
High quality sequence stop: 290.

FEATURES
Source 1..290
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_1ib="FT0175"
/note="Organ: prostate.tumor; Vector: puc18; Site:1: SmaI; Site:2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

BASE COUNT
78 a 73 c 53 g 86 t

Query Match 6.6%; Score 238; DB 10; Length 290;
Best Local Similarity 100.0%; Pred. No. 8.3e-94;
Matches 238; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 762 GGGAGAGATTAACACGGGGGAGAGGGTGTGCTGCTGCTTAACGTGGG 821
|||||
DB 21 GGGAGAGATTAACACGGGGGAGAGGGTGTGCTGCTGCTTAACGTGGG 80
822 TTCTATACCAATTCATTTCTAATTCCTCAATATATATATATATATATAT 881
81 TTCTATACCAATTCATTTCTAATTCCTCAATATATATATATATATATAT 140
882 CTCTACGCTTCTCTGGGCCCAACATTCCTCATATATATATATATATAT 941
141 CTCTACGCTTCTCTGGGCCCAACATTCCTCATATATATATATATATATAT 200
QY 942 TTTAGTCCAGATCTGTACTGTGACCTTTTCTACACTGTAGATAATTA 999
|||||
DB 201 TTTAGTCCAGATCTGTACTGTGACCTTTTCTACACTGTAGATAATTA 258

RESULT 11
B0338234 304 bp mRNA linear EST 20-MAY-2002
LOCUS B0338234
DEFINITION CM2-NN0116-100700-257-e11 NN0116 Homo sapiens cDNA, mRNA sequence.
ACCESSION B0338234
VERSION B0338234.1 GI:20996652
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
1 (bases 1 to 304)
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H., Brunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V., O'hare

TITLE 'M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.G.
Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE 20202663
PUBMED 10737800
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=CM2<2=CM2-NN0116-100700-257-e11<3=2000-07-10<4=1)
Seq primer: puc 18 forward
High quality sequence start: 304.
High quality sequence stop: 304.

FEATURES
Source 1..304
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_1ib="NN0116"
/note="Organ: nervous.normal; Vector: puc18; Site:1: SmaI; Site:2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

BASE COUNT
66 a 98 c 45 g 95 t

Query Match 6.6%; Score 238; DB 13; Length 304;
Best Local Similarity 99.7%; Pred. No. 8.2e-94;
Matches 288; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2745 GTCCCATCTCTGTGAGCCACACCAACAGACAGACCAAGCATGCTGATCC 2804
|||||
DB 1 GTCCCATCTCTGTGAGCCACACCAACAGACAGACCAAGCATGCTGATCC 60
2805 ATCAAGAAACAGCTGATGATGATTTCTTATATATATATATATATAT 2864
61 ATCAAGAAACAGCTGATGATGATTTCTTATATATATATATATATATAT 120
QY 2865 CTCTGCTCTCTCTTGACACATATATAGCTTCTGCTCCACGACTTTAT 2924
|||||
DB 121 CTCTGCTCTCTCTTGACACATATATAGCTTCTGCTCCACGACTTTAT 180
2925 TTCTCCACACATCGTTACCATCTCTCTGCTGCTGCTTGGAGCTCCGACA 2984
|||||
DB 181 TTCTCCACACATCGTTACCATCTCTCTGCTGCTGCTTGGAGCTCCGACA 240

QY 2985 GAATTTCAAGCACTCTCAAGTCTTTTCTTCATCCACACACATCACTG 3033
|||||
DB 241 GAATTTCAAGCACTCTCAAGTCTTTTCTTCATCCACACACATCACTG 289

RESULT 12
BF858371 226 bp mRNA linear EST 16-JAN-2001
LOCUS BF858371
DEFINITION RCS-FT0193-211100-012-E11 FT0193 Homo sapiens cDNA, mRNA sequence.
ACCESSION BF858371
VERSION BF858371.1 GI:12246115
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
PUBMED
COMMENT

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
1 (bases 1 to 226)
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Britones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordini, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bala, G.S., Simpson, D.H., Brunstein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.
Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
10737800
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?cl=RC56t2-RC5-FT0193-21100-012-El16t3-2000-11-216t4-1)
Seq primer: puc 18 forward
High quality sequence stop: 226.
Location/Qualifiers
1..226
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="FT0193"
/note="Organ: prostate; tumor; Vector: puc18; Site: 1: SmaI; Site: 2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
BASE COUNT
79 a 29 c 59 g 59 t
ORIGIN

Query Match 6.0%; Score 214; DB 10; Length 226;
Best Local Similarity 100.0%; Pred. No. 3.5e-83;
Matches 214; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 809 CCTAATGTCGCTTCATTAACCAATCATTTCTATTTCTAACCTCAAAACAAAGCTGT 868
DB 226 CCTAATGTCGCTTCATTAACCAATCATTTCTATTTCTAACCTCAAAACAAAGCTGT 167
QY 869 TGTAAATGTCGATCTACAGGTTCTCTGGGCCCAACATCTCATATATCCAGCCACA 928
DB 166 TGTAAATGTCGATCTACAGGTTCTCTGGGCCCAACATCTCATATATCCAGCCACA 107
QY 929 CTCATTTTAAATTAATTTAGTTCCAGATCTGTAGTACCTTTCTACACTAGAAATAC 988
DB 106 CTCATTTTAAATTAATTTAGTTCCAGATCTGTAGTACCTTTCTACACTAGAAATAC 47
QY 989 ATTACATTTTGTTCAAAGACCTTGCTGTGC 1022
DB 46 ATTACATTTTGTTCAAAGACCTTGCTGTGC 13

RESULT 13
AQ206972/c 394 bp DNA linear GSS 17-SEP-1998
LOCUS
DEFINITION
HS_3238_B1_G11_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3238 Col=21 Row=N, genomic survey
sequence.
ACCESSION
AQ206972

VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
PUBMED
COMMENT

AQ206972.1 GI:3617542
GSS.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
1 (bases 1 to 394)
Mahairas, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T., Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D. and Hood, L.
Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome
Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
99380589
10449764
Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Sequence Tagged Connector
Plate: 3238 row: N column: 21
Class: BAC ends
High quality sequence stop: 394.
Location/Qualifiers
1..394
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/clone_plate=3238 Col=21 Row=N"
/sex="male"
/clone_lib="CIT Approved Human Genomic Sperm Library D"
/note="Organ: sperm; Vector: pBelBAC11; BAC clones in E-Coli DH10B"
BASE COUNT
134 a 62 c 93 g 103 t 2 others
ORIGIN

Query Match 6.0%; Score 214; DB 28; Length 394;
Best Local Similarity 99.4%; Pred. No. 3.2e-83;
Matches 314; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 905 ACATTTCTCCATATATATCCAGCCACACTATTTTATATATTTAGTCCAGATCTACTGT 964
DB 381 ACATTTCTCCATATATATCCAGCCACACTATTTTATATATTTAGTCCAGATCTACTGT 322
QY 965 GACCTTTCTACAGTGAATATACATTAATCTATTTGTTCAAAGACCTTGCTGTCTG 1024
DB 321 GACCTTTCTACAGTGAATATACATTAATCTATTTGTTCAAAGACCTTGCTGTCTG 262
QY 1025 CCTAATATGTCGACGTGTTTCTTAAGAGAGTCTGCGCCAGGAGATCTGTAGACA 1084
DB 261 CCTAATATGTCGACGTGTTTCTTAAGAGAGTCTGCGCCAGGAGATCTGTAGACA 202
QY 1085 GCGTGGAGATCTCAAGATCTTTCACAGGTTATTAATCTAGACACAGATGATCAT 1144
DB 201 GCGTGGAGATCTCAAGATCTTTCACAGGTTATTAATCTAGACACAGATGATCAT 142
QY 1145 TAGGAGGAGATTTTCATCAATCATCATCTCGTGTGCGCCATAGGAATTCAT 1204
DB 141 TAGGAGGAGATTTTCATCAATCATCATCTCGTGTGCGCCATAGGAATTCAT 82
QY 1205 TTCCCACTTTTGTGCC 1220
DB 81 TTCCCACTTTTGTGCC 66

RESULT 14
BF858286 332 bp mRNA linear EST 16-JAN-2001
LOCUS
DEFINITION
RC5-FT0193-201100-012-D06 FT0193 Homo sapiens cDNA, mRNA sequence.
ACCESSION
BF858286

VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL	MEDLINE	PUBMED	COMMENT									
BF858286.1	GI:12246030	EST	Homo sapiens (human)	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.	Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsumura, A., Bala, G.S., Simpson, D.H., Brunstein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson A.J.	Shotgun sequencing of the human transcriptome with ORF expressed sequence tags	Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)	20202663	10737800	Contact: Simpson A.J.G. Laboratory of Cancer Genetics Ludwig Institute for Cancer Research Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil Tel: +55-11-2704922 Fax: +55-11-2707001 Email: asimpson@ludwig.org.br This sequence was derived from the FAPESP/ICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=RC5&tl2=RC5-FT0193-201100-012-006&tl3=2000-11-20&tl4=1) Seq primer: puc 18 forward High quality sequence stop: 332. Location/Qualifiers									
FEATURES	source	<pre> 1..332 /mol_type="Homo sapiens" /org_id="Homo sapiens" /db_xref="taxon:9606" /dev_stage="Adult" /clone_id="FT0193" /note="Organ: prostate tumor; Vector: puc18; Site: 1: SmaI; Site 2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions." low stringency conditions." </pre>																	
BASE COUNT	90 a 84 c 64 g 94 t																		
ORIGIN																			
Query Match	5.9%; Score 213; DB 10; Length 332;																		
Best Local Similarity	100.0%; Pred. No. 9.2e-83;																		
Matches 213; Conservative	0; Mismatches 0; Indels 0; Gaps 0;																		
OY	763	GGAGGAGATACACACGGGGGAGAGGGTCGAGATTCTGGCCCTGCTCTAAACGTGTGGCT	822																
Db	61	GGAGGAGATACACACGGGGGAGAGGGTCGAGATTCTGGCCCTGCTCTAAACGTGTGGCT	120																
OY	823	TCATTAACCAATATCATTTTCATATTTCTCTAACCTCAACCAAGAGCTGTGTATATCTGATC	882																
Db	121	TCATTAACCAATATCATTTTCATATTTCTCTAACCTCAACCAAGAGCTGTGTATATCTGATC	180																
OY	883	TCTACGGTTCCTTCTGGGCCCAACATCTTCCATATATCCACGACACATTTTAAATAT	942																
Db	181	TCTACGGTTCCTTCTGGGCCCAACATCTTCCATATATCCACGACACATTTTAAATAT	240																
OY	943	TTAGTTCACAGATCTGACTGTGACCTTTTAC	975																
Db	241	TTAGTTCACAGATCTGACTGTGACCTTTTAC	273																
RESULT 15																			
BF373581/c																			
LOCUS	BF373581	282 bp	mrna	linear	EST 24-NOV-2000														

DEFINITION	MR0-F0175-210800-101-d05 F0175 Homo sapiens cDNA, mRNA sequence.
ACCESSION	BF373581
VERSION	BF373581.1 GI:11335606
KEYWORDS	EST.
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
AUTHORS	1 (bases 1 to 282) Dias Neto,E., Garcia Correa,R., Verjovsky-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare ,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.J.
TITLE	Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE	20202653
PUBMED	10737800
COMMENT	Contact: Simpson A.J.G. Laboratory of Cancer Genetics Ludwig Institute for Cancer Research Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil Tel: +55-11-2704922 Fax: +55-11-2707001 Email: asimpson@ludwig.org.br This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL. (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=MR0&t2=MR0-F0175-210800-101-d05&t3=2000-08-21&t4=1) Seq primer: puc 18 forward High quality sequence start: 35 High quality sequence stop: 282.
FEATURES	Location/Qualifiers
SOURCE	1..282
<pre> /ororganism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /def_stage="Adult" /clone_lib="F0175" /note="Organ: prostate,tumor; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the puc 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions." </pre>	
BASE COUNT	85 a 51 c 76 t
ORIGIN	
Query Match	5.5%; Score 198; DB 10; Length 282;
Best Local Similarity	100.0%; Pctd. No. 4.1e-76;
Matches 198; Conservative	0; Mismatches: 0; Indels 0; Gaps 0;
OY	775 CACGGGCGAGGGGTCAAGATTTCGGCCCTCTGCTCAAACTGTGCGTTCATAACCAAT 834
Db	
262 CACGGGGCAGAGGGTCAAGATTTCGGCCCTCTGCTCAAACTGTGCGTTCATAACCAAT 203	
OY	835 CATTTCATATTTCCTAACCCCTCAAAACAAGCTGTTGTAATATTCGATCTCAGGGTTCCT 894
Db	
202 CATTTCATATTTCCTAACCCCTCAAAACAAGCTGTTGTAATATTCGATCTCAGGGTTCCT 143	
OY	895 TCTGGGGCCCAACATTCCTCCATATATCCACGACACACTATTTTAATATTAGTTCACAGA 954
Db	
142 TCTGGGGCCCAACATTCCTCCATATATCCACGACACACTATTTTAATATTAGTTCACAGA 83	
OY	955 TCTGTACTGTGACCTTTC 972
Db	
82 TCTGTACTGTGACCTTTC 65	

Mon Sep 29 08:56:35 2003

us-09-402-713a-6.olig.rst

Page 10

Search completed: September 27, 2003, 11:35:49
Job time : 7519.98 secs
